

Result No.	Score	Query		Length	DB	ID	Description
		Match	%				
1	38	46.9	20	1	R92907	HLA-B*2702 CTL modu	
2	38	46.9	20	1	R95428	HLA-B*2702 84-75-84	
3	38	46.9	20	1	W33778	Immunomodulating d	
4	38	46.9	513	1	R79945	Helicobacter pylori	
5	36	44.4	176	1	W55346	H. pylori ORF 07ep	
6	36	44.4	178	1	Y11022	H. pylori ORF 02qe	
7	36	44.4	852	1	W79065	FIV-NCsU1 clone J5	
8	36	44.4	854	1	R44957	Feline Immunodefic	
9	36	44.4	854	1	R51250	FIV PPR envelope p	
10	36	44.4	855	1	R51255	FIV SWISS22 envelo	
11	36	44.4	855	1	R58585	FIV UK8 envelope p	
12	36	44.4	856	1	R51247	FIV envelope prote	
13	36	44.4	856	1	R51248	FIV petaluma envel	
14	36	44.4	856	1	R51249	FIV PPT-F14 envelo	
15	36	44.4	856	1	R51254	FIV DUTCHI19K1 enve	
16	36	44.4	856	1	W53671	FIV PPR clone 34 O	
17	36	44.4	870	1	R51246	Composite sequence	
18	36	44.4	1287	1	R79944	Helicobacter pylori	
19	36	44.4	1288	1	W55547	H. pylori ORF 14ee	
20	36	44.4	1288	1	W55685	H. pylori ORF 07ee	
21	36	44.4	1296	1	R41198	CT. Recombinant He	
22	35	43.2	20	1	R95430	HLA-B*2702 84-75T/7	
23	35	43.2	207	1	R32202	Broad bean leaf PP	
24	35	43.2	267	1	W32427	Mycobacterium tube	
25	35	43.2	267	1	W32359	Mycobacterium tube	
26	35	43.2	267	1	W64299	Mycobacterium tube	
27	35	43.2	267	1	M81662	M. tuberculosis im	
28	35	43.2	435	1	R32999	Rat choline kinase	
29	35	43.2	511	1	R81161	Recombinant alpha-	
30	35	43.2	511	1	P81180	Sequence of alpha-	
31	35	43.2	512	1	R07574	Alpha-amylase enco	
32	35	43.2	855	1	R28033	Env polypeptide of	
33	35	43.2	855	1	R51251	FIV JAPANTM2 envel	
34	35	43.2	855	1	R51252	FIV UK2 envelope p	

PR 02-APR-1996; US-758731.
PR 25-OCT-1996; US-736905.
PR 28-OCT-1996; US-738859.
PA (ASTR.) ASTRA AB.
PI Alm RA, Smith D;
DR WPI; 97-503122/46.
DR N-PSDB; V24755.
PT Helicobacter pylori nucleic acid sequences and encoded
PT polypeptide(s) - useful in vaccines to treat or prevent H. pylori
PT infection and for diagnosis of H. pylori infection
PS Claim 14; Page 570-571; 1145pp; English.
CC This sequence is a H. pylori protein of unspecified function.
CC The protein may be used in a vaccine to prevent or treat H. pylori
CC infection or to identify H. pylori polypeptide binding compounds,
CC useful as potential H. pylori life cycle activators or inhibitors. The
CC DNA and probes derived from it may be used for the identification of
CC H. pylori in a sample and the diagnosis of H. pylori infection. Nucleic
CC acid sequences complementary to the DNA act as antisense sequences and
CC can be used to prevent the translation of H. pylori mRNA. Antibodies
CC against the protein can be used in immunoassays to evaluate the abundance
CC and distribution of H. pylori-specific antigens. The genomic sequence of
CC H. pylori (ATCC 55679) was determined from overlapping contigs generated
CC by mechanically shearing the bacterial DNA. The sequences were analysed
CC for ORF of at least 180 nucleotides, and the predicted coding regions
CC were analysed by computer evaluation. To identify likely H. pylori antigens for
CC vaccine development, the amino acid sequences predicted from various ORF
CC were analysed for significant homology to other known or exported
CC membrane proteins. Having identified and determined the sequences of
CC interest, particular regions can be isolated from H. pylori by PCR
CC amplification for recombinant polypeptide production, e.g. in E. coli
CC hosts.
SQ Sequence 176 AA;

Query Match 44.4%; Score 36; DB 1; Length 176;
Best Local Similarity 46.7%; Pred. No. 40;
Matches 7; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 2 YKLVKINNIRIVK 16
|| :|||: : :||
DB 16 YKPLKINSADLLK 30

RESULT 6

ID Y11022 standard; Protein; 178 AA.
AC Y11022; 1999 (first entry).
DE H. pylori ORF 02gei0116_15632000_c2_114 cell envelope protein.
KW Vaccine; probe; diagnostic; ORF; cell envelope protein;
KW secreted protein; cytoplasmic protein; cellular protein.
OS Helicobacter pylori.
PN W09824475-AL.
PD 11-JUN-1998.
PF 05-DEC-1997; U22104.
PR 14-JUL-1997; US-891928.
PR 05-DEC-1996; US-759625.
PR 25-MAR-1997; US-823745.
PA (ASTR.) ASTRA AB.
PI Alm RA, Castriotta LM, Doig PC, Kabok Z, Smith D;
DR WPI; 98-333051/29.
DR N-PSDB; X30551.
PT New isolated Helicobacter pylori nucleic acids - used to develop
PT products for the diagnosis, prevention and treatment of infection by
PT H. pylori and other Helicobacter species
PS Claims 37, 41; Page 184; 339pp; English.
CC Recombinant or substantially pure preparations of H. pylori polypeptides
CC are disclosed, together with the nucleic acids encoding them. In all,
CC 97 ORFs are shown. The proteins are variously cell envelope proteins,
CC cytoplasmic proteins, secreted proteins or other cellular proteins.
CC Vaccines containing the nucleic acids or proteins are claimed, as are
CC probes containing at least 8 nucleotides from the nucleic acid
CC sequences. The vaccines are useful for treating or reducing the risk of

CC H. pylori infections, and the probes can be used diagnostically for
CC detecting the presence of Helicobacter in a sample. The products are
CC also of use in screening for compounds having the ability to interfere
CC with the H. pylori life cycle or to inhibit H. pylori infection.
SQ Sequence 178 AA;

Query Match 44.4%; Score 36; DB 1; Length 178;
Best Local Similarity 50.0%; Pred. No. 41;
Matches 7; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 3 KLVKINNIRIVK 16
| : :||| : :|
DB 90 KSVLPNNIEIRK 103

RESULT 7

W79065
ID W79065 standard; Protein; 852 AA.
AC W79065;
DT 11-JAN-1999 (first entry)
DE FIV-NCSU1 clone JSY3 envelope protein (env).
KW FIV; retrovirus; immunodeficiency; diagnosis; vaccine;
KW envelope protein; env; cat; animal model.
OS Feline immunodeficiency virus isolate NCSU1 clone JSY3.
FH Key Location/Qualifiers
FT Domain 691..702
FT /label= TM
FT /note= "transmembrane domain (Claim 19)"

PN W09839451-AL.
PD 11-SEP-1998.
PF 04-MAR-1998; U04147.
PF 05-MAR-1997; US-811682.
PA (UYNC-) UNIV NORTH CAROLINA STATE.
PI Tompkins WB, Tompkins WAF, Tang J;
DR WPI; 98-506365/43.
DR N-PSDB; V57355-56.
PT Feline immunodeficiency virus clone, JSY3 - retaining in vivo
PT characteristics of parent virus, useful e.g. to produce vaccines to
PT protect felines against feline immunodeficiency virus
PS Claim 19; Page 44-47; 128pp; English.
CC This is the amino acid sequence of the FIV isolate NCSU1 clone JSY3
CC envelope protein (env). The sequence was deduced from JSY3
CC proviral DNA (see V57355-56). The JSY3 clone, polypeptides and
CC encoding nucleic acids are useful for producing vaccines to protect
CC feline species against FIV; such vaccines may contain e.g. live
CC attenuated JSY3 virus, antigenic fragments (e.g. the env
CC transmembrane peptide), or host cells transformed with nucleic
CC acids and expressing virus antigen on the surface etc. They are
CC also useful diagnostically. Since JSY3 retains the essential in
CC vivo biological characteristics of the parent virus (including
CC induction of immunodeficiency and inversion of the CD4+CD8+ ratio
CC by 6 weeks post infection), it is useful for producing animal
CC models for studying the virus and other retroviral diseases, e.g.
CC HIV-1 infection, and testing possible treatments.
SQ Sequence 852 AA;

Query Match 44.4%; Score 36; DB 1; Length 852;
Best Local Similarity 66.7%; Pred. No. 2.2e+02;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 6 IKINNIRIV 14
: :|||: :|
DB 656 LKINNRLRV 664

RESULT 8

R44957
ID R44957 standard; Protein; 854 AA.
AC R44957;
DT 05-JUL-1994 (first entry)
DE Feline Immunodeficiency Virus (Wo isolate) ENV protein.

KW FIV; French virus strain; Wo isolate; envelope glycoprotein;
 KW feline acquired immunodeficiency syndrome; cat; vaccine;
 OS Retrovirus; lentivirus.
 FH Feline immunodeficiency virus (Wo isolate).
 FT Key Location/Qualifiers
 FT 26..72
 FT /label= V1
 FT /note= "variable region capable of inducing a
 FT Wo strain-specific immune response"
 FT 96..174
 FT /label= V2
 FT /note= "variable region capable of inducing a
 FT Wo strain-specific immune response"
 FT 253..289
 FT /label= SU1
 FT /note= "part of external surface glycoprotein"
 FT 388..424
 FT /label= SU2
 FT /note= "part of external surface glycoprotein"
 FT 361..422
 FT /label= V3
 FT /note= "variable region capable of inducing a
 FT Wo strain-specific immune response"
 FT 467..492
 FT /label= SU3
 FT /note= "part of external surface glycoprotein"
 FT 452..487
 FT /label= V4
 FT /note= "variable region capable of inducing a
 FT Wo strain-specific immune response"
 FT 508..528
 FT /label= SU4
 FT /note= "part of external surface glycoprotein"
 FT 541..570
 FT /label= V5
 FT /note= "variable region capable of inducing a
 FT Wo strain-specific immune response"
 FT 572..606
 FT /label= SU5
 FT /note= "part of external surface glycoprotein"
 FT 586..612
 FT /label= V6
 FT /note= "variable region capable of inducing a
 FT Wo strain-specific immune response"
 FT 595..647
 FT /label= TM1
 FT /note= "part of transmembrane glycoprotein"
 FT 681..711
 FT /label= TM2
 FT /note= "part of transmembrane glycoprotein"
 FT 710..718
 FT /label= V7
 FT /note= "variable region capable of inducing a
 FT Wo strain-specific immune response"
 FT 765..778
 FT /label= V8
 FT /note= "variable region capable of inducing a
 FT Wo strain-specific immune response"
 FT 832..842
 FT /label= V9
 FT /note= "variable region capable of inducing a
 FT Wo strain-specific immune response"
 EP-577458-A.
 PD 05-JAN-1994.
 PD 401538.
 PF 16-JUN-1993; FR-007257.
 PR 16-JUN-1992; FR-007257.
 PR 23-NOV-1992; FR-014026.
 PR (CNRS) CNRS CENT NAT RECH SCI.
 PI Avrameas A, Chappay C, Hurlrel B, Klatzmann D, Moraillon A;
 PI Pancelo G, Saurin W, Sonigo P, Strosberg AD;
 DR WPI: 94-009689/02.
 DR N-PSDB; 054396.

PT Nucleic acid sequences of GAG and ENV genes - of feline immune
 PT deficiency virus, strain Wo, and derived probes, primers, vectors
 PT and peptide(s), for diagnosis and vaccination
 PS Claim 20; Page 34-36; 56pp; French.
 CC Peripheral blood mononuclear cells (PBMC) from cats naturally
 CC infected with the FIV French strain Wo were co-cultured with PBMC
 CC from uninfected cats in the presence of recombinant human IL-2 and
 CC concanavalin A. After 15 days, total cellular DNA was extracted
 CC from cells positive for Mg-dependent reverse transcriptase activity
 CC and was used as starting material for amplifying FIV env and gag
 CC genes. PCR primers were designed based on conserved regions in the
 CC Petalum isolate of FIV. The env gene was obtained from 3
 CC overlapping subfragments. Sequence analysis and comparison with
 CC other FIV isolates identified 9 variable regions suitable for
 CC designing strain-specific diagnostic and therapeutic agents.
 SQ Sequence 854 AA;
 Query Match 44.4%; Score 36; DB 1; Length 854;
 Best Local Similarity 66.7%; Pred. No. 2.2e+02;
 Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
 QY 6 IKINNIRIV 14
 DB 658 LKINNLRV 666
 RESULT 9
 R51250
 ID R51250 standard; peptide; 854 AA.
 AC R51250;
 DT 08-OCT-1994 (first entry)
 DE FIV PPR envelope protein sequence.
 KW Feline immunodeficiency virus; FIV; vaccine; diagnostic; AIDS;
 KW T-lymphotropic lentivirus; FIV UR8; FIV Petalum; envelope protein.
 OS Synthetic.
 FH Key Location/Qualifiers
 FT peptide 1..178
 FT region /note= "Hydrophobic leader peptide"
 FT 51..66
 FT /note= "V1 region"
 FT 95..173
 FT /note= "V2 region"
 FT 179..608
 FT /note= "Surface glycoprotein"
 FT 360..424
 FT /note= "V3 region"
 FT 451..483
 FT /note= "V4 region"
 FT 539..565
 FT /note= "V5 region"
 FT 609..854
 FT /note= "Transmembrane protein"
 FT WO9406471-A.
 PD 31-MAR-1994.
 PD 20-SEP-1993; G01974.
 PR 21-SEP-1992; GB-019936.
 PA (PITM) PITMAN MOORE INC.
 PI Francis MJ;
 DR WPI: 94-118158/14.
 PT Feline immunodeficiency virus antigenic polypeptide(s) and
 PT nucleic acid - used to prepare prods. for combating or diagnosis
 PT of feline immunodeficiency infection
 PS Disclosure; Figure 2; 68pp; English.
 CC The sequences given in R51248-R51262 and R58584-85 represent the
 CC feline immunodeficiency virus (FIV) envelope protein from different
 CC strains and serotypes. The consensus sequence based on these, is given
 CC in R51247. The synthetic FIV peptides of the invention were derived
 CC principally from a combination of the sequences of the FIV UK 8 and
 CC Petalum isolates, a composite sequence of which is given in R51246.
 CC Variations in the sequence may occur between different strains or
 CC serotypes, isolates of different geographical origin or even between
 CC different isolates from the same host.

SQ Sequence 854 AA;

Query Match 44.4%; Score 36; DB 1; Length 854;
 Best Local Similarity 66.7%; Pred. No. 2.2e+02;
 Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 6 IKINNIRIV 14

Db 658 LKINNRLV 666
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RESULT 10

ID R51255 standard; peptide; 855 AA.

AC R51255;

DT 08-OCT-1994 (first entry)

DE FIV SWISS22 envelope protein sequence.

KW Feline immunodeficiency virus; FIV; vaccine; diagnostic; AIDS;

KW T-lymphotropic lentivirus; FIV UK8; FIV Petaluma; envelope protein.

OS Synthetic.

FH Key

FT Location/Qualifiers

FT peptide

FT 1..178

FT /note= "Hydrophobic leader peptide"

FT region

FT 51..66

FT /note= "v1 region"

FT region

FT 95..173

FT /note= "v2 region"

FT protein

FT 179..609

FT /note= "Surface glycoprotein"

FT region

FT 360..424

FT /note= "v3 region"

FT region

FT 451..483

FT /note= "v4 region"

FT region

FT 539..566

FT /note= "v5 region"

FT protein

FT 610..855

FT /note= "Transmembrane protein"

FT WO9406471-A.

PN 31-MAR-1994.

PD 20-SEP-1993; G01974.

PF 21-SEP-1992; GB-019936.

PA (PITM) PITMAN MOORE INC.

PI Francis MJ;

DR WPI; 94-118168/14.

PT Feline immunodeficiency virus antigenic polypeptide(s) and

PT nucleic acid - used to prepare prods. for combating or diagnosis

PT of feline immunodeficiency infection

PS Disclosure; Figure 2; 68pp; English.

CC The sequences given in R51248-R51262 and R58584-85 represent the

CC feline immunodeficiency virus (FIV) envelope protein from different

CC strains and serotypes. The consensus sequence based on these, is given

CC in R51247. The synthetic FIV peptides of the invention were derived

CC principally from a combination of the sequences of the FIV UK 8 and

CC Petaluma isolates, a composite sequence of which is given in R51246.

CC Variations in the sequence may occur between different strains or

CC serotypes, isolates of different geographical origin or even between

CC different isolates from the same host.

CC Sequence 855 AA;

SQ

Query Match

Best Local Similarity 44.4%; Score 36; DB 1; Length 855;
 Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 6 IKINNIRIV 14

Db 659 LKINNRLV 667
 :||||:|

RESULT 11

R58585

ID R58585 standard; peptide; 855 AA.

AC

DT

DE

KW

OS

FH

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R58585;

DT 08-OCT-1994 (first entry)

DE FIV UK8 envelope protein sequence.

KW Feline immunodeficiency virus; FIV; vaccine; diagnostic; AIDS;

KW T-lymphotropic lentivirus; FIV UK8; FIV Petaluma; envelope protein.

OS Synthetic.

FH Key

FT Location/Qualifiers

FT peptide

FT 1..178

FT /note= "Hydrophobic leader peptide"

FT region

FT 51..66

FT /note= "v1 region"

FT region

FT 95..173

FT /note= "v2 region"

FT protein

FT 179..609

FT /note= "Surface glycoprotein"

FT region

FT 360..424

FT /note= "v3 region"

FT region

FT 451..483

FT /note= "v4 region"

FT region

FT 539..566

FT /note= "v5 region"

FT protein

FT 610..855

FT /note= "Transmembrane protein"

FT WO9406471-A.

PN 31-MAR-1994.

PD 20-SEP-1993; G01974.

PF 21-SEP-1992; GB-019936.

PA (PITM) PITMAN MOORE INC.

PI Francis MJ;

DR WPI; 94-118168/14.

PT Feline immunodeficiency virus antigenic polypeptide(s) and

PT nucleic acid - used to prepare prods. for combating or diagnosis

PT of feline immunodeficiency infection

PS Disclosure; Figure 2; 68pp; English.

CC The sequences given in R51248-R51262 and R58584-85 represent the

CC feline immunodeficiency virus (FIV) envelope protein from different

CC strains and serotypes. The consensus sequence based on these, is given

CC in R51247. The synthetic FIV peptides of the invention were derived

CC principally from a combination of the sequences of the FIV UK 8 and

CC Petaluma isolates, a composite sequence of which is given in R51246.

CC Variations in the sequence may occur between different strains or

CC serotypes, isolates of different geographical origin or even between

CC different isolates from the same host.

CC Sequence 855 AA;

SQ

Query Match

Best Local Similarity

Matches 6; Conservative

66.7%; Pred. No. 2.2e+02;

Mismatches 0; Indels

0; Gaps

0;

44.4%; Score 36; DB 1; Length 855;

66.7%; Pred. No. 2.2e+02;

3; Mismatches

0; Indels

0; Gaps

0;

QY 6 IKINNIRIV 14

Db 659 LKINNRLV 667

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FT region 360..424
 FT /note= "V3 region"
 FT 451..483
 FT /note= "V4 region"
 FT 539..567
 FT /note= "V5 region"
 FT 611..856
 FT /note= "Transmembrane protein"
 PN WO9406471-A.
 PD 31-MAR-1994.
 PF 20-SEP-1993; G01974.
 PR 21-SEP-1992; GB-019936.
 PA (PITM) PITMAN MOORE INC.
 PI Francis MJ;
 DR WPI: 94-118168/14.
 PT Feline immunodeficiency virus antigenic polypeptide(s) and
 PT nucleic acid - used to prepare prods. for combating or diagnosis
 PT of feline immunodeficiency infection
 PS Disclosure; Figure 2; 68pp; English.
 CC The sequences given in R51248-R51262 and R58584-85 represent the
 CC feline immunodeficiency virus (FIV) envelope protein from different
 CC strains and serotypes. The consensus sequence basedon these, is given
 CC in R51247. The synthetic FIV peptides of the invention were derived
 CC Petaluma isolates, a composite sequence of which is given in R51246.
 CC Variations in the sequence may occur between different strains or
 CC serotypes, isolates of different geographical origin or even between
 CC different isolates from the same host.
 CC Sequence 856 AA;
 SQ

Query Match 44.4%; Score 36; DB 1; Length 856;
 Best Local Similarity 66.7%; Pred. No. 2.2e+02;
 Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 6 IKINNIRIV 14
 Db 660 LKINNRLV 668
 :||||:|

RESULT 13
 R51248
 ID R51248 standard; peptide; 856 AA.
 AC R51248;
 DT 08-OCT-1994 (first entry)
 DE FIV petaluma envelope protein sequence.
 KW Feline immunodeficiency virus; FIV; vaccine; diagnostic; AIDS;
 KW T-lymphotropic lentivirus; FIV UK8; FIV Petaluma; envelope protein.
 OS Synthetic.
 FH Key Location/Qualifiers
 FT peptide 1..178
 FT /note= "Hydrophobic leader peptide"
 FT region 51..66
 FT /note= "V1 region"
 FT region 95..173
 FT /note= "V2 region"
 FT protein 179..610
 FT /note= "Surface glycoprotein"
 FT region 360..424
 FT /note= "V3 region"
 FT region 451..483
 FT /note= "V4 region"
 FT region 539..567
 FT /note= "V5 region"
 FT protein 611..856
 FT /note= "Transmembrane protein"
 PN WO9406471-A.
 PD 31-MAR-1994.
 PF 20-SEP-1993; G01974.
 PR 21-SEP-1992; GB-019936.
 PA (PITM) PITMAN MOORE INC.
 PI Francis MJ;
 DR WPI: 94-118168/14.
 PT Feline immunodeficiency virus antigenic polypeptide(s) and
 PT nucleic acid - used to prepare prods. for combating or diagnosis
 PT of feline immunodeficiency infection
 PS Disclosure; Figure 2; 68pp; English.
 CC The sequences given in R51248-R51262 and R58584-85 represent the
 CC feline immunodeficiency virus (FIV) envelope protein from different
 CC strains and serotypes. The consensus sequence basedon these, is given
 CC in R51247. The synthetic FIV peptides of the invention were derived
 CC Petaluma isolates, a composite sequence of which is given in R51246.
 CC Variations in the sequence may occur between different strains or
 CC serotypes, isolates of different geographical origin or even between
 CC different isolates from the same host.
 CC Sequence 856 AA;
 SQ

PT Feline immunodeficiency virus antigenic polypeptide(s) and
 PT nucleic acid - used to prepare prods. for combating or diagnosis
 PT of feline immunodeficiency infection
 PS Disclosure; Figure 2; 68pp; English.
 CC The sequences given in R51248-R51262 and R58584-85 represent the
 CC feline immunodeficiency virus (FIV) envelope protein from different
 CC strains and serotypes. The consensus sequence basedon these, is given
 CC in R51247. The synthetic FIV peptides of the invention were derived
 CC Petaluma isolates, a composite sequence of which is given in R51246.
 CC Variations in the sequence may occur between different strains or
 CC serotypes, isolates of different geographical origin or even between
 CC different isolates from the same host.
 CC Sequence 856 AA;
 SQ

Query Match 44.4%; Score 36; DB 1; Length 856;
 Best Local Similarity 66.7%; Pred. No. 2.2e+02;
 Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 6 IKINNIRIV 14
 Db 660 LKINNRLV 668
 :||||:|

RESULT 14
 R51249
 ID R51249 standard; peptide; 856 AA.
 AC R51249;
 DT 08-OCT-1994 (first entry)
 DE FIV PET-FL4 envelope protein sequence.
 KW Feline immunodeficiency virus; FIV; vaccine; diagnostic; AIDS;
 KW T-lymphotropic lentivirus; FIV UK8; FIV Petaluma; envelope protein.
 OS Synthetic.
 FH Key Location/Qualifiers
 FT peptide 1..178
 FT /note= "Hydrophobic leader peptide"
 FT region 51..66
 FT /note= "V1 region"
 FT region 95..173
 FT /note= "V2 region"
 FT protein 179..610
 FT /note= "Surface glycoprotein"
 FT region 360..424
 FT /note= "V3 region"
 FT region 451..483
 FT /note= "V4 region"
 FT region 539..567
 FT /note= "V5 region"
 FT protein 611..856
 FT /note= "Transmembrane protein"
 PN WO9406471-A.
 PD 31-MAR-1994.
 PF 20-SEP-1993; G01974.
 PR 21-SEP-1992; GB-019936.
 PA (PITM) PITMAN MOORE INC.
 PI Francis MJ;
 DR WPI: 94-118168/14.
 PT Feline immunodeficiency virus antigenic polypeptide(s) and
 PT nucleic acid - used to prepare prods. for combating or diagnosis
 PT of feline immunodeficiency infection
 PS Disclosure; Figure 2; 68pp; English.
 CC The sequences given in R51248-R51262 and R58584-85 represent the
 CC feline immunodeficiency virus (FIV) envelope protein from different
 CC strains and serotypes. The consensus sequence basedon these, is given
 CC in R51247. The synthetic FIV peptides of the invention were derived
 CC Petaluma isolates, a composite sequence of which is given in R51246.
 CC Variations in the sequence may occur between different strains or
 CC serotypes, isolates of different geographical origin or even between
 CC different isolates from the same host.
 CC Sequence 856 AA;
 SQ

Query Match 44.4%; Score 36; DB 1; Length 856;
 Best Local Similarity 66.7%; Pred. NO. 2.2e+02;
 Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

OY 6 IKINNIRIV 14
 :||||:|
 Db .660 LKINLRV 668

RESULT 15

R51254
 ID R51254 standard; peptide: 856 AA.
 AC R51254;
 DE 08-OCT-1994 (first entry)
 DE FIV DUTCH19K1 envelope protein sequence.
 KW Feline immunodeficiency virus; FIV; vaccine; diagnostic; AIDS;
 KW T-lymphotropic lentivirus; FIV UK8; FIV Petaluma; envelope protein.
 OS Synthetic.
 FH Key
 FT peptide
 FT region
 FT region
 FT region
 FT protein
 FT region
 FT region
 FT region
 FT region
 FT protein
 FT protein
 FT WO9406471-A.
 PN 31-MAR-1994.
 PD 20-SEP-1993; G01974.
 PR 21-SEP-1992; GB-019936.
 PA (PTM) PITMAN MOORE INC.
 PI Francis MJ;
 DR WPI; 94-118168/14.
 PT Feline immunodeficiency virus antigenic polypeptide(s) and
 PT nucleic acid - used to prepare prods. for combating or diagnosis
 PT of feline immunodeficiency infection
 PS Disclosure; Figure 2; 68pp; English.
 CC The sequences given in R51248-R51262 and R58584-85 represent the
 CC feline immunodeficiency virus (FIV) envelope protein from different
 CC strains and serotypes. The consensus sequence based on these, is given
 CC in R51247. The synthetic FIV peptides of the invention were derived
 CC principally from a combination of the sequences of the FIV UK 8 and
 CC Petaluma isolates, a composite sequence of which is given in R51246.
 CC Variations in the sequence may occur between different strains or
 CC serotypes, isolates of different geographical origin or even between
 CC different isolates from the same host.
 SQ Sequence 856 AA;

Query Match 44.4%; Score 36; DB 1; Length 856;
 Best Local Similarity 66.7%; Pred. NO. 2.2e+02;
 Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

OY 6 IKINNIRIV 14
 :||||:|
 Db .660 LKINLRV 668

Search completed: February 8, 2000, 04:05:41
 Job time: 9358 sec

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: February 7, 2000, 18:04:35 ; Search time 111.22 Seconds
(without alignments)
7,210 Million cell updates/sec

Title: US-08-653-294-22

Perfect score: 81
Sequence: 1 SYKLVIKINNIRIVVKF 17

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 142080 seqs, 47169319 residues

Total number of hits satisfying chosen parameters: 142080

Minimum DB seq length: 0

Maximum DB seq length: 1000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : PIR_62:*

1: p1r1:.*
2: p1r2:.*
3: p1r3:.*
4: p1r4:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	44	54.3	471	2 F71618	adenylosuccinate l
2	43	53.1	265	2 S32735	AAF protein - Esch
3	41	50.6	364	2 S05434	hypothetical prote
4	41	50.6	459	2 G71619	PINT domain protei
5	40	49.4	294	2 H38888	COI intron 15 prot
6	40	49.4	334	2 A70101	hypothetical prote
7	40	49.4	579	2 T01160	hypothetical prote
8	40	49.4	1204	2 S62506	hypothetical prote
9	39	48.1	275	2 F71714	2-dehydro-3-deoxyp
10	39	48.1	624	2 E64483	hypothetical prote
11	38.5	47.5	2875	1 RRVUTW	genome polypeptin
12	38	46.9	82	2 S07332	hypothetical prote
13	38	46.9	338	2 F71690	hypothetical prote
14	38	46.9	373	2 D71636	hypothetical prote
15	38	46.9	436	2 E70387	conserved hypotet
16	38	46.9	513	2 A53739	hypothetical vacuo
17	38	46.9	763	2 S51300	probable membrane
18	38	46.9	801	2 D70309	ribonucleoside-dip
19	38	46.9	835	2 F70363	cation transportin
20	38	46.9	4572	2 S57908	hypothetical 527K
21	37.5	46.3	354	2 A69877	anion permease hom
22	37	45.7	197	1 YTBST	tunicamycin resist
23	37	45.7	254	2 S23475	rod-core linker po
24	37	45.7	320	2 T02285	hypothetical prote
25	37	45.7	325	2 B72475	probable transcrip
26	37	45.7	543	2 I40545	oligopeptide ABC t
27	37	45.7	1487	2 S62048	probable membrane
28	36	44.4	91	2 F70142	glu-tRNA amidotran
29	36	44.4	178	2 B71942	glucose inhibited
30	36	44.4	235	1 SQMS	parotid secretory

```

31      36      44.4      240      2      E71898      uridylate kinase -
32      36      44.4      240      2      A64617      uridine 5'-monopho
33      36      44.4      241      2      A64155      hypothetical prote
34      36      44.4      353      2      S29788      glucose 1-dehydrog
35      36      44.4      358      2      D70138      hypothetical prote
36      36      44.4      433      2      A75125      hypothetical prote
37      36      44.4      576      2      G72277      NH(3)-dependent NA
38      36      44.4      765      2      S72278      ATP-dependent Clp
39      36      44.4      795      1      S22804      replication licens
40      36      44.4      808      1      S62594      replication licens
41      36      44.4      827      2      S29955      surface glycoprote
42      36      44.4      855      1      JQ2004      env polyprotein -
43      36      44.4      856      1      VCLJFP      env polyprotein pr
44      36      44.4      856      2      S23823      env polyprotein -
45      36      44.4      857      2      S19886      env polyprotein E

```

ALIGNMENTS

```

RESULT 1
F71618
adenylosuccinate lyase (OO) PFB0295W - malaria parasite (Plasmodium falciparum)
C:Species: Plasmodium falciparum
C:Date: 13-Nov-1998 #sequence_revision 13-Nov-1998 #text_change 07-May-1999
C:Accession: F71618
.: Gardner, M.J.; Tettelin, H.; Carucci, D.J.; Cummings, L.M.; Aravind, L.; Koonin, E.
.: Perlea, M.; Salzberg, S.; Zhou, L.; Sutton, G.G.; Clayton, R.; White, O.; Smith, H
Science 282, 1126-1132, 1998
A:Title: Chromosome 2 sequence of the human malaria parasite Plasmodium falciparum.
A:Reference number: A71600; MUID:99021743
A:Accession: F71618
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-471 <GAR>
A:Cross-references: GB:AE001385; GB:AE001362; NID:g3845143; PID:g3845146; TIGR:PFB029
A:Experimental source: clone 3D7
C:Genetics:
A:Gene: PFB0295W

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Query Match      54.3%      Score 44; DB 2; Length 471;
Best Local Similarity 56.2%      Pred. No. 5;
Matches 9; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY      2 YKLVIKINNIRIVVKF 17
      || : || | ||
Db      194 YKHINKLNIEIVVKF 209

RESULT 2
S32735
AAF protein - Escherichia coli
C:Species: Escherichia coli
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 26-Aug-1999
C:Accession: S32735
R:Nataro, J.P.; Deng, Y.; Deng, Y.
A:Description: Region 2 of aggregative adherence fimbriae I encodes an rns-like prote
submitted to the EMBL Data Library, November 1992
A:Reference number: S32735
A:Accession: S32735
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-265 <NAT>
A:Cross-references: EMBL:Z18751; NID:g296992; PIDN:CAA79242.1; PID:g296993
C:Superfamily: fapR protein

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```

Query Match      53.1%      Score 43; DB 2; Length 265;
Best Local Similarity 81.8%      Pred. No. 4.1;
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      3 KLVIKINNIRI 13

```

Db 9 KEIINKINIRI 19
| : ||| ||| |||

RESULT 3

S05434

hypothetical protein A3 - Emericella nidulans mitochondrion (SGC3)
C:Species: mitochondrion Emericella nidulans, Aspergillus nidulans
C:Date: 01-Dec-1989 #sequence_revision 01-Dec-1989 #text_change 09-Sep-1997
C:Accession: S05434

R:Brown, T.A.; Constable, A.; Waring, R.B.; Scazzocchio, C.; Davies, R.W.

Nucleic Acids Res. 17, 5838, 1989

A:Title: Nucleotide sequence of the only unidentified reading frame in the Aspergillus nidulans
A:Reference number: S05434; MUID:89345173

A:Accession: S05434

A:Molecule type: DNA

A:Residues: 1-364 <BRO>

A:CROSS-references: EMBL:X15442; NID:gl2720; PID:gl2721

C:Genetics:

A:Genome: mitochondrion

A:Genetic code: SGC3

C:Keywords: mitochondrion

Query Match 50.6%; Score 41; DB 2; Length 364;

Best Local Similarity 40.0%; Pred. No. 13;

Matches 6; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

QY 3 KLVIKINIRIVKVF 17

| : ||| ||| : |

Db 71 KIIRINTVKIITIF 85

RESULT 4

G71619

PINT domain protein (proteasomal subunit) PFB0240w - malaria parasite (Plasmodium falciparum)
C:Species: Plasmodium falciparum

C:Date: 13-Nov-1998 #sequence_revision 13-Nov-1998 #text_change 07-May-1999

C:Accession: G71619

R:Gardner, M.J.; Tettelin, H.; Carucci, D.J.; Cummings, L.M.; Aravind, L.; Koonin, E.V.;

.; Pertea, M.; Salzberg, S.; Zhou, L.; Sutton, G.G.; Clayton, R.; White, O.; Smith, H.O.;

Science 282, 1128-1132, 1998

A:Title: Chromosome 2 sequence of the human malaria parasite Plasmodium falciparum.

A:Reference number: A71600; MUID:99021743

A:Accession: G71619

A:Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-459 <GAR>

A:CROSS-references: GB:AE001382; GB:AE001362; NID:g3845130; PID:g3845132; TIGR:PFB0240w

A:Experimental source: clone 3D7

C:Genetics:

A:Gene: PFB0240w

Query Match 50.6%; Score 41; DB 2; Length 459;

Best Local Similarity 47.1%; Pred. No. 16;

Matches 8; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 1 SYKLVIKINIRIVKVF 17

| : ||| ||| : |

Db 219 SIKLCMKLNMQITTSF 235

RESULT 5

H38888

COI intron 15 protein - Podospora anserina mitochondrion (SGC3)

C:Species: mitochondrion Podospora anserina

C:Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 09-Sep-1997

C:Accession: H38888

R:Cummings, D.J.; Michel, F.; McNally, K.L.

Curr. Genet. 16, 381-406, 1989

A:Title: DNA sequence analysis of the 24.5 kilobase pair cytochrome oxidase subunit I md

A:Reference number: A48327; MUID:90124722

A:Accession: H38888

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-294 <CDW>

A:CROSS-references: GB:X55026; NID:gl4030; PID:e33710; PID:gl334548; GB:M30937; GB:M6

C:Genetics:

A:Genome: mitochondrion

A:Genetic code: SGC3

C:Keywords: mitochondrion

Query Match 49.4%; Score 40; DB 2; Length 294;

Best Local Similarity 63.6%; Pred. No. 15;

Matches 7; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 2 YKLVIKINIR 12

| : ||| ||| : |

Db 91 YRLVTKLSNIQ 101

RESULT 6

A70101

hypothetical protein BB0009 - Lyme disease spirochete

C:Species: Borrelia burgdorferi (Lyme disease spirochete)

C:Date: 13-Feb-1998 #sequence_revision 13-Feb-1998 #text_change 05-Jun-1998

C:Accession: A70101

R:Fraser, C.M.; Casjens, S.; Huang, W.M.; Sutton, G.G.; Clayton, R.; Lathigra, R.; Wh

son, D.; Peterson, J.; Kerlavage, A.R.; Quackenbush, J.; Salzberg, S.; Hanson, M.; Vu

; Bowman, C.; Garland, S.; Fujii, C.; Cotton, M.D.; Horst, K.; Roberts, K.; Hatch, B.

Nature 390, 580-586, 1997

A:Authors: Smith, H.O.; Venter, J.C.

A:Title: Genomic sequence of a Lyme disease spirochete, Borrelia burgdorferi.

A:Reference number: A70100; MUID:98065943

A:Accession: A70101

A:Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-334 <KLE>

A:CROSS-references: GB:AE001115; GB:AE000783; NID:g2687879; PID:g2687892; TIGR:BB00009

A:Experimental source: strain B31

Query Match 49.4%; Score 40; DB 2; Length 334;

Best Local Similarity 57.1%; Pred. No. 17;

Matches 8; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 SYKLVIKINIRIV 14

| : ||| ||| : |

Db 101 SYKLPIKIKLNISI 114

RESULT 7

T01160

hypothetical protein F7N22.6 - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)

C:Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 14-May-1999

C:Accession: T01160

R:Dante, M.

submitted to the EMBL Data Library, April 1998

A:Description: The sequence of A. thaliana F7N22.

A:Reference number: Z14250

A:Accession: T01160

A:Status: translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-579 <DAN>

A:CROSS-references: EMBL:AF058825; NID:g3047060; PID:g3047066

A:Experimental source: cultivar Columbia

C:Genetics:

A:Map position: 4

A:Introns: 70/2; 380/1

A>Note: F7N22.6

Query Match 49.4%; Score 40; DB 2; Length 579;

Best Local Similarity 35.3%; Pred. NO. 30;
Matches 6; Conservative 7; Mismatches 4; Indels 0; Gaps 0;

Qy 1 SYKLVIKINIRIVVKF 17
:|::|:|:|:|:|
Db 426 NYKIMRKQNMNLIKPF 442

RESULT 8
S62506
hypothetical protein SPAC23D3.15 - fission yeast (Schizosaccharomyces pombe) (fragment)
C:Species: Schizosaccharomyces pombe
C:Date: 16-May-1996 #sequence_revision 13-Mar-1997 #text_change 31-Oct-1997
C:Accession: S62506
R:Niblett, D.; Harris, D.
submitted to the EMBL Data Library, October 1995
A:Reference number: S62492
A:Accession: S62506
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1204 <NTB>
A:Cross-references: EMBL:Z64354; NID:g1039338; PID:g1039353
C:Genetics:
A:Map position: 1R

Query Match 49.4%; Score 40; DB 2; Length 1204;
Best Local Similarity 46.7%; Pred. NO. 64;
Matches 7; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

Qy 3 KLVIKINIRIVVKF 17
:|::|:|:|:|:|
Db 735 RLVIPLKRLIIVEF 749

RESULT 9
F71714
2-dehydro-3-deoxyphosphooctonate aldolase (kdsA) RP062 - Rickettsia prowazekii
C:Species: Rickettsia prowazekii
C:Date: 21-Nov-1998 #sequence_revision 21-Nov-1998 #text_change 26-Aug-1999
C:Accession: F71714
R:Andersson, S.G.E.; Zomorodipour, A.; Andersson, J.O.; Sicheritz-Ponten, T.; Alsmark, U.
Nature 396, 133-140, 1998
A:Title: The genome sequence of Rickettsia prowazekii and the origin of mitochondria.
A:Reference number: A71630; MUID:99039499
A:Accession: F71714
A>Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-275 <AND>
A:Cross-references: GB:AJ235270; GB:AJ235269; NID:g3860572; PID:el342376; PID:g3860632
A:Experimental source: strain Madrid E
C:Genetics:
A:Gene: kdsA: RP062
C:Superfamily: phospho-2-dehydro-3-deoxyoctonate aldolase

Query Match 48.1%; Score 39; DB 2; Length 275;
Best Local Similarity 63.6%; Pred. NO. 21;
Matches 7; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 3 KLVIKINIRI 13
|:|:|:|:|
Db 2 KKVVKLNINIKI 12

RESULT 10
E64483
hypothetical protein MJ1470 - Methanococcus jannaschii
C:Species: Methanococcus jannaschii
C:Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 10-Oct-1997
C:Accession: E64483
R:Bult, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blake, R.; Reich, C.I.; Overbeek, R.; Kirkness, E.F.; Weinstock, K.G.; Merrick, J.M.; Glodek, A.

rson, J.D.; Sadow, P.W.; Hanna, M.C.; Cotton, M.D.; Roberts, K.M.; Hurst, M.A.
Science 273, 1058-1073, 1996
A:Authors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese
A:Title: Complete genome sequence of the methanogenic archaeon, Methanococcus jannaschii
A:Reference number: A64300; MUID:96337999
A:Accession: E64483
A>Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-624 <BUL>
A:Cross-references: GB:U67588; GB:L77117; NID:g1592111; PID:g1500355; TIGR:MJ1470
C:Genetics:
A:Map position: FOR1440749-1442623

Query Match 48.1%; Score 39; DB 2; Length 624;
Best Local Similarity 53.3%; Pred. NO. 49;
Matches 8; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy 2 YKLVIKINIRIVVK 16
|:|:|:|:|
Db 609 YLTLSPNNVTIVK 623

RESULT 11
RVVUTW
genome polyprotein - tomato spotted wilt virus (strain BR-01)
N:Alternate names: L protein
N:Contains: RNA-directed RNA polymerase (EC 2.7.7.48)
C:Species: tomato spotted wilt virus
C:Date: 30-Sep-1992 #sequence_revision 30-Sep-1992 #text_change 29-May-1998
C:Accession: J01335
R:de Haan, P.; Kormelink, R.; de Oliveira Resende, R.; van Poelwijk, F.; Peters, D.; J. Gen. Virol. 71, 2207-2216, 1991
A:Title: Tomato spotted wilt virus L RNA encodes a putative RNA polymerase.
A:Reference number: J01335
A:Accession: J01335
A:Molecule type: genomic RNA
A:Residues: 1-2875 <DEH>
C:Genetics:
A:Map position: segment L
C:Superfamily: bunyavirus RNA-directed RNA polymerase
C:Keywords: nucleotidyltransferase

Query Match 47.5%; Score 38.5; DB 1; Length 2875;
Best Local Similarity 30.4%; Pred. NO. 2.8e+02;
Matches 7; Conservative 7; Mismatches 0; Indels 9; Gaps 1;

Qy 3 KLVIKIN-----NIRIVVK 16
|:|:|:|:|
Db 2322 KMIVKNATSRQIRLENVKLVK 2344

RESULT 12
S07352
hypothetical protein 82 - fava bean chloroplast
C:Species: chloroplast Vicia faba (fava bean)
C:Date: 02-Dec-1993 #sequence_revision 01-Dec-1995 #text_change 09-Sep-1997
C:Accession: S07352
R:Kuntz, M.; Weil, J.H.; Steinmetz, A.
Nucleic Acids Res. 12, 5037-5047, 1984
A:Title: Nucleotide sequence of a 2 kbp BamH I fragment of Vicia faba chloroplast DNA
A:Reference number: S07352; MUID:84247356
A:Accession: S07352
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-82 <KUN>
A:Cross-references: EMBL:X00682; NID:g12385; PID:g12386
A:Note: the authors translated the codon CAA for residue 51 as Glu
C:Keywords: chloroplast

Query Match 46.9%; Score 38; DB 2; Length 82;


```

RESULT 5
ID YE70_METJA STANDARD; PRT; 624 AA.
AC Q58865;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE HYPOTHETICAL PROTEIN MJ1470.
GN MJ1470
OS Methanococcus jannaschii.
OC Archaea; Euryarchaeota; Methanococcales; Methanococcaceae;
OC Methanococcus.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-JAL-1 / DSM 2661 / ATCC 43067;
RX MEDLINE; 96337999.
RA BULT C.J., WHITE O., OLSEN G.J., ZHOU L., FLEISCHMANN R.D.,
RA SUTTON G.G., BLAKE J.A., FITZGERALD L.M., CLAYTON R.A., GOCAYNE J.D.,
RA KERLAVAGE A.R., DOUGHERTY B.A., TOMB J.-F., ADAMS M.D., REICH C.I.,
RA OVERBECK R., KIRKNESS E.F., WEINSTOCK K.G., MERRICK J.M., GLODEK A.,
RA SCOTT J.L., GEOGHAGEN N.S.M., WEIDMAN J.F., FUHRMANN J.L., NGUYEN D.,
RA UTTERBACK T.R., KELLEY J.M., PETERSON J.D., SADOW P.W., HANNA M.C.,
RA COTTON M.D., ROBERTS K.M., HURST M.A., RAINE B.P., BORODOVSKIY M.,
RA KLENK H.-P., FRASER C.M., SMITH H.O., WOESE C.R., VENTER J.C.;
RT "Complete genome sequence of the methanogenic archaeon, Methanococcus
jannaschii."
RL Science 273:1058-1073(1996).
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CC -----
DR EMBL; U67588; AAB99485.1; -.
KW Hypothetical protein; Transmembrane.
FT TRANSMEM 10 30 POTENTIAL.
SQ SEQUENCE 624 AA; 72857 MW; 4C4411ED CRC32;

Query Match 48.1%; Score 39; DB 1; Length 624;
Best Local Similarity 53.3%; Pred. No. 25;
Matches 8; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy 2 YKLVKINNIRIVK 16
| | | | |
Db 609 YVLTSPNNVTIVK 623

RESULT 6
ID RRPL_TSWV1 STANDARD; PRT; 2875 AA.
AC P28976;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE RNA-DIRECTED RNA POLYMERASE (EC 2.7.7.46) (L PROTEIN).
GN L.
OS Tomato spotted wilt virus (strain Brazilian Br-01) (TSWV).
OC Viruses; ssRNA negative-strand viruses; Bunyaviridae; Tospovirus.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 91374019.
RA DE HAAN P., KORMELINK R., DE OLIVEIRA RESENDE R., VAN POELWIJK F.,
RA PETERS D., GOLDBACH R.;
RT "Tomato spotted wilt virus L RNA encodes a putative RNA polymerase.";
RL J. Gen. Virol. 72:2207-2216(1991).
CC -!- CATALYTIC ACTIVITY: N NUCLEOSIDE TRIPHOSPHATE = N PYROPHOSPHATE
CC + RNA(N).
CC -----

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CC -----
DR EMBL; X00682; CAA25290.1; -.
KW PIR; S07352; S07352.
KW Chloroplast; Hypothetical protein.
SQ SEQUENCE 82 AA; 9935 MW; 18728241 CRC32;

Query Match 46.9%; Score 38; DB 1; Length 82;
Best Local Similarity 58.3%; Pred. No. 4.3;
Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 2 YKLVKINNIRI 13
| | | | |
Db 35 YRLVIGMNNLEI 46

RESULT 8
ID YNS1_YEAST STANDARD; PRT; 763 AA.
AC P42843;

```


DR EMBL; U29401; AAA86834.1; -
 KW Cytotoxin; Toxin; Signal.
 FT SIGNAL 1 30
 FT CHAIN 31 ?
 FT PROPEP ? 1310
 FT POTENTIAL: VACUOLATING CYTOTOXIN.
 SQ SEQUENCE 1310 AA; 141988 MW; BDE25580 CRC32;

Query Match 46.9%; Score 38; DB 1; Length 1310;
 Best Local Similarity 53.3%; Pred. No. 83;
 Matches 8; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Oy 2 YKLVKINNIRIVK 16
 || :|||| : :
 Db 725 YKPLKINNAQLTK 739

RESULT 11
 TMRB_BACSU STANDARD; PRT; 197 AA.
 AC P12921;
 DT 01-OCT-1989 (Rel. 12, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DE TUNICAMYCIN RESISTANCE PROTEIN.
 GN TMRB.
 OS Bacillus subtilis.
 OC Bacteria; Firmicutes; Bacillus/Clostridium group;
 CC Bacillus/Staphylococcus group; Bacillus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RA HARADA S., YODA K., MORI M., TANIMOTO A., FURUSATO T., YAMANE K.,
 RA TAKATSUKI A., YAMASAKI M., TAMURA G.;
 RT "The gene responsible for tunicamycin resistance, tnrB, in Bacillus
 RT subtilis";
 RL Agric. Biol. Chem. 52:1785-1789(1988).
 RN [2]
 RP PARTIAL SEQUENCE OF 1-10, AND CHARACTERIZATION.
 RX MEDLINE; 92325013.
 RA NODA V., YODA K., TAKATSUKI A., YAMASAKI M.;
 RT "TnrB protein, responsible for tunicamycin resistance of Bacillus
 RT subtilis, is a novel ATP-binding membrane protein.";
 RL J. Bacteriol. 174:4302-4307(1992).
 CC -1- FUNCTION: INVOLVED IN THE RESISTANCE TO TUNICAMYCIN. BINDS ATP.
 CC -1- SUBCELLULAR LOCATION: MEMBRANE-ASSOCIATED.

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 CC -----
 DR EMBL; D13793; BAA02946.1; -
 DR EMBL; D13793; BAA02944.1; ALT_INIT.
 DR EMBL; D13793; BAA02945.1; ALT_INIT.
 DR PIR; JT0240; YTEST.
 DR SUBILLIST; BG10456; TMRB.
 KW Antibiotic resistance; ATP-binding; Membrane.
 FT NP_BIND 7 14
 FT ATP (POTENTIAL).
 SQ SEQUENCE 197 AA; 22730 MW; 264B136D CRC32;

Query Match 45.7%; Score 37; DB 1; Length 197;
 Best Local Similarity 54.5%; Pred. No. 16;
 Matches 6; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

Oy 3 KLVKINNIRI 13
 :||:|:|:|
 Db 186 RLWKLNHIRI 196

RESULT 12
 PYG3_MASLA STANDARD; PRT; 253 AA.

ID PYG3_MASLA
 AC P29733;
 DT 01-APR-1993 (Rel. 25, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 01-OCT-1996 (Rel. 34, Last annotation update)
 DE PHYCOBILISOME ROD-CORE LINKER POLYPEPTIDE CPCG3 (L-RC 29.6).
 GN CPCG3.

OS Mastigocladus laminosus (Fischerella sp.)
 OC Bacteria; Cyanobacteria; Stigonematales; Fischerella.

RN [1]
 RP SEQUENCE FROM N.A.

RC STRAIN-PCG 7603;
 RX MEDLINE; 92249337.

RA GLAUSER M., STIREWALT V.L., BRYANT D.A., SIDLER W., ZUBER H.;
 RT "Structure of the genes encoding the rod-core linker polypeptides of the
 RT Mastigocladus laminosus phycobilisomes and functional aspects of the
 RT phycobiliprotein/linker-polypeptide interactions.";
 RL Eur. J. Biochem. 205:927-937(1992).

CC -1- FUNCTION: ROD-CORE LINKER PROTEIN REQUIRED FOR ATTACHMENT OF
 CC PHYCOCYANIN TO ALLOPHYCOCYANIN IN CORES OF PHYCOBILISOMES.
 CC -1- FUNCTION: LINKER POLYPEPTIDES DETERMINE THE STATE OF AGGREGATION
 CC AND THE LOCATION OF THE DISC-SHAPED PHYCOBILIPROTEIN UNITS WITHIN
 CC THE PHYCOBILISOME AND MODULATE THEIR SPECTROSCOPIC PROPERTIES IN
 CC ORDER TO MEDIATE A DIRECTED AND OPTIMAL ENERGY TRANSFER.
 CC -1- SUBUNIT: THE PHYCOBILISOME IS A HEMIDISCOIDAL STRUCTURE THAT IS
 CC COMPOSED OF TWO DISTINCT SUBSTRUCTURES: A CORE COMPLEX (THAT IS
 CC CONTAINS PHYCOBILIPROTEINS) AND A NUMBER OF RODS RADIATING FROM
 CC THE CORE.

CC -1- SIMILARITY: TO OTHER PHYCOBILISOME LINKER PROTEINS.

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 CC -----

DR EMBL; X59763; CAA42435.1; -
 DR PIR; S16060; S16060.
 DR PIR; S23475; S23475.
 DR PFAM; PF00427; PBS_linker_poly; 1.
 KW Phycobilisome; Photosynthesis; Multigene family.
 FT INIT_MET 0
 FT BY SIMILARITY
 SQ SEQUENCE 253 AA; 29493 MW; 820A835D CRC32;

Query Match 45.7%; Score 37; DB 1; Length 253;
 Best Local Similarity 36.8%; Pred. No. 21;
 Matches 7; Conservative 6; Mismatches 2; Indels 4; Gaps 1;

Oy 2 YKLVKINNIRIVK 16
 :||:|:|:|
 Db 94 YRLVSVNNRYRLVDVVLK 112

RESULT 13
 SMLA_DICDI STANDARD; PRT; 284 AA.

ID SMLA_DICDI
 AC P54661; Q23850;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DE SMALL AGGREGATE FORMATION PROTEIN.
 GN SMLA.

OS Dictyostelium discoideum (Slime mold).
 OC Eukaryota; Dictyostelida; Dictyostelium.

RN [1]
 RP SEQUENCE FROM N.A.

RX MEDLINE; 96379719.
 RA BROCK D.A., BUCZYNSKI G., SPANN T.P., WOOD S.A., CARDELLI J.,

RA GOMER R.H.;
 RT "A Dictyostellium mutant with defective aggregate size determination.";
 RL Development 122:2569-2578(1996).
 RN [2]
 RP SEQUENCE OF 1-92 FROM N.A.
 RC STRAIN=AX3;
 RX MEDLINE; 89178644.
 RA GORDA R., OHMACHI T., ENNIS H.L.;
 RT "Organization of a gene family developmentally regulated during
 RT Dictyostellium discoideum spore germination.";
 RL J. Mol. Biol. 205:63-69(1989).
 CC -!- FUNCTION: KNOCKOUT OF THE GENE FOR THIS PROTEIN CAUSES SMALL
 CC AGGREGATE FORMATION. MAY REGULATE THE SECRETION OR PROCESSING OF A
 CC SECRETED FACTOR THAT REGULATES AGGREGATE SIZE.
 CC -!- SUBCELLULAR LOCATION: CYTOPLASMIC.
 CC -!- DEVELOPMENTAL STAGE: EXPRESSED IN VEGETATIVE AND EARLY DEVELOPING
 CC CELLS, ITS LEVEL DECREASES AT ABOUT 10 HOURS OF DEVELOPMENT.
 CC -----
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 CC -----
 DR EMBL; U48706; AAB19231.1; -;
 DR EMBL; M19469; AAA67428.1; -;
 DR DICTYDB; DD02058; SMLA.
 FT CONFLICT 9 9 V -> E (IN REF. 2).
 FT CONFLICT 34 34 P -> Q (IN REF. 2).
 FT CONFLICT 52 67 PNLGFGKMLKLPPIW -> QNFDFENAKIVSTNF (IN
 FT REF. 2).
 SQ SEQUENCE 284 AA; 33227 MW; BBDF1F98 CRC32;
 Query Match 45.7%; Score 37; DB 1; Length 284;
 Best Local Similarity 40.0%; Pred. No. 24;
 Matches 6; Conservative 6; Mismatches 3; Indels 0; Gaps 0;
 QY 2 YKLVIKINNIRIVK 16
 ||::: |||::: |
 DB 21 YKTIISGNIKVLPK 35
 RESULT 14
 ID RNC_CAEEL STANDARD; PRT; 412 AA.
 AC 001326;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DE PUTATIVE RIBONUCLEASE III (EC 3.1.26.3) (RNAse III).
 GN F26E4.13.
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida;
 OC Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BRISTOL N2;
 RA LIGHTNING J.;
 RL Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.
 CC -!- SIMILARITY: BELONGS TO THE RNAse III FAMILY.
 CC -----
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 CC -----
 DR EMBL; Z81070; CAB03005.1; -;

DR WORMPEP; F26E4.13; CE09697.
 DR PROSITE; PS00517; RIBONUCLEASE_III; 2.
 DR PFAM; PF00636; Ribonuclease_3; 2.
 KW Hypothetical protein; Hydrolase; Nuclease; Endonuclease.
 SQ SEQUENCE 412 AA; 47087 MW; B6C1ICDI CRC32;
 Query Match 45.7%; Score 37; DB 1; Length 412;
 Best Local Similarity 50.0%; Pred. No. 36;
 Matches 7; Conservative 4; Mismatches 3; Indels 0; Gaps 0;
 QY 3 KLVKINNIRIVK 16
 ||::: |||::: |
 DB 168 RLGIQFNIRLLAK 181
 RESULT 15
 ID APPA_BACSU STANDARD; PRT; 543 AA.
 AC P42061;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 01-NOV-1995 (Rel. 32, Last annotation update)
 DE OLIGOPEPTIDE-BINDING PROTEIN APPA PRECURSOR.
 GN APPA.
 OS Bacillus subtilis.
 OC Bacteria; Firmicutes; Bacillus/Clostridium group;
 OC Bacillus/Staphylococcus group; Bacillus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=168;
 RX MEDLINE; 95089678.
 RA KOIDE A., HOCH J.A.;
 RT "Identification of a second oligopeptide transport system in Bacillus
 RT subtilis and determination of its role in sporulation.";
 RL Mol. Microbiol. 13:417-426(1994).
 CC -!- FUNCTION: THIS PROTEIN IS A COMPONENT OF AN OLIGOPEPTIDE
 CC PERMEASE, A BINDING PROTEIN-DEPENDENT TRANSPORT SYSTEM. THIS
 CC APP SYSTEM CAN COMPLETELY SUBSTITUTE FOR THE OPP SYSTEM IN BOTH
 CC SPOULATION AND GENETIC COMPETENCE. APPA CAN BIND AND TRANSPORT
 CC TETRA- AND PENTAPEPTIDES BUT NOT TRIPEPTIDES.
 CC -!- SUBCELLULAR LOCATION: ATTACHED TO THE MEMBRANE BY A LIPID ANCHOR
 CC (PROBABLE).
 CC -!- SIMILARITY: BELONGS TO THE BACTERIAL EXTRACELLULAR SOLUTE-BINDING
 CC PROTEIN FAMILY 5.
 CC -----
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 CC -----
 DR EMBL; U20909; AAA62358.1; -;
 DR EMBL; Z99110; CAB12995.1; -;
 DR SUBTILIST; BG11087; APPA.
 DR PROSITE; PS00013; PROKAR_LIPOPROTEIN; 1.
 DR PROSITE; PS01040; SBP_BACTERIAL_5; 1.
 DR PFAM; PF00496; SBP_bac_5; 1.
 KW Peptide transport; Transport; Membrane; Signal; Sporulation;
 KW Lipoprotein.
 FT SIGNAL 1 23 POTENTIAL.
 FT CHAIN 24 543 OLIGOPEPTIDE-BINDING PROTEIN APPA.
 FT LIPID 24 24 N-ACYL DIGLYCERIDE (PROBABLE).
 SQ SEQUENCE 543 AA; 61947 MW; C52C0ICE CRC32;
 Query Match 45.7%; Score 37; DB 1; Length 543;
 Best Local Similarity 53.8%; Pred. No. 48;
 Matches 7; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
 QY 2 YKLVIKINNIRIV 14

Wed Feb 9 08:48:34 2000

us-08-653-294-22.rsp

page 7

Db 270 YKTAEKFNKIV 282
|| | ||: ||

Search completed: February 8, 2000, 01:25:57
Job time: 1557 sec

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: February 8, 2000, 19:16:09 ; Search time 176.54 Seconds
(without alignments)
6.677 Million cell updates/sec

Title: US-08-653-294-22

Perfect score: 81
Sequence: 1 SYKLVIKINNIRIVVKF 17

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 225878 seqs, 69334122 residues

Total number of hits satisfying chosen parameters: 225878

Minimum DB seq length: 0
Maximum DB seq length: 1000000

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database : SPTRMBL12.*
1: sp_archaea.*
2: sp_bacteria.*
3: sp_fungi.*
4: sp_human.*
5: sp_invertebrate.*
6: sp_mammal.*
7: sp_mbc.*
8: sp_organelle.*
9: sp_phage.*
10: sp_plant.*
11: sp_rodent.*
12: sp_virus.*
13: sp_vertebrate.*
14: sp_unclassified.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	47	58.0	475	2 O32315	O32315 bacillus th
2	44	54.3	471	5 O15918	O15918 plasmidum
3	41	50.6	240	2 O85022	O85022 helicobacte
4	41	50.6	240	2 O9X414	O9X414 helicobacte
5	41	50.6	364	8 O33805	O33805 emericella
6	41	50.6	459	5 O96149	O96149 plasmidum
7	40	49.4	235	2 O85023	O85023 helicobacte
8	40	49.4	253	5 O15869	O15869 plasmidum
9	40	49.4	294	8 O02676	O02676 podospira a
10	40	49.4	579	10 O65223	O65223 arabidopsis
11	40	49.4	584	2 O9XAS5	O9XAS5 staphylococ
12	39	48.1	275	2 O9ZERA	O9ZERA rickettsia
13	39	48.1	339	2 O9Z4S2	O9Z4S2 thermotoga
14	39	48.1	547	10 Q9XIA4	Q9XIA4 arabidopsis
15	39	48.1	727	10 Q9ZWC2	Q9ZWC2 arabidopsis
16	38	46.9	240	2 O85029	O85029 helicobacte
17	38	46.9	240	2 O9X413	O9X413 helicobacte
18	38	46.9	240	2 O9X410	O9X410 helicobacte
19	38	46.9	248	2 Q9ZIE7	Q9ZIE7 helicobacte
20	38	46.9	338	2 Q9ZDI8	Q9ZDI8 rickettsia

21	38	46.9	345	12 Q9YW40	Q9YW40 melanoplus
22	38	46.9	373	2 Q9ZC10	Q9ZC10 rickettsia
23	38	46.9	403	2 O86251	O86251 helicobacte
24	38	46.9	403	2 O86252	O86252 helicobacte
25	38	46.9	403	2 O86253	O86253 helicobacte
26	38	46.9	436	2 O67128	O67128 aquifex aeo
27	38	46.9	513	2 Q48246	Q48246 helicobacte
28	38	46.9	576	11 O62970	O62970 rattus norv
29	38	46.9	835	2 O66938	O66938 aquifex aeo
30	38	46.9	1323	2 O87018	O87018 helicobacte
31	38	46.9	1736	10 O23025	O23025 arabidopsis
32	38	46.9	4572	10 Q40712	Q40712 oryza sativ
33	37.5	46.3	354	2 O34734	O34734 bacillus su
34	37	45.7	130	2 Q44641	Q44641 buchnera ap
35	37	45.7	132	12 O66232	O66232 cacao swoll
36	37	45.7	197	2 P94385	P94385 bacillus su
37	37	45.7	240	2 O9X415	O9X415 helicobacte
38	37	45.7	240	2 O9X412	O9X412 helicobacte
39	37	45.7	240	2 O9X409	O9X409 helicobacte
40	37	45.7	320	10 O80756	O80756 arabidopsis
41	37	45.7	325	1 O9Y942	O9Y942 aeropyrum p
42	37	45.7	347	6 O97526	O97526 saimiri bol
43	37	45.7	402	6 O9XS98	O9XS98 cebus apell
44	37	45.7	405	6 O97527	O97527 saimiri sci
45	37	45.7	405	6 O97528	O97528 callithrix

ALIGNMENTS

RESULT 1

O32315
ID O32315 PRELIMINARY: PRT; 475 AA.
AC O32315;
DT 01-JAN-1998 (TREMBlrel. 05, Created)
DT 01-JAN-1998 (TREMBlrel. 05, Last sequence update)
DT 01-NOV-1998 (TREMBlrel. 08, Last annotation update)
DE HYPOTHETICAL 53.7 KD PROTEIN.
OS Bacillus thuringiensis.
OG Plasmid pGI3.
OC Bacteria; Firmicutes; Bacillus/Clostridium group;
OC Bacillus/Staphylococcus group; Bacillus.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 97405895.
RA HOFACK L., SEURINCK J., MAHILLON J.;
RT "Nucleotide sequence and characterization of the cryptic Bacillus
RT thuringiensis plasmid pGI3 reveal a new family of rolling circle
RT replicons."
RL J. Bacteriol. 179:5000-5008(1997).
DR EMBL; Y11173; CAA72058.1;
KW Hypothetical protein; Plasmid.
SQ SEQUENCE 475 AA; 53733 MW; FCE7AEC8 CRC32;

Query Match 58.0%; Score 47; DB 2; Length 475;
Best Local Similarity 50.0%; Pred. No. 5.1;
Matches 8; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

Qy 2 YKLVIKINNIRIVVKF 17

Db 48 YNLIIKVNMMKDVYSF 63

RESULT 2

O15918
ID O15918 PRELIMINARY: PRT; 471 AA.
AC O15918;
DT 01-JAN-1998 (TREMBlrel. 05, Created)
DT 01-JAN-1998 (TREMBlrel. 05, Last sequence update)
DT 01-NOV-1998 (TREMBlrel. 12, Last annotation update)
DE ADENYLOSUCCINATE LYASE (EC 4.3.2.2).
GN PFB0295W.

OS Plasmodium falciparum.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=B8;
RX MEDLINE; 97418807.
RA MARSHALL V.M., COPPEL R.L.;
RT "Characterisation of the gene encoding adenylosuccinate lyase of
Plasmodium falciparum";
RL Mol. Biochem. Parasitol. 88:237-241(1997).
[2]
RN SEQUENCE FROM N.A.
RP STRAIN=B8;
RX MEDLINE; 98384012.
RA MARSHALL V.M., TIEQUAO W., COPPEL R.L.;
RT "Close linkage of three merozoite surface protein genes on chromosome
2 of Plasmodium falciparum";
RL Mol. Biochem. Parasitol. 94:13-25(1998).
[3]
RN SEQUENCE FROM N.A.
RP MEDLINE; 99021743.
RA GARDNER M.J., TETTELIN H., CARUCCI D.J., CUMMINGS L.M., ARAVIND L.,
RA KOONIN E.V., SHALLOO S., MASON T., YU K., FUJII C., PEDERSON J.,
RA SHEN K., JING J., ASTON C., LAI Z., SCHWARTZ D.C., PERTEA M.,
RA SALZBERG S., ZHOU L., SUTTON G.G., CLAYTON R., WHITE O., SMITH H.O.,
RA FRASER C.M., ADAMS M.D., VENTER J.C., HOFFMAN S.L.;
RT "Chromosome 2 sequence of the human malaria parasite Plasmodium
falciparum";
RL Science 282:1126-1132(1998).
DR EMBL; AF033037; AAC32788.1; -.
DR EMBL; AE001385; AAC71848.1; -.
DR PROSITE; PS00163; FUMARATE_LYASES; 1.
DR PFAM; PF00206; lyase_1; 2.
KW Lyase.
SQ SEQUENCE 471 AA; 55176 MW; A7EC2F0B CRC32;

Query Match 54.3%; Score 44; DB 5; Length 471;
Best Local Similarity 56.2%; Pred. No. 16;
Matches 9; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 2 YKLVKINNIRIVVKF 17
||:|:|||||
DB 194 YKHINKLNIEIVVKF 209

RESULT 3
ID O85022 PRELIMINARY; PRT; 240 AA.
AC O85022;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
DE VACUOLATING CYTOTOXIN PRECURSOR (FRAGMENT).
GN VACA.
OS Helicobacter pylori (Campylobacter pylori).
OC Bacteria; Proteobacteria; epsilon subdivision; Helicobacter group;
OC Helicobacter.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=R10A;
RX MEDLINE; 98314552.
RA PAN Z.J., BERG D.E., VAN DER HULST R.W., SU W.W., RAUDONIKIENE A.,
RA XIAO S.D., BARKERT J., TYTGAT G.N., VAN DER ENDE A.;
RT "Prevalence of vacuolating cytotoxin production and distribution of
distinct vacA alleles in Helicobacter pylori from China.";
RL J. Infect. Dis. 178:220-226(1998).
DR EMBL; AF035609; AAC31125.1; -.
FT NON_TER 1
FT NON_TER 240
SQ SEQUENCE 240 AA; 26722 MW; 6A5AD7A4 CRC32;

Query Match 50.6%; Score 41; DB 2; Length 240;
Best Local Similarity 53.3%; Pred. No. 26;
Matches 8; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 2 YKLVKINNIRIVVK 16
||:|||||:|
DB 176 YKPLIKINNAQDLIK 190

RESULT 4
ID Q9X414 PRELIMINARY; PRT; 240 AA.
AC Q9X414;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
DE VACUOLATING CYTOTOXIN PRECURSOR (FRAGMENT).
GN VACA.
OS Helicobacter pylori (Campylobacter pylori).
OC Bacteria; Proteobacteria; epsilon subdivision; Helicobacter group;
OC Helicobacter.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=T-25;
RA LIN C.W.;
RT "Helicobacter pylori Taiwanese isolates";
RL Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF091822; AAD23359.1; -.
FT NON_TER 1
FT NON_TER 240
SQ SEQUENCE 240 AA; 26608 MW; OD37C8B0 CRC32;

Query Match 50.6%; Score 41; DB 2; Length 240;
Best Local Similarity 53.3%; Pred. No. 26;
Matches 8; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 2 YKLVKINNIRIVVK 16
||:|||||:|
DB 176 YKPLIKINNAQDLIK 190

RESULT 5
ID Q33805 PRELIMINARY; PRT; 364 AA.
AC Q33805;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
DE ASPERGILLUS NIDULANS MITOCHONDRIAL DNA FOR URF A3.
OG Emericella nidulans (Aspergillus nidulans).
OC Mitochondrion.
OC Eukaryota; Fungi; Ascomycota; Euascomycetes; Plectomycetes;
OC Eurotiiales; Trichocomaceae; Emericella.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 89345173.
RA BROWN T.A., CONSTABLE A., WARING R.B., SCAZZOCCHIO C., DAVIES R.W.;
RT "Nucleotide sequence of the only unidentified reading frame in the
Aspergillus nidulans mitochondrial genome.";
RL Nucleic Acids Res. 17:5838-5838(1989).
DR EMBL; X15442; CAA33482.1; -.
KW Mitochondrion.
SQ SEQUENCE 364 AA; 42482 MW; 89011CF2 CRC32;

Query Match 50.6%; Score 41; DB 8; Length 364;
Best Local Similarity 40.0%; Pred. No. 38;
Matches 6; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

QY 3 KLVKINNIRIVVKF 17
||:||||:|
DB 71 KIIIRINTVKIITIF 85

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RESULT 6
O96149
ID O96149 PRELIMINARY; PRT; 459 AA.
AC O96149;
DT 01-MAY-1999 (TRENBLrel. 10, Created)
DT 01-MAY-1999 (TRENBLrel. 10, Last sequence update)
DT 01-MAY-1999 (TRENBLrel. 10, Last annotation update)
DE PINT DOMAIN PROTEIN (PROTEASOMAL SUBUNIT).
GN PFB0240W.
OS Plasmodium falciparum.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE: 99021743.
RA GARDNER M.J., TETTELIN H., CARUCCI D.J., CUMMINGS L.M., ARAVIND L.,
RA KOONIN E.V., SHALLOM S., MASON T., YU K., FUJII C., PEDERSON J.,
RA SHEN K., JING J., ASTON C., LAI Z., SCHWARTZ D.C., PERTEA M.,
RA SALZBERG S., ZHOU L., SUTTON G.G., CLAYTON R., WHITE O., SMITH H.O.,
RA FRASER C.M., ADAMS M.D., VENTER J.C., HOFFMAN S.L.;
RT "Chromosome 2 sequence of the human malaria parasite Plasmodium
RT falciparum.";
RL Science 282:1126-1132(1998).
DR EMBL; AE001382; AAC71837.1; -.
SQ SEQUENCE 459 AA; 54610 MW; E86BDE0D CRC32;

Query Match 50.6%; Score 41; DB 5; Length 459;
Best Local Similarity 47.1%; Pred. No. 47;
Matches 8; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 1 SYKLVIKINNIRIVVKF 17
Db 219 SIKLCMKLNMMQITTSF 235

RESULT 7
O85023 PRELIMINARY; PRT; 235 AA.
AC O85023;
DT 01-NOV-1998 (TRENBLrel. 08, Created)
DT 01-NOV-1998 (TRENBLrel. 08, Last sequence update)
DT 01-NOV-1998 (TRENBLrel. 08, Last annotation update)
DE VACUOLATING CYTOTOXIN PRECURSOR (FRAGMENT).
GN VACA.
OS Helicobacter pylori (Campylobacter pylori).
OC Bacteria; Proteobacteria; epsilon subdivision; Helicobacter group;
OC Helicobacter.
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=R13A;
RX MEDLINE: 98314552.
RA PAN Z.J., BERG D.E., VAN DER HULST R.W., SU W.W., RAUDONIKIENE A.,
RA XIAO S.D., DANKERT J., TYTGAT G.N., VAN DER ENDE A.;
RT "Prevalence of vacuolating cytotoxin production and distribution of
RT distinct vacA alleles in Helicobacter pylori from China.";
RL J. Infect. Dis. 178:220-226(1998).
DR EMBL; AF035610; AAC31126.1; -.
FT NON_TER 235
FT NON_TER 235
SQ SEQUENCE 235 AA; 25955 MW; B2C778AC CRC32;

Query Match 49.4%; Score 40; DB 2; Length 235;
Best Local Similarity 53.3%; Pred. No. 37;
Matches 8; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 2 YKLVIKINNIRIVVK 16
Db 176 YAPLIKINSARDLIK 190

RESULT 8
O15869 PRELIMINARY; PRT; 253 AA.
AC O15869;
DT 01-JAN-1998 (TRENBLrel. 05, Created)
DT 01-JAN-1998 (TRENBLrel. 05, Last sequence update)
DT 01-NOV-1998 (TRENBLrel. 08, Last annotation update)
DE ORNITHINE DECARBOXYLASE (EC 4.1.1.17) (FRAGMENT).
GN ODC.
OS Plasmodium falciparum.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
RN [1]
RP SEQUENCE FROM N.A.
RA MADHUBALA R.;
RL Submitted (JUL-1997) to the EMBL/GenBank/DBJ databases.
CC -1- CATALYTIC ACTIVITY: L-ORNITHINE - PUTRESCINE + CO(2).
CC -1- COFACTOR: PYRIDOXAL-PHOSPHATE.
DR EMBL; Y14231; CAA74609.1; -.
DR PFAM; PF00278; Orn_DAP_Arg_dec; 1.
KW Lyase.
FT NON_TER 1
FT NON_TER 253
SQ SEQUENCE 253 AA; 29489 MW; 4218E85B CRC32;

Query Match 49.4%; Score 40; DB 5; Length 253;
Best Local Similarity 50.0%; Pred. No. 40;
Matches 7; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 4 LVIKINNIRIVVKF 17
Db 4 LCVKCNDEVVVKF 17

RESULT 9
Q02676 PRELIMINARY; PRT; 294 AA.
AC Q02676;
DT 01-NOV-1996 (TRENBLrel. 01, Created)
DT 01-NOV-1996 (TRENBLrel. 01, Last sequence update)
DT 01-NOV-1998 (TRENBLrel. 08, Last annotation update)
DE HYPOTHETICAL 34.0 KD PROTEIN IN COI INTRON 15 REGION.
OS Podospora anserina.
OG Mitochondrion.
OC Eukaryota; Fungi; Ascomycota; Euascomycetes; Pyrenomycetes;
OC Sordariales; Sordariaceae; Podospora.
RN [1]
RP COMPLETE MITOCHONDRIAL GENOME.
RX STRAIN=S;
RX MEDLINE: 90291512.
RA CUMMINGS D.J., MCNALLY K.L., DOMENICO J.M., MATSUURA E.T.;
RT "The complete DNA sequence of the mitochondrial genome of Podospora
RT anserina.";
RL Curr. Genet. 17:375-402(1990).
DR EMBL; X55026; CAA38793.1; -.
DR PFAM; PF00961; Intron_maturase; 2.
KW Hypothetical protein; Mitochondrion.
SQ SEQUENCE 294 AA; 33970 MW; 387D9E8E CRC32;

Query Match 49.4%; Score 40; DB 8; Length 294;
Best Local Similarity 63.6%; Pred. No. 46;
Matches 7; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 2 YKLVIKINNIR 12
Db 91 YRLVIKLSNIQ 101

RESULT 10
O65223 PRELIMINARY; PRT; 579 AA.
AC O65223;

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DT 01-AUG-1998 (TReMBLrel. 07, Created)
 DT 01-AUG-1998 (TReMBLrel. 07, Last sequence update)
 DT 01-NOV-1999 (TReMBLrel. 12, Last annotation update)
 DE F7N22.6 PROTEIN.
 GN F7N22.6.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons;
 OC core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae;
 OC Arabidopsis.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CV. COLUMBIA;
 RA WASHU;
 RL Submitted (APR-1998) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CV. COLUMBIA;
 RA DANTE M.;
 RL Submitted (APR-1998) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CV. COLUMBIA;
 RA WATERSTON R.;
 RL Submitted (APR-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF058825; AAC13580.1; -;
 DR PRINTS: PR00939; C2HCZNFINGER.
 SQ SEQUENCE 579 AA; 66041 MW; 1E97C420 CRC32;

Query Match 49.4%; Score 40; DB 10; Length 579;
 Best Local Similarity 35.3%; Pred. No. 85;
 Matches 6; Conservative 7; Mismatches 4; Indels 0; Gaps 0;
 QY 1 SYKLVIKINIRIVVKF 17
 :||::|:|:|:|
 Db 426 NYKIMRKQNNLIPKF 442

RESULT 11
 Q9XAS5 PRELIMINARY; PRT; 584 AA.
 ID Q9XAS5
 AC Q9XAS5;
 DT 01-NOV-1999 (TReMBLrel. 12, Created)
 DT 01-NOV-1999 (TReMBLrel. 12, Last sequence update)
 DT 01-NOV-1999 (TReMBLrel. 12, Last annotation update)
 DE MAP-7. PROTEIN PRECURSOR.
 GN MAP-7.
 OS Staphylococcus aureus.
 OC Bacteria; Firmicutes; Bacillus/Clostridium group;
 OC Bacillus/Staphylococcus group; Staphylococcus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CLINICAL ISOLATE 7;
 RA HUSSAIN SHAIKH M., HEILMANN C., PETERS G., HERRMAN M.;
 RT "Cloning, sequencing and expression of map-7 from Staphylococcus
 aureus clinical isolate 7";
 RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AJ243790; CAB50820.1; -;
 KW Signal.
 FT SIGNAL 1 30 POTENTIAL.
 FT CHAIN 31 584 POTENTIAL.
 SQ SEQUENCE 584 AA; 65173 MW; 49AE4DA5 CRC32;

Query Match 49.4%; Score 40; DB 2; Length 584;
 Best Local Similarity 62.5%; Pred. No. 86;
 Matches 10; Conservative 3; Mismatches 1; Indels 2; Gaps 1;
 QY 3 KLVIKI--NNIRIVVK 16
 ||||| |::|:|
 Db 185 KLVIKILENNVKSIVK 200

RESULT 12
 Q9ZE84 PRELIMINARY; PRT; 275 AA.
 ID Q9ZE84
 AC Q9ZE84;
 DT 01-MAY-1999 (TReMBLrel. 10, Created)
 DT 01-MAY-1999 (TReMBLrel. 10, Last sequence update)
 DT 01-MAY-1999 (TReMBLrel. 10, Last annotation update)
 DE 2-DEHYDRO-3-DEOXYPHOSPHOCTONATE ALDOLASE (KDSA).
 GN RP062.
 OS Rickettsia prowazekii.
 OC Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;
 OC Rickettsiaceae; Rickettsiae; Rickettsia.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=MADRID E;
 RX MEDLINE: 99039499.
 RA ANDERSSON S.G.E., ZOMORODIPOUR A., ANDERSSON J.O.,
 RA SICHERTZ-PONTEN T., ALSMARK U.C.M., PODOMSKI R.M., NAESLUND A.K.,
 RA ERIKSSON A.S., WINKLER H.H., KURLAND C.G.;
 RT "The genome sequence of Rickettsia prowazekii and the origin of
 RT mitochondria";
 RL Nature 396:133-140(1998).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=MADRID E;
 RA ANDERSSON S.G.E.;
 RL Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AJ235270; CAA14533.1; -;
 SQ SEQUENCE 275 AA; 30245 MW; 3E960290 CRC32;

Query Match 48.1%; Score 39; DB 2; Length 275;
 Best Local Similarity 63.6%; Pred. No. 62;
 Matches 7; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
 QY 3 KLVIKINNIRI 13
 |::|:|:|:|
 Db 2 KVVVKLNINIKI 12

RESULT 13
 Q9Z4S2 PRELIMINARY; PRT; 339 AA.
 ID Q9Z4S2
 AC Q9Z4S2;
 DT 01-MAY-1999 (TReMBLrel. 10, Created)
 DT 01-MAY-1999 (TReMBLrel. 10, Last sequence update)
 DT 01-MAY-1999 (TReMBLrel. 10, Last annotation update)
 DE N-ACETYL-GAMMA-GLUTAMYL-PHOSPHATE REDUCTASE (EC 1.2.1.38).
 GN ARGC.
 OS Thermotoga neapolitana.
 OC Bacteria; Thermotogales; Thermotoga.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=NS-E;
 RA MARC F., WEIGEL P., SANTROT M., SAKANYAN V.;
 RT "Comparative enzymatic analysis of bi- and monofunctional ornithine
 acetyltransferases from thermophilic microorganisms";
 RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=NS-E;
 RA DIMOVA D., WEIGEL P., TAKAHASHI M., MARC F., SAKANYAN V.;
 RT "Gene regulation at high temperatures : characterization of the
 RT autoreglatable arginine repressor of the hyperthermophile Thermotoga
 neapolitana";
 RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AJ009897; CAB38109.1; -;
 KW Oxidoreductase.
 SQ SEQUENCE 339 AA; 37911 MW; 697E3D80 CRC32;

Query Match 48.1%; Score 39; DB 2; Length 339;

Best Local Similarity 35.7%; Pred. No. 76;
Matches 5; Conservative 7; Mismatches 2; Indels 0; Gaps 0;

QY 1 SYKLVIKINNIRIV 14
||:|::|::|:
Db 79 SYRLAMELQNVKII 92

QY 1 SYKLVIKINNIRIVVKF 17
|:|::|:|:
Db 253 SFVLCLRSNNLRVCVIF 269

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Job time: 21499 sec

RESULT 14
Q9XIA4 PRELIMINARY; PRT: 547 AA.
AC Q9XIA4
DT 01-NOV-1999 (TReMBLrel. 12, Created)
DT 01-NOV-1999 (TReMBLrel. 12, Last sequence update)
DE 01-NOV-1999 (TReMBLrel. 12, Last annotation update)
GN F13F21.19
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons;
OC core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae;
OC Arabidopsis.
RN [1]
RP SEQUENCE FROM N.A.
RA FEDERSPIEL N.A., PALM C.J., CONWAY A.B., CONN L., HANSEN N.F.,
RA ALTAFI H., ARAUJO R., HUIZAR L., ROWLEY D., BUEHLER E., DUNN P.,
RA GONZALEZ A., KREMENTSKAIA I., KIM C., LENZ C., LI J., LIU S.,
RA LUROS S., SCHWARTZ J., SHINN P., TORIUMI M., VYSOTSKAIA V.S.,
RA WALKER M., YU G., ECKER J., THEOLOGIS A., DAVIS R.W.,
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC007504; AAD43162.1; -
SQ SEQUENCE 547 AA; 59392 MW; AEC76952 CRC32;

Query Match 48.1%; Score 39; DB 10; Length 547;

Best Local Similarity 50.0%; Pred. No. 1.2e+02;
Matches 8; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 1 SYKLVIKINNIRIVVK 16
|:|:|:|:|:
Db 444 SSKLPFIEINGMKVIE 459

RESULT 15
Q9ZWC2 PRELIMINARY; PRT: 727 AA.
AC Q9ZWC2
DT 01-MAY-1999 (TReMBLrel. 10, Created)
DT 01-MAY-1999 (TReMBLrel. 10, Last sequence update)
DE F21M11.4 PROTEIN.
GN F21M11.4
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons;
OC core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae;
OC Arabidopsis.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. COLUMBIA;
RA FEDERSPIEL N.A., PALM C.J., CONWAY A.B., CONN L., HANSEN N.F.,
RA ALTAFI H., ARAUJO R., HUIZAR L., ROWLEY D., BUEHLER E., DUNN P.,
RA GONZALEZ A., KREMENTSKAIA I., KIM C., LENZ C., LI J., LIU S.,
RA LUROS S., SCHWARTZ J., SHINN P., TORIUMI M., VYSOTSKAIA V.S.,
RA WALKER M., YU G., ECKER J., THEOLOGIS A., DAVIS R.W.,
RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC003027; AAD10669.1; -
SQ SEQUENCE 727 AA; 81342 MW; 5316180B CRC32;

Query Match 48.1%; Score 39; DB 10; Length 727;

Best Local Similarity 47.1%; Pred. No. 1.5e+02;
Matches 8; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

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Date: Feb 8, 2000 10:21 PM
About: Results were produced by the GenCore software, version 4.5,
Copyright (c) 1993-2000 CompuGen Ltd.

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gb_hg3:AC009186	+	49.00	107.53	575.94	48600	Oryza sativa genomic
gb_hg4:AC010873	-	49.00	98.26	1.9e+03	127240	Oryza sativa genomic
gb_hg3:AC011386	-	49.00	96.58	2.3e+03	217175	Oryza sativa genomic
gb_in2:AF021084	-	48.00	138.56	10.76	465	AF021084 Dianous nitidulus cyt
gb_in1:MSQNCAR	-	48.00	112.94	287.55	15455	L04272 Anopheles quadrimacul
gb_hg4:AC012417	-	48.00	103.53	962.00	56025	AC012417 Homo sapiens chromo
em_in:AC004375	-	48.00	100.28	1.5e+03	87325	AC004375 Drosophila melanoga
gb_in:AC007765	-	48.00	95.70	2.6e+03	163403	AC007765 Drosophila melanoga
gb_pl2:CNS019CV	-	47.00	131.82	25.55	780	AL111479 Botrytis cinerea strai
gb_ba1:BTGP3REP	+	47.00	112.23	315.09	11365	Y11173 B.thuringiensis plasmi
gb_hg4:AC010688	-	47.00	97.88	2.0e+03	80958	AC010688 Drosophila melanoga
gb_pl1:AB006598	-	47.00	97.56	2.1e+03	84510	AB006598 Arabidopsis thaliana
gb_hg4:AC008308	-	47.00	93.30	3.6e+03	151373	AC008308 Drosophila melanoga
gb_pl2:HSAC02064	-	47.00	93.07	3.7e+03	156214	AC002064 Human BAC clone RGO
gb_hg5:AC013460	+	47.00	92.74	3.8e+03	163346	AC013460 Homo sapiens clone
gb_hg7:AC009555	-	47.00	92.68	3.9e+03	164713	AC009555 Homo sapiens chrom
gb_hg4:AC010859	-	47.00	90.45	5.1e+03	223594	AC010859 Homo sapiens clone
gb_hg2:AC006889	-	47.00	89.15	6.1e+03	267118	AC006889 Caenorhabditis eleg
gb_v1:PHV1VGB	-	46.00	118.84	134.96	3069	Z68147 Phocid herpesvirus type
gb_pl2:ATF1111	+	46.00	93.14	3.6e+03	103150	AL079347 Arabidopsis thalian
gb_pl1:ATT22BA	-	46.00	92.77	3.8e+03	108598	AL049876 Arabidopsis thalian
gb_hg2:AC008311	-	46.00	92.67	3.9e+03	109826	AC008311 Drosophila melanoga
gb_hg2:AC007194_3	-	46.00	92.67	3.9e+03	110000	Continuation (4 of 5) of AC0
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gb_hg4:AC011177	+	46.00	89.55	5.8e+03	158660	AC011177 Homo sapiens clone
gb_hg1:AP000811	+	46.00	88.97	6.2e+03	182508	AP000811 Homo sapiens chrom
gb_pl4:AC007364	-	46.00	88.27	6.8e+03	200908	AC007364 Homo sapiens clone
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gb_sts:G53007	+	45.00	134.79	17.45	231	G53007 SHGC-81794 Human Homo sa
gb_sts:G53006	+	45.00	134.48	18.15	241	G53006 SHGC-81793 Human Homo sa
gb_ov:GGRNACP49	+	45.00	120.82	104.66	1561	X84806 G.gallus mRNA for CP49
gb_pl4:AF137131	+	45.00	108.04	539.34	8970	AF137131 Homo sapiens downstre
gb_ba2:AE001116	-	45.00	107.27	595.14	9363	AE001116 Borrelia burgdorferi
gb_in2:MSQNTCC	-	45.00	104.11	893.27	15363	L20934 Anopheles gambiae comp
gb_v1:MHVGENE1	-	45.00	101.55	1.2e+03	21798	M55148 Murine coronavirus ope
gb_ba2:AF036485	+	45.00	96.61	2.3e+03	42810	AF036485 Plasmid pNZ4000, con
gb_in1:CELB0563	+	45.00	96.45	2.4e+03	43801	U28740 Caenorhabditis elegans
gb_in2:AF160864	+	45.00	95.88	2.6e+03	47296	AF160864 Tetrahymena pyriform
gb_pl2:ATAC007584	+	45.00	91.63	4.4e+03	84592	AC007584 Arabidopsis thaliana
gb_pl2:ATAC006918	+	45.00	90.10	5.4e+03	104292	AC006918 Arabidopsis thalian

gb_hg2:AC008209 - 45.00 88.84 6.3e+03 123872 ! AC008209 Drosophila melan
gb_hg5:AC010836 + 45.00 86.81 8.2e+03 163667 ! AC010836 Homo sapiens clo
gb_hg5:AC012594 + 45.00 86.75 8.3e+03 164997 ! AC012594 Homo sapiens clo

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seq_documentation_block:

LOCUS AP000399 154180 bp DNA PLN 03-DEC-1999
DEFINITION Oryza sativa genomic DNA, chromosome 6, clone:P0535G04.

ACCESSION AP000399

VERSION AP000399.1 GI:5803242

KEYWORDS

SOURCE Oryza sativa (cultivar:Nipponbare) DNA, clone:P0535G04.

ORGANISM

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
euphyllophytes; Spermatophyta; Magnoliophyta; Liliopsida; Poales;
Poaceae; Oryza.

REFERENCE

1 (bases 1 to 154180)
Sasaki,T., Matsumoto,T. and Yamamoto,K.

Oryza sativa nipponbare (GA3) genomic DNA, chromosome 6, PAC
clone:P0535G04

TITLE

Published Only in DataBase (1999) In press

JOURNAL

2 (bases 1 to 154180)

AUTHORS

Sasaki,T., Matsumoto,T. and Yamamoto,K.

TITLE

Submitted (25-AUG-1999) to the DDBJ/EMBL/GenBank databases. Takuji
Sasaki, National Institute of Agrobiological Resources, Rice Genome
Research Program; Kanno dai 2-1-2, Tsukuba, Ibaraki 305-8602, Japan
(E-mail:tsasaki@abrr.affrc.go.jp,
URL:http://www.dna.affrc.go.jp:82/, Tel:81-298-38-7441,
Fax:81-298-38-7468)

COMMENT

The orientation of the sequence is from T7 to SP6 of the PAC clone.
Genes were predicted from the integrated results of the
following:GENSCAN1.0, BLASTX2.0, BLASTX2.0 as well as
SplicePredictor (October1998 version). The genomic sequence was
searched against the non-redundant database NRP (PIR,SWISSPROT,
GENPEPT, PDB) from MAFF DNABank and the cDNA sequence database at
RGP. Protein similarities of the coding regions were searched
against NRP with BLASTX2.0. ESTs represent the identified cDNA
sequences using BLASTX1.4 with the corresponding DDBJ accession no.
and RGP clone ID.

FEATURES

Location/Qualifiers

1..154180
/organism="Oryza sativa"
/cultivar="Nipponbare"
/db_xref="taxon:4530"
/chromosome="6"
/clone="P0535G04"
complement(10850..10856)
/note="ESTs AU078033(R0160),D23790(R0160) correspond to a
region of the predicted gene; hypothetical protein"

CDS

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/db_xref="GI:5803243"
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GGPPTFGEVLSRLDRDSATIV"
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/note="similar to hexose carrier protein HEX6 sRCCHCP_1
(Q07423)"

CDS

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FAASRVAGRGKRRFLLGGLGAAVGAAGVSDIIVLIGRLVGLGUGFANQAVP
LYSEMAPRMRGAFSGFQVGVGALAAVINGTEKIRGGWGVSLAAAPVAG
LLTIGALFLPTEPNSLIQQQKVERCDVQLLKIRGADDDVDELDTVAANSATAPAG
GGGLMLLORRRVPLQAAVMTIFFQOVTGGINAIFAPVLLRTIGMGESASLLSAV
VTGVVGATLLSFEAFDGRGRTFLFAGGQMLASQVLGGINAAKLDDGGVSRW
AAALILIAVAGFGWSGVLGVPFLEVRSAQSQVTAISFVTFVFAQAF
LAMLCURRVRGPIEFVLAAMTAFVLLLPETKGVPIEEVAGVWRGHWFSRVVGG
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complement(join(16352..16617,17437..17488,18513..19025))

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 DVPDAFVLGAGHEGKEAAAYWADVSEKRGAGGDSAFVDLRLKAVDMDRK
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 NOICKGVKRRQISADLKIESEPAPFVPGPYAIAHLISSWAFEGAPKAPSSFNL
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 complement(join(21523..21536,22175..22245,22419..22771))
 /notes="ESTs AU077984(C62969),D41648(S4289),
 AU063584(C62969) correspond to a region of the predicted
 gene: similar to putative Ser/Thr protein kinase
 (AC003105)"
 /codon_start=1
 /protein_id="BAA83556.1"
 /db_xref="GI:5803246"
 /translation="MNIQRKPGDWCKSCQHLNFRSDYCORCHTQPDQLDGDGYVP
 GGLTSLDIRPDCWYCNCGVNFASRSCFKCGAIVKDLDPAGGGGVANGDFARALDS
 SAVRQKAGDWICTRPGCNVHNFASRIEYECNAPREAGNVK"
 complement(join(29617..29738,29858..29936,30110..30171,
 30324..30396))
 /notes="similar to OSENOD93a gene for early nodulin
 (AB018375)"
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 join(30628..30744,32792..32887)
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 nodulin (AB018375)"
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 /db_xref="GI:5803249"
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 FOGTGRPHPAFFRP"
 complement(join(38870..39091,39193..39254,39364..39427))
 /notes="EST AU077941(C12908) corresponds to a region of the
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 nodulin (AB018375)"
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 /db_xref="GI:5803250"
 /translation="MSTVTRAYLDOKLALAKRCSRENTLAGAKAAVATVASVPTLA
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 44305..44333))
 /notes="hypothetical protein"
 /codon_start=1
 /protein_id="BAA83561.1"
 /db_xref="GI:5803251"
 /translation="MTNYSYSTRNGGGGGDEAEGNGGGGGWGAATAVAGSSCGGL
 VTPDGTGTLKLLIWTSTYGTITLLIIVAFTSALRKEELAGDEHLHVSPLPAAP
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 FMPLCVG"
 join(45402..45435,46888..46954,46962..47139)
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/translation="MHPYSGGVAVRPRQSGYPPVRAPASTLLPLRLAFSTATVP
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 51205..51338,51584..51770)
 /notes="ESTs AU068856(C50756),AU077979(C61370) correspond
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 protease (AF097709)"
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 /db_xref="GI:5803253"
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 RVQVGFPOSALLESPLHGVLAVGHDTGEIMVETVELAGDSKVSDEDDRLHCKISKP
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 SILNRNVVALASNGFFIEMSGSKMILTASLRVDSGDENKIDENUKIRKVFNNQCKE
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 /notes="ESTs C97429(C60159),D22427(C11106),
 AU078031(E31854),D15683(C1084) correspond to a region of
 the predicted gene: hypothetical protein"
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 SCFLSHALEQLEIRYCDRIVCLKVPCLQRLISLKVFCDNLKLIENAPNVSTFA
 FOGDKTQLKGETLQWKSCLWVRSGVYHARALPSIMENLAKMSKETAFAFKL
 CSKFLRLHSIALIGYPAYDYSIASYIHAAPSLLETFLYLMORYQNVQNSIFAHPA
 DARSREGHSLKSVRYTSFISVSLVELTCHILESTSLCCLILDASQTFRCDDTP
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 complement(join(58107..58328,58503..58564,58688..58751))
 /notes="ESTs C98096(C0688),C98097(C0688) correspond to a
 region of the predicted gene: similar to OSENOD93a gene
 for early nodulin (AB018375)"
 /codon_start=1
 /protein_id="BAA83565.1"
 /db_xref="GI:5803255"
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 QGTGRPHPAFFRP"
 complement(join(64318..64539,64634..64695,64782..64845))
 /notes="ESTs C98280(C1391),D15843(C1391) correspond to a
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 for early nodulin (AB018375)"
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 complement(join(67321..67542,67657..67718,67829..67895))
 /notes="EST C97982(C0324) corresponds to a region of the
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DEFINITION	Homo sapiens chromosome unknown clone NH012N16, WORKING DRAFT				
ACCESSION	AC010873				
VERSION	AC010873.2 GI:6139274				

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repeat_region 13461..13532 /rpt_family="MIR"
repeat_region 14028..14317 /rpt_family="Alu"
repeat_region 15788..15873 /rpt_family="MIR"
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repeat_region 17036..17079 /rpt_family="TGGA)n"
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repeat_region 26531..26718 /rpt_family="MERL_type"
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repeat_region 30412..30705 /rpt_family="Alu"
repeat_region 30706..30971 /rpt_family="L1"
repeat_region 31074..31103 /rpt_family="(CA)n"
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    DEFINITION Homo sapiens chromosome 5 clone CIT978SKB_15P5, *** SEQUENCING IN
    PROGRESS ***, 45 unordered pieces.
    ACCESSION AC011386
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    KEYWORDS HTG; HTGS_PHASE1.
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SOURCE human.
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 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 217175)
 REFERENCE DOE Joint Genome Institute.
 AUTHORS Sequencing of Human Chromosome 5
 JOURNAL Unpublished
 2 (bases 1 to 217175)
 REFERENCE DOE Joint Genome Institute.
 AUTHORS Direct Submission
 JOURNAL Submitted (06-Oct-1999) Production Sequencing Facility, DOE Joint
 Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
 www.tgi.doe.gov.
 COMMENT * NOTE: This is a 'working draft' sequence. It currently
 * consists of 45 contigs. The true order of the pieces
 * is not known and their order in this sequence record is
 * arbitrary. Gaps between the contigs are represented as
 * runs of N, but the exact sizes of the gaps are unknown.
 * This record will be updated with the finished sequence
 * as soon as it is available and the accession number will
 * be preserved.
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 encoding mitochondrial protein, partial cds.
 ACCESSION AF021084
 VERSION AF021084.1 GI:4103228
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 SOURCE Dianous nitidulus.
 ORGANISM Mitochondrion Dianous nitidulus


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seq_name: gb_htg4:AC012417

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DEFINITION Homo sapiens chromosome 18 clone 408_H_20 map 18, LOW-PASS SEQUENCE
SAMPLING.
ACCESSION AC012417
VERSION AC012417.1 GI:6136401
KEYWORDS HTG; HTGS_PHASE0.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 56025)
AUTHORS Birren,B., Linton,L., Nusbaum,C. and Lander,E.
TITLE Homo sapiens chromosome 18, clone 408_H_20
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 56025)
AUTHORS Birren,B., Linton,L., Nusbaum,C., Lander,E., Allen,N., Anderson,M.,
Baldwin,J., Barna,N., Beckerly,R., Boguslavsky,L., Bouckhalter,B.,
Brown,A., Castle,A., Collangelo,M., Collins,S., Collamore,A.,
Cooke,P., Dearellano,K., Dewar,K., Domino,M., Donelan,L., Doyle,M.,
Ferreira,P., FitzHugh,W., Forrest,C., Funke,R., Gage,D.,
Gallagan,J., Gardyna,S., Grant,G., Hagos,B., Heaford,A., Horton,L.,
Howland,J.C., Johnson,R., Jones,C., Kann,L., Karatas,A., Klein,J.,
Lehoczky,J., Lieu,C., Locke,K., Macdonald,P., Marquis,N.,

```

McEwan, P., McGurk, A., McKernan, K., McLaughlin, J., Meldrim, J.,
Morrow, J., Naylor, J., Norman, C. H., O'Connor, T., O'Donnell, P.,
Peterson, K., Pollara, V., Riley, R., Roy, A., Santos, R., Severy, P.,
Stange-Rothmann, N., Stojanovic, N., Subramanian, A., Talamas, J.,
Tesfaye, S., Tirrell, A., Vassiliev, H., Vo, A., Wheeler, J., Wu, X.,
Wyman, D., Ye, W. J., Zimmer, A. and Zody, N.
Direct Submission
Submitted (27-OCT-1999) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
All repeats were identified using RepeatMasker: Smit, A.F.A. &
Green, P. (1996-1997)
<http://ftp.genome.washington.edu/RM/RepeatMasker.html>.

* NOTE: This record contains 70 individual
* sequencing reads that have not been assembled into
* contigs. Runs of N are used to separate the reads
* and the order in which they appear is completely
* arbitrary. Low-pass sequence sampling is useful for
* identifying clones that may be gene-rich and allows
* overlap relationships among clones to be deduced.
* However, it should not be assumed that this clone
* will be sequenced to completion. In the event that
* the record is updated, the accession number will
* be preserved.

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FEATURES

Location/Qualifiers

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ORIGIN

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Ratio:	3.692	Gaps:	0
Percent Similarity:	81.250	Percent Identity:	62.500

alignment block:

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seq_name: em_in:AC004375

seq_documentation_block:

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ID AC004375 standard; DNA; INV; 87325 BP.
XX AC004375; AC003631; AC003632; AC003633; AC003634; AC003635;
SV AC004375.1

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XX 13-MAR-1998 (Rel. 55, Created)
DT 08-JUL-1998 (Rel. 56, Last updated, Version 9)
XX Drosophila melanogaster DNA sequence (P1 DS02190 (D82)), complete
DE sequence.
XX HTG.

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XX Drosophila melanogaster (fruit fly)
OS Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea;
OC Drosophilidae; Drosophila.

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RN [1]
RA Celniker S.E., George R.A., Galle R.F., Hoskins R.A., Svirskas R.R.,
RA Harris N.L., Agbayani A., Arcaina T.T., Baxter E., Blazej R.G., Chavez C.,
RA Chew M., Doyle C.M., Farfan D.E., Flanagan J., Houston K.A., Hummasti S.R.,
RA Karra K., Kearney L., Kim S.H., Lee B., Lomotan M.A., Mak J., Mazda P.,
RA Mok M.S., Moshrefi A.R., Moshrefi M., Nixon K., Pacleb J.M., Park S.,
RA Pfeiffer B., Punch E., Snir E., Twomey B., Wan K.H., Whitelaw K.R., Yee A.,
RA Zhang R., Zieran L.L., Kimmel B.

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"Sequencing of Drosophila chromosome, region 23c1-23c5";
Unpublished.

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RT
RL
XX
RN
RP
RA Celniker S.E., George R.A., Galle R., Svirskas R.R., Hoskins R.A.,
RA Agbayani A., Arcaina T.T., Baxter E., Blazej R.G., Chavez C., Chew M.,
RA Doyle C.M., Farfan D.E., Flanagan J., Houston K.A., Hummasti S.R.,
RA Karra K., Kearney L., Kim S.H., Lee B., Lomotan M.A., Mak J., Mazda P.,
RA Mok M.S., Moshrefi A.R., Moshrefi M., Nixon K., Pacleb J.M., Park S.,
RA Pfeiffer B., Punch E., Snir E., Twomey B., Wan K.H., Whitelaw K.R., Yee A.,
RA Zhang R., Zieran L.L., Kimmel B.E.;

```

Submitted (07-MAR-1998) to the EMBL/GenBank/DBJ databases.

RL Drosophila Genome Center, Lawrence Berkeley Laboratory, MS 64-121,
Berkeley, CA 94720, USA

Sequence submitted by:

CC Berkeley Drosophila Genome Project
CC Lawrence Berkeley National Laboratory, MS 64-121
CC Berkeley, CA 94720

CC For further information about this sequence, including its location
CC and relationship to other sequences, please visit our sequence
CC archive Web site (<http://fruitfly.berkeley.edu/sequence/>) or send
CC email to drosophila@hg.lbl.gov.
CC Library location: 78-23.

XX Key Location/Qualifiers

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Quality:	48.00	Length:	12
Ratio:	4.000	Gaps:	0
Percent Similarity:	100.000	Percent Identity:	66.667

alignment_block:

US-08-653-294-22 x AC004375/rev ..

Align seg 1/1 to reverse of: AC004375 from: 1 to: 87325

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seq_documentation_block:

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LOCUS AC007765 163403 bp DNA INV 09-JUN-1999
DEFINITION Drosophila melanogaster, chromosome 2L, region 23c1-23c5, P1 clones
DS02190 and DS0906, complete sequence.
ACCESSION AC007765 AC004375 AC003631 AC003632 AC003633 AC003634 AC003635
AC004154 AC002028 AC002976 AC002029 AC002977 AC002030 AC002031
AC002032 AC002033 AC002562 AC002034 AC002035
VERSION AC007765.1 GI:5030435
KEYWORDS HTG.
SOURCE fruit fly.
ORGANISM Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

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REFERENCE

1 (bases 1 to 163403)

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AUTHORS Celniker S.E., Agbayani A., Arcaina T.T., Baxter E., Blazej R.G.,
Belenkoff, C., Champe, M., Chavez, C., Chew, M., Ciesiolka, L.,
Doyle, C.M., Farfan D.E., Galle, R., George, R.A., Harris, N.L.,

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  Ratio: 3.357        Gaps: 0
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Align seg 1/1 to: BTPGI3REP from: 1 to: 11365

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LOCUS      AC010688      80958 bp      DNA              16-OCT-1999
DEFINITION Drosophila melanogaster chromosome 3L/73B5 clone RPC198-11G5, ***
SEQUENCING HTG; HTGS_PHASE1.
ACCESSION  AC010688
VERSION    AC010688.3  GI:6056139
KEYWORDS   HTG; HTGS_PHASE1.
SOURCE     fruit fly.
ORGANISM   Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
REFERENCE  Muzny,D.M., Adams,C., Bailey,M., Barbara,J., Blankenburg,K.,
AUTHORS    Bodota,B., Bouck,J., Bowie,S., Brooks,A., Buhay,C., Bunac,C.,
            Burkett,C., Burrows,J., Carter,M., Chacko,J., Chen,Z., Cox,C.,
            David,R., Deigado,O., Deshazo,D., Ding,Y., Doman-Rashid,N.,
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            Taylor,T., Vasquez,L., Vinson,R., Vo,Q., Wambah,M., Watlington,S.,
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TITLE
JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
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Wrensford,G., Yu,W., Zhou,X., Nelson,D. and Gibbs,R.
Direct Submission
Unpublished
2 (bases 1 to 80958)
Worley,K.C.
Direct Submission
Submitted (18-SEP-1999) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
On Oct 16, 1999 this sequence version replaced gi:5916430.
* NOTE: This is a 'working draft' sequence. It currently
* consists of 56 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence.
* as soon as it is available and the accession number will
* be preserved.
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* 799: contig of 799 bp in length
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* 5601: contig of 1063 bp in length
* 6664: contig of 1051 bp in length
* 7715: contig of 1297 bp in length
* 9012: contig of 1398 bp in length
* 10410: contig of 881 bp in length
* 11291: contig of 1222 bp in length
* 12513: contig of 865 bp in length
* 13378: contig of 773 bp in length
* 14151: contig of 1240 bp in length
* 15391: contig of 1355 bp in length
* 16746: contig of 1378 bp in length
* 18124: contig of 1348 bp in length
* 19472: contig of 1219 bp in length
* 20691: contig of 1051 bp in length
* 21742: contig of 831 bp in length
* 22573: contig of 625 bp in length
* 23199: contig of 838 bp in length
* 24037: contig of 1495 bp in length
* 25332: contig of 1135 bp in length
* 26667: contig of 922 bp in length
* 27589: contig of 1236 bp in length
* 28824: contig of 1194 bp in length
* 30018: contig of 973 bp in length
* 30991: contig of 1496 bp in length
* 32489: contig of 873 bp in length
* 33362: contig of 1261 bp in length
* 34623: contig of 1539 bp in length
* 36162: contig of 1693 bp in length
* 37855: contig of 1214 bp in length
* 39089: contig of 1561 bp in length
* 40630: contig of 936 bp in length
* 42530: contig of 1408 bp in length
* 43466: contig of 772 bp in length
* 45646: contig of 1881 bp in length
* 47527: contig of 2132 bp in length
* 49659: contig of 1817 bp in length
* 51476: contig of 1559 bp in length
* 53035: contig of 2220 bp in length
* 55255: contig of 1474 bp in length
* 56729: contig of 1732 bp in length
* 58451: contig of 2092 bp in length
* 60553: contig of 2280 bp in length
* 62833: contig of 1707 bp in length
* 64540: contig of 2241 bp in length
* 66781: contig of 2650 bp in length
* 69431: contig of 2076 bp in length
* 71507: contig of 3212 bp in length
* 74719: contig of 3003 bp in length
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* 77723 80958: contig of 3236 bp in length.
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 /db_xref="taxon:7227"
 /chromosome="3L/73B5"
 /clone="RPCI98-11G5"
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 ORIGIN

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 Ratio: 3.615 Gaps: 0
 Percent Similarity: 76.471 Percent Identity: 47.059
 alignment_block:
 US-08-653-294-22 x AC010688 ..
 Align seg 1/1 to: AC010688 from: 1 to: 80958
 1 SerTyrLysLeuValIleLysIleAsnIleArgIleValValLys 17
 |||||:||||| ||| |||||:|||||:||||| |||||
 32302 TCCTACAGCCCTTTATACATATACAACTTACAGTTATTACAAATT 32351

17 e 17

32352 T 32352

seq_name: gb_pl1:AB006698

seq_documentation_block:

LOCUS AB006698 84510 bp DNA PLN 20-NOV-1999
 DEFINITION Arabidopsis thaliana genomic DNA, chromosome 5, p1 clone: MCL19,
 complete sequence.
 ACCESSION AB006698
 VERSION AB006698.1 GI:2351063
 KEYWORDS HTG.
 SOURCE Arabidopsis thaliana (strain:Columbia) DNA, clone_lib:Mitsui P1
 clone:MCL19.
 ORGANISM Arabidopsis thaliana
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons; core
 eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae;
 Arabidopsis.
 REFERENCE 1 (sites)
 AUTHORS Kotani,H., Nakamura,Y., Sato,S., Kaneko,T., Asamizu,E., Miyajima,N.
 and Tabata,S.

TITLE Structural analysis of Arabidopsis thaliana chromosome 5. II.
 Sequence features of the regions of 1,044,062 bp covered by
 thirteen physically assigned p1 clones
 JOURNAL DNA Res. 4 (4), 291-300 (1997)

MEDLINE 98069011
 REFERENCE 2 (bases 1 to 84510)
 AUTHORS Nakamura,Y.
 TITLE Direct Submission
 JOURNAL Submitted (22-AUG-1997) to the DDBJ/EMBL/Genbank databases.
 Yasukazu Nakamura, Kazusa DNA Research Institute, Laboratory of
 Gene Structure 2; 1532-3, Yana, Kisarazu, Chiba 292, Japan
 (E-mail:ynakamura@kazusa.or.jp, Tel:++81-438-52-3935,
 Fax:++81-438-52-3934)

FEATURES Location/Qualifiers
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 /strain="Columbia"
 /db_xref="taxon:3702"
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 BASE COUNT 28311 a 14338 c 14358 g 27503 t
 ORIGIN

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 Align seg 1/1 to reverse of: AB006698 from: 1 to: 84510

4 LeuValIleLysIleAsnIleArgIleValValLys 16

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seq_name: gb_htg4:AC008308

seq_documentation_block:

LOCUS AC008308 151373 bp DNA HTG 20-OCT-1999
 DEFINITION Drosophila melanogaster chromosome 3 clone BACR10M16 (D743) RPCI-98
 10.M.16 map 93C-93D strain y; cn bw sp, *** SEQUENCING IN PROGRESS
 ***, 186 unordered pieces.

ACCESSION AC008308

VERSION AC008308.3 GI:6087905

KEYWORDS HTG; HTGS-PHASE1.

SOURCE fruit fly.

ORGANISM Drosophila melanogaster

Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
 Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

REFERENCE 1 (bases 1 to 151373)

AUTHORS

Celniker,S.E., Agbayani,A., Arcaina,T.T., Baxter,E., Blazej,R.G.,
 Butenhoff,C., Champe,M., Chavez,C., Chew,M., Ciesiolka,L.,
 Doyle,C.M., Farfan,D.E., Galle,R., George,R.A., Harris,N.L.,
 Hoskins,R.A., Houston,K.A., Hummasti,S.R., Karra,K., Kearney,L.,
 Kim,E., Lee,B., Lewis,S., Li,P., Lomotan,M.A., Mazda,P.,
 Moshrefi,A.R., Moshrefi,M., Nixon,K., Pacleb,J.M., Park,S.,
 Pfeiffer,B., Poon,L., Sequeira,A., Sethi,H., Snir,E.,
 Svirskas,R.R., Wan,K.H., Weinburg,T., Zhang,R., Zieran,L.L. and
 Rubin,G.M.

Sequencing of Drosophila melanogaster

TITLE

JOURNAL

REFERENCE

AUTHORS

2 (bases 1 to 151373)
 Celniker,S.E., Agbayani,A., Arcaina,T.T., Baxter,E., Blazej,R.G.,
 Butenhoff,C., Champe,M., Chavez,C., Chew,M., Ciesiolka,L.,
 Doyle,C.M., Farfan,D.E., Galle,R., George,R.A., Harris,N.L.,
 Hoskins,R.A., Houston,K.A., Hummasti,S.R., Karra,K., Kearney,L.,
 Kim,E., Lee,B., Lewis,S., Li,P., Lomotan,M.A., Mazda,P.,
 Moshrefi,A.R., Moshrefi,M., Nixon,K., Pacleb,J.M., Park,S.,
 Pfeiffer,B., Poon,L., Sequeira,A., Sethi,H., Snir,E.,
 Svirskas,R.R., Wan,K.H., Weinburg,T., Zhang,R., Zieran,L.L. and
 Rubin,G.M.

Direct Submission

TITLE

JOURNAL

COMMENT

Submitted (02-AUG-1999) Drosophila Genome Center, Lawrence Berkeley
 Laboratory, MS 64-121, Berkeley, CA 94720, USA
 On Oct 20, 1999 this sequence version replaced gi:6067129.
 For further information about this sequence, including its location
 and relationship to other sequences, please visit our sequence
 archive Web site (<http://www.fruitfly.org/sequence/>) or send email
 to bagp@fruitfly.berkeley.edu. All contigs in this submission meet
 the following cutoffs: length >= 200 bases.
 * NOTE: This is a 'working draft' sequence. It currently
 * consists of 186 contigs. The true order of the pieces
 * is not known and their order in this sequence record is
 * arbitrary. Gaps between the contigs are represented as
 * runs of N, but the exact sizes of the gaps are unknown.
 * This record will be updated with the finished sequence.
 * as soon as it is available and the accession number will
 * be preserved.

* 1 270: contig of 270 bp in length
 * 271 350: gap of unknown length
 * 351 1076: contig of 726 bp in length
 * 1077 1156: gap of unknown length
 * 1157 1787: contig of 631 bp in length

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1868	2168: contig of 301 bp in length	32579	32658: gap of unknown length
2169	2248: gap of unknown length	33384	3384: contig of 726 bp in length
2249	2801: contig of 553 bp in length	33464	3464: gap of unknown length
2802	2881: gap of unknown length	33465	35293: contig of 1829 bp in length
2882	3182: contig of 301 bp in length	33573	35373: gap of unknown length
3183	3262: gap of unknown length	35294	36220: contig of 847 bp in length
3263	3885: contig of 623 bp in length	36221	36300: gap of unknown length
3886	3965: gap of unknown length	36301	37223: contig of 1023 bp in length
3966	4450: contig of 485 bp in length	37324	37403: gap of unknown length
4451	4530: gap of unknown length	38441	38441: contig of 1038 bp in length
4531	5295: contig of 765 bp in length	38442	38521: gap of unknown length
5296	5375: gap of unknown length	38522	39603: contig of 1082 bp in length
5376	6199: contig of 824 bp in length	39604	39683: gap of unknown length
6200	6279: gap of unknown length	39684	40530: contig of 847 bp in length
6280	7185: contig of 906 bp in length	40531	40610: gap of unknown length
7186	7265: gap of unknown length	40611	41832: contig of 1222 bp in length
7266	7844: contig of 579 bp in length	41833	41912: gap of unknown length
7845	7924: gap of unknown length	41913	43390: contig of 1478 bp in length
7925	8688: contig of 764 bp in length	43391	43470: gap of unknown length
8689	8768: gap of unknown length	43471	44364: contig of 894 bp in length
8769	9397: contig of 629 bp in length	44365	44444: gap of unknown length
9398	9477: gap of unknown length	44445	45927: contig of 1483 bp in length
9478	9994: contig of 517 bp in length	45928	46007: gap of unknown length
9995	10074: gap of unknown length	46008	47580: contig of 1573 bp in length
10075	10705: contig of 631 bp in length	47581	47660: gap of unknown length
10706	10785: gap of unknown length	47661	48605: contig of 945 bp in length
10786	11807: contig of 1022 bp in length	48606	48685: gap of unknown length
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11888	12654: contig of 767 bp in length	50086	50165: gap of unknown length
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12735	13432: contig of 698 bp in length	51445	51524: gap of unknown length
13433	13512: gap of unknown length	51525	53165: contig of 1641 bp in length
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15263	15342: gap of unknown length	54715	56896: contig of 2182 bp in length
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16039	16118: gap of unknown length	56977	58340: contig of 1364 bp in length
16119	17043: contig of 925 bp in length	58341	58420: gap of unknown length
17044	17123: gap of unknown length	58421	59885: contig of 1565 bp in length
17124	17775: contig of 652 bp in length	59886	60065: gap of unknown length
17776	17855: gap of unknown length	60066	63185: contig of 3120 bp in length
17856	18158: contig of 303 bp in length	63186	63265: gap of unknown length
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18239	18767: contig of 529 bp in length	65462	65541: gap of unknown length
18768	18847: gap of unknown length	65542	67549: contig of 2008 bp in length
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20272	20785: contig of 514 bp in length	70855	70934: gap of unknown length
20786	20865: gap of unknown length	70935	75464: gap of unknown length
20866	21878: contig of 1013 bp in length	75465	75544: gap of unknown length
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21959	22626: contig of 668 bp in length	76232	78311: gap of unknown length
22627	22706: gap of unknown length	76312	78866: contig of 555 bp in length
22707	23349: contig of 643 bp in length	76867	76946: gap of unknown length
23350	23429: gap of unknown length	76947	77554: contig of 608 bp in length
23430	24076: contig of 647 bp in length	77555	77634: gap of unknown length
24077	24156: gap of unknown length	77635	78331: contig of 597 bp in length
24157	25336: contig of 1180 bp in length	78232	78311: gap of unknown length
25337	25416: gap of unknown length	78312	78927: contig of 616 bp in length
25417	26672: contig of 1256 bp in length	78928	79007: gap of unknown length
26673	26752: gap of unknown length	79008	79649: contig of 642 bp in length
26753	27512: contig of 760 bp in length	79650	79729: gap of unknown length
27513	27592: gap of unknown length	79730	80365: contig of 636 bp in length
27593	28805: contig of 1213 bp in length	80366	80445: gap of unknown length
28806	28885: gap of unknown length	80446	80780: contig of 335 bp in length
28886	29725: contig of 840 bp in length	80781	80860: gap of unknown length
29726	29805: gap of unknown length	80861	81485: contig of 625 bp in length
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OM of: US-08-653-294-22 to: N_Geneseq_36:* out_format : pfs

Date: Feb 8, 2000 7:30 PM

About: Results were produced by the Gencore software, version 4.5,
Copyright (c) 1993-2000 CompuGen Ltd.

Command line parameters:

-MODEL=frame+p2n.model -DEV=xlp
-O=/cgn1_1/USPTO_spool/US08653294/runat_04022000_160701_15807/app_query.fasta.2
-DB=N_Geneseq_36 -QFMT=fastap -SUFFIX=eng -GAPOP=12.000
-GAPEXT=4.000 -MINMATCH=0.100 -LOOPEXT=0.000
-OGAPOP=4.500 -OGAPEXT=0.050 -XGAPOP=10.000 -XGAPEXT=0.500
-FGAPOP=6.000 -FGAPEXT=7.000 -YGAPOP=10.000 -YGAPEXT=0.500
-DELOP=6.000 -DELEXT=7.000 -START=1 -MATRIX=blossum62
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR_SCORE=pct
-ALIGN=15 -MODE=LOCAL -OUTFMT=pfs -NORM=ext -MINLEN=0
-MAXLEN=1000000 -USER=US08653294 -NCPU=6 -ICPU=3 -NO_XLPXY -WAIT
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Search information block:

Query: US-08-653-294-22
Query length: 17
Database: N_Geneseq_36:*
Database sequences: 311585
Database length: 125096042
Search time (sec): 873.190000

score_list:

Sequence	Strd Orig	Zscore	EScore	Len	Documentation
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N_Geneseq_36:V21209_08	+ 42.00	77.22	1.1e+04	110000	Continuation (9 of 17) of
N_Geneseq_36:X20248_00	+ 42.00	77.22	1.1e+04	110000	Borrelia burgdorferi polyn
N_Geneseq_36:X20248_03	+ 42.00	77.22	1.1e+04	110000	Continuation (4 of 10) of
N_Geneseq_36:X20248_04	+ 41.50	112.19	119.79	1673	B. fragilis DNA probe BF-35.1
N_Geneseq_36:X20248_05	+ 41.50	75.67	1.3e+04	110000	Continuation (5 of 10) of
N_Geneseq_36:X20248_06	+ 41.50	126.74	18.52	116277	Borrelia burgdorferi polynuc
N_Geneseq_36:X20248_07	+ 41.00	115.35	79.80	974	DNA encoding a Staphylococcus a
N_Geneseq_36:X20248_08	+ 41.00	113.58	100.23	1194	Staphylococcus aureus contig S
N_Geneseq_36:X20248_09	+ 41.00	97.51	786.47	7528	Enterococcus faecalis genome c
N_Geneseq_36:X20248_10	+ 41.00	88.49	2.5e+03	21170	Polynucleotide sequence from
N_Geneseq_36:X20248_11	+ 41.00	74.12	1.6e+04	110000	Continuation (6 of 17) of
N_Geneseq_36:X20248_12	+ 41.00	74.12	1.6e+04	110000	Continuation (8 of 17) of
N_Geneseq_36:X20248_13	+ 40.00	110.44	149.81	1198	Nucleotide sequence of cluster
N_Geneseq_36:X20248_14	+ 40.00	108.62	189.36	1477	Helicobacter polypeptide GHPO
N_Geneseq_36:X20248_15	+ 40.00	97.93	745.94	5030	Staphylococcus aureus contig S
N_Geneseq_36:X20248_16	+ 40.00	94.69	1.1e+03	7291	ALVAC subgenomic fragment cont
N_Geneseq_36:X20248_17	+ 40.00	94.62	1.1e+03	7350	Canarypox virus DNA containing
N_Geneseq_36:X20248_18	+ 40.00	94.62	1.1e+03	7351	Canarypox virus BgIII fragment
N_Geneseq_36:X20248_19	+ 40.00	94.62	1.1e+03	7351	Canarypox virus DNA containing
N_Geneseq_36:X20248_20	+ 40.00	93.54	1.3e+03	8318	Borrelia burgdorferi polynucle
N_Geneseq_36:X20248_21	+ 40.00	93.36	1.3e+03	8486	Enterococcus faecalis genome c
N_Geneseq_36:X20248_22	+ 40.00	92.30	1.5e+03	9589	Enterococcus faecalis genome c
N_Geneseq_36:X20248_23	+ 40.00	91.33	1.7e+03	10715	Continuation (10 of 10) of
N_Geneseq_36:X20248_24	+ 40.00	76.54	1.1e+04	58407	Methanococcus jannaschii larg
N_Geneseq_36:X20248_25	+ 40.00	71.01	2.3e+04	110000	Continuation (2 of 6) of TS
N_Geneseq_36:X20248_26	+ 40.00	71.01	2.3e+04	110000	Continuation (8 of 10) of
N_Geneseq_36:X20248_27	+ 40.00	71.01	2.3e+04	110000	Continuation (9 of 10) of
N_Geneseq_36:X20248_28	+ 39.00	115.65	76.83	462	Polynucleotide sequence from th
N_Geneseq_36:X20248_29	+ 39.00	114.14	93.18	549	Borrelia burgdorferi polynucle
N_Geneseq_36:X20248_30	+ 39.00	110.97	140.02	790	H. influenzae DNA fragment conta
N_Geneseq_36:X20248_31	+ 39.00	110.33	151.97	850	Sequence of Haemophilus influen
N_Geneseq_36:X20248_32	+ 39.00	99.45	613.78	2960	Adzuki bean endo-xyloglucan tr
N_Geneseq_36:X20248_33	+ 39.00	96.81	860.12	4002	Yeast transcription regulatory
N_Geneseq_36:X20248_34	+ 39.00	94.22	1.2e+03	5391	Upstream sequence of the ACC S
N_Geneseq_36:X20248_35	+ 39.00	94.19	1.2e+03	5407	Upstream sequence of the ACC S
N_Geneseq_36:X20248_36	+ 39.00	67.91	3.4e+04	110000	Continuation (5 of 6) of TS
N_Geneseq_36:X20248_37	+ 39.00	67.91	3.4e+04	110000	Methanococcus jannaschii c
N_Geneseq_36:X20248_38	+ 39.00	66.19	4.2e+04	13894	ACNPV genomic DNA clone 6. A
N_Geneseq_36:X20248_39	+ 38.50	94.31	1.2e+03	4462	3' Terminal of TSWV L RNA. DNA

N_Geneseq_36:V76315 - 38.00 124.91 23.44 112 ! Staphylococcus aureus contig
N_Geneseq_36:Q05757 - 38.00 116.34 70.31 299 ! Clone CBP408 with homology t
N_Geneseq_36:Q05756 - 38.00 114.62 87.62 364 ! Clone CBP405 with homology t
N_Geneseq_36:Q05755 - 38.00 114.16 93.02 384 ! Clone CBP401 with homology t

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seq_documentation_block:

Continuation (9 of 10) of X20248 from base 800001 (Borrelia burgdorferi polynucleotid
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Fragment Name Begin End
WP X20248_00 1 110000
WP X20248_01 100001 210000
WP X20248_02 210001 310000
WP X20248_03 310001 410000
WP X20248_04 410001 510000
WP X20248_05 510001 610000
WP X20248_06 610001 710000
WP X20248_07 710001 810000
WP X20248_08 810001 910000
WP X20248_09 910001 910715

alignment_scores:

Quality: 45.00 Length: 16
Ratio: 3.462 Gaps: 0
Percent Similarity: 81.250 Percent Identity: 62.500

alignment_block:

US-08-653-294-22 x X20248_08

Align seg 1/1 to: X20248_08 from: 1 to: 110000

1 SerTyrLysLeuValIleLysIleAsnAsnIleArgIleValVallys 16
|||||
94894 AGCTACAGCTAGTACTTCTACTTGAATTCTATATTAATTGCAAAA 94941

seq_name: N_Geneseq_36:V21209_08

seq_documentation_block:

Continuation (9 of 17) of V21209 from base 800001 (Methanococcus jannaschii circular
WP Sequence split into 17 fragments LOCUS V21209 Accession V21209
Fragment Name Begin End
WP V21209_00 1 110000
WP V21209_01 100001 210000
WP V21209_02 210001 310000
WP V21209_03 310001 410000
WP V21209_04 410001 510000
WP V21209_05 510001 610000
WP V21209_06 610001 710000
WP V21209_07 710001 810000
WP V21209_08 810001 910000
WP V21209_09 910001 1010000
WP V21209_10 1010001 1110000
WP V21209_11 1110001 1210000
WP V21209_12 1210001 1310000
WP V21209_13 1310001 1410000
WP V21209_14 1410001 1510000
WP V21209_15 1510001 1610000
WP V21209_16 1610001 1664976

alignment_scores:

Quality: 42.00 Length: 16
Ratio: 3.500 Gaps: 0
Percent Similarity: 75.000 Percent Identity: 56.250

alignment_block:

US-08-653-294-22 x V21209_08

Align seg 1/1 to: V21209_08 from: 1 to: 110000

2 TyrLysLeuValIleLysIleAsnAsnIleArgIleValVallysPhe 17

||||| ||||| ::||| ||::||| ||||| ::|||
71863 TATAACCAAGTCCTCTTAATTATATCAAAATAGTTTTTAAGTTT 71910

seq_name: N_Geneseq_36:X20248_00

seq_documentation_block:

WP Sequence split into 10 fragments LOCUS X20248 Accession X20248

Fragment Name	Begin	End
WP X20248_00	1	110000
WP X20248_01	100001	210000
WP X20248_02	200001	310000
WP X20248_03	300001	410000
WP X20248_04	400001	510000
WP X20248_05	500001	610000
WP X20248_06	600001	710000
WP X20248_07	700001	810000
WP X20248_08	800001	910000
WP X20248_09	900001	910715

ID X20248 standard; DNA; 910715 BP.

AC X20248:

DT 04-MAY-1999 (first entry)

DE Borrelia burgdorferi polynucleotide sequence #1.

KW Borrelia burgdorferi; Spirochete; Bacterium; Pathogen; Lyme disease;

KW epidemic relapsing fever; endemic relapsing fever; Lyme borreliosis;

KW infection; diagnosis; characterisation; detection; ds.

OS Borrelia burgdorferi.

PN W09858943-A1.

PD 30-DEC-1998.

PF 18-JUN-1998; U12764.

PR 03-SEP-1997; US-057483.

PR 20-JUN-1997; US-050359.

PR 22-JUL-1997; US-053344.

PR 22-JUL-1997; US-053377.

PA (HUMA-) HUMAN GENOME SCI INC.

PA (MEDI-) MEDIMMUNE INC.

PI Clayton R, Dougherty BA, Fraser C, Lathigra R, Smith HO,

PI White OR;

DR WPI; 99-081217/07.

PT New isolated Borrelia burgdorferi nucleic acids - used to develop

PT products for the detection, diagnosis, characterisation, prevention

PT and therapy of infections, particularly Lyme disease

PS Claim 1; Page 157-671; 1128pp; English.

CC X20248 to X20402 represent polynucleotide sequences isolated from

CC Borrelia burgdorferi (Bb). Products derived from Bb can be used for

CC the detection, diagnosis, characterisation, prevention and therapy of

CC Bb infections, e.g. Lyme disease. They can also be used for the

CC production of biosynthetic products, e.g. enzymes. Borrelia belongs

CC to a family of motile, spiral-shaped bacteria called Spirochetes.

CC Spirochetes are pathogenic in humans and Borrelia causes epidemic and

CC endemic relapsing fever, and Lyme borreliosis, more commonly known as

CC Lyme disease.

SQ Sequence 910715 BP; 327171 A; 129646 C; 130753 G; 323091 T;

alignment_scores:

Quality: 42.00 Length: 14

Ratio: 3.818 Gaps: 0

Percent Similarity: 78.571 Percent Identity: 71.429

alignment_block:

US-08-653-294-22 x X20248_00/rev ..

Align seg 1/1 to reverse of: X20248_00 from: 1 to: 110000

3 LysLeuValIleuYltsnAsnIleArgIleValValLys 16

||||| ||||| ||||| ||||| |||||

44990 AAACCTTTTAAATAATCTTGATATGAGATATGCGTAAAG 44949

seq_name: N_Geneseq_36:X20248_03

seq_documentation_block:

Continuation (4 of 10) of X20248 from base 300001 (Borrelia burgdorferi polynucleotide s

WP Sequence split into 10 fragments LOCUS X20248 Accession X20248

Fragment Name	Begin	End
WP X20248_00	1	110000
WP X20248_01	100001	210000
WP X20248_02	200001	310000
WP X20248_03	300001	410000
WP X20248_04	400001	510000
WP X20248_05	500001	610000
WP X20248_06	600001	710000
WP X20248_07	700001	810000
WP X20248_08	800001	910000
WP X20248_09	900001	910715

alignment_scores:

Quality: 42.00 Length: 17

Ratio: 3.500 Gaps: 0

Percent Similarity: 70.588 Percent Identity: 52.941

alignment_block:

US-08-653-294-22 x X20248_03 ..

Align seg 1/1 to: X20248_03 from: 1 to: 110000

1 SerTyLysLeuValIleYltsnAsnIleArgIleValValLysPh 17

:::||||| ::| ||||| ||||| |||||

67263 ACATACAAGAGATCTGCAAGATTTTCAACATATAAGATAAAAAATCAAGTT 67312

17 e 17

67313 T 67313

seq_name: N_Geneseq_36:X22323

seq_documentation_block:

ID X22323 standard; DNA; 1673 BP.

AC X22323;

DT 19-MAY-1999 (first entry)

DE B. fragilis DNA probe BF-35.

KW Probe; diagnosis; infection; specific; blood; detection; BF-35; ds.

OS Bacterioides fragilis.

PN W09842844-A1.

PD 01-OCT-1998.

PF 23-MAR-1998; J01287.

PR 25-MAR-1997; JP-071079.

PA (FUSO) FUSO PHARM IND LTD.

PA (FUSO) FUSO YAKUHIN KOGYO KK.

PI Abe K, Keshi H, Matsuhisa A, Ueyama H;

DR WPI; 99-070072/06.

PT DNA probes for diagnosis of infection with Bacterioides fragilis -

PT are obtained by HindIII digestion of genomic B. fragilis DNA and

PT selection of bacterial-binding fragments

PS Claim 2; Page 25-26; 36pp; Japanese.

CC X22318-X22323 are DNA probes used for the diagnosis of infection with

CC Bacterioides fragilis. The probes are obtained by isolation of genomic

CC DNA from this bacterium, digesting it with HindIII restriction enzyme,

CC and identifying clones capable of binding to the bacterium then isolating

CC and sequencing the HindIII fragments involved. The method allows simple

CC and highly specific detection of Bacterioides fragilis in biological

CC samples such as blood, for diagnosis of Bacterioides fragilis infections.

CC This sequence represents genomic DNA probe BF-35.

SQ Sequence 1673 BP; 528 A; 408 C; 249 G; 488 T;

alignment_scores:

Quality: 41.50 Length: 18

Ratio: 2.964 Gaps: 1

Percent Similarity: 77.778 Percent Identity: 55.556

alignment_block:

US-08-653-294-22 x X22323 ..

Align seg 1/1 to: X22323 from: 1 to: 1673

CC	Spirochetes are pathogenic in humans and Borrelia causes epidemic and		
CC	endemic relapsing fever, and Lyme borreliosis, more commonly known as		
CC	Lyme disease.		
SQ	Sequence	116277 BP; 42656 A; 19868 C; 14490 G; 39250 T;	

alignment_scores:		
Quality:	41.50	Length: 16
Ratio:	2.964	Gaps: 1
Percent Similarity:	87.500	Percent Identity: 56.250

Align seq 1/1 to reverse of: X20249 from: 1 to: 116277

TyrLysLeuValIleLysIleAsnAsnIleArgIleValValLysPhe 17

seq_name: N_Geneseq_36:V76754

```
seq_documentation_block:
ID      V76754 standard; DNA; 264 BP.
```

16-MAR-1999 (first entry)
Staphylococcus aureus contig SEQ ID #2443.
Computer readable medium; vaccine; S.aureus infection; immunodetection;
cellulitis; eyelid infection; food poisoning; osteomyelitis; therapy;
skin infection; surgical wound infection; scalded skin syndrome;
toxic shock syndrome; ds.

Staphylococcus aureus

```

-08-653-294-22 x X20248_04
ign seg 1/1 to: X20248_04 from: 1 to: 110000
2 TvrLysLeuValIleLysIleAsnAsnIleArgIleValValIysPhe 17
|||||:|||||
89154 CATAAACTGATTTT...TTAAATAATAATAAAATGTTTACCTTTT 89198

```

PT Polynucleotide(s) and proteins derived from *Staphylococcus aureus*
PT stored on computer readable medium and used in the production of
PT stored on computer readable medium and used in the production of
WPI; 97-374922/33.

stored on computer readable medium and used in the production of anti-S.aureus vaccines

Claim 1; Page 2240; 3271pp; English.

This sequence represents one of 5191 *Staphylococcus aureus* DNA sequences of the invention. The DNA sequences are recorded on a computer readable medium, preferably selected from a floppy or hard disk, random access memory (RAM), read-only memory (ROM) or CD-ROM. Homology searches using the S.aureus DNA sequences allows putative functions to be assigned so that protein-encoding or regulatory regions of commercial, therapeutic or industrial importance can be obtained. Specifically, sequences which are likely to encode antigens have been identified and these polypeptides can be used in a vaccine composition against S.aureus infection. The polypeptides can also be used in a kit for the immunodetection of S.aureus in a sample. S.aureus is implicated in numerous human diseases, including cellulitis, eyelid infections, food poisoning, osteomyelitis, skin and surgical wound infections, scalded skin syndrome, toxic shock syndrome, etc. Organisms transformed with the DNA sequences can be used for recombinant production of the polypeptides. The new DNA sequences (and their fragments) are useful as primers or probes for isolating homologues of any of the S.aureus DNA sequences contained on the computer readable medium.

264 BP; 100 A; 34 C; 39 G; 89 T; 100 C

ID X20249 standard; DNA; 116277 BP.

04-MAY-1999 (first entry)
 Borrelia burgdorferi polynucleotide sequence #2.
 Borrelia burgdorferi; spirochete; bacterium; pathogen; Lyme disease;
 epidemic relapsing fever; endemic relapsing fever; Lyme borreliosis;
 infection; diagnosis; characterisation; detection; ds.

OS Borrelia burgdorferi

PN W09858943-A1.

PD 30-DEC-1998.

PF 18-JUN-1998; U12764.

PR 03-SEP-1997; US-057483.

PR 20-JUN-1997; US-050359.

PR 22-JUL-1997; US-053344.

PR 22-JUL-1997; US-053377.

PA (HUMA-) HUMAN GENOME SC.

PA (MEDI-) MEDIMMUNE INC.

PI Clayton R, Dougherty BA

PI White OR;

DR WPI; 99-081217/07.

NT New isolated *Borrelia* b

products for the detection and therapy of infectious

Claim 1: Page 672-737.

P3 CLAIM I; Page 012-137;
 CC X20248 to X20402 represent

CC AZ0248 LU AZ0402 Iepres
CC Borrelia burgdorferi (B)

the detection, diagnosis

CC Bb infections, e.g. Lyme disease, meningitis, arthritis, etc.

CC-2 production of biosynthe

to a family of motile, flagellated, ciliated, and biflagellated forms.

Introduction

AN
THE
INTELLIGENCE, EARLY THAT MORNING INTERSECTION,
SCATTERED WITH SYMPHONY,

CC A computer readable medium has been developed which has recorded on it
 CC 982 nucleotide sequences isolated from the *Enterococcus faecalis* genome.
 CC X12938 to X13919 represent these nucleotide sequences which are primary
 CC nucleotide sequences, also known as contigs. The computer-based system
 CC can identify fragments of the *Enterococcus faecalis* genome with
 CC commercial importance. The products can be used to detect the presence
 CC of *Enterococcus faecalis* in samples. They can also be used for
 CC diagnosing *Enterococcal* infection in an animal and monitoring
 CC progression of disease, and for identifying agents which can be used to
 CC modulate the growth or pathogenicity of *Enterococcus faecalis*, or
 CC another related organism, in vivo or in vitro. In particular the
 CC polypeptides encoded by the *Enterococcus faecalis* nucleotide sequences
 CC can be used in vaccines to prevent or attenuate an *Enterococcal*
 CC infection.
 SQ Sequence 7528 BP; 2483 A; 1225 C; 1645 G; 2167 T;

alignment_scores:
 Quality: 41.00 Length: 15
 Ratio: 3.154 Gaps: 0
 Percent Similarity: 86.667 Percent Identity: 60.000

alignment_block:

US-08-653-294-22 x X12992/rev ..

Align seg 1/1 to reverse of: X12992 from: 1 to: 7528

3 LysLeuValIleLysIleAsnAsnIleArgIleValValLysPhe 17
 ::::::::::::::::::::::||| ::::::::::::::

264 CGGTTAACTAAATCAATAACGATCGGATATGGTGCTTC 220

seq_name: N_Geneseq_36:X20535

seq_documentation_block:

ID X20535 standard; DNA; 21170 BP.

AC X20535;

DT 05-MAY-1999 (first entry)

DE Polynucleotide sequence from the genome of *Treponema pallidum*.

KW *Treponema pallidum* infection; syphilis; *Borrelia* infection; animal;

OS enzyme production; ds.

OS *Treponema pallidum*.

PN WO9859034-A2.

PD 30-DEC-1998.

PF 23-JUN-1998; UI13041.

PR 24-JUN-1997; US-050667.

PA (HUMA-) HUMAN GENOME SCI INC.

PI Fraser CM;

DR WPI: 99-081273/07.

PT New isolated *Treponema pallidum* nucleic acids - used to develop

PT products for the detection, diagnosis, characterisation, prevention

PT and therapy of *T. pallidum* infections, particularly syphilis

PS Claim 1: Page 389-401; 1150pp; English.

CC X20500-21243 represent polynucleotide sequences from the genome of

CC *Treponema pallidum*. The sequences can be used for detection,

CC diagnosis, characterisation, prevention and therapy for *T. pallidum*

CC infections, particularly syphilis. They can also be used for detecting

CC diseases related to *Borrelia* infections in animals, and for the

CC production of biosynthetic products such as enzymes.

SQ Sequence 21170 BP; 4629 A; 5015 C; 6107 G; 5390 T;

alignment_scores:
 Quality: 41.00 Length: 14
 Ratio: 3.154 Gaps: 0
 Percent Similarity: 92.857 Percent Identity: 50.000

alignment_block:

US-08-653-294-22 x X20535/rev ..

Align seg 1/1 to reverse of: X20535 from: 1 to: 21170

4 LeuValIleLysIleAsnAsnIleArgIleValValLysPhe 17
 ::::::::::||| ::::::::::||| ::::::::::||| ::::::::::||| ::::::::::|||

18517 GTAATCATCAAGACTAATCATCGGATCGGATCAACCAAGTAC 18476

seq_name: N_Geneseq_36:V21209_05

seq_documentation_block:

Continuation (6 of 17) of V21209 from base 500001 (*Methanococcus jannaschii* circular
 WP Sequence split into 17 fragments LOCUS V21209 Accession V21209

Fragment Name	Begin	End
WP V21209_00	1	110000
WP V21209_01	100001	210000
WP V21209_02	200001	310000
WP V21209_03	300001	410000
WP V21209_04	400001	510000
WP V21209_05	500001	610000
WP V21209_06	600001	710000
WP V21209_07	700001	810000
WP V21209_08	800001	910000
WP V21209_09	900001	1010000
WP V21209_10	1000001	1110000
WP V21209_11	1100001	1210000
WP V21209_12	1200001	1310000
WP V21209_13	1300001	1410000
WP V21209_14	1400001	1510000
WP V21209_15	1500001	1610000
WP V21209_16	1600001	1664976

alignment_scores:
 Quality: 41.00 Length: 11
 Ratio: 3.727 Gaps: 0
 Percent Similarity: 100.000 Percent Identity: 72.727

alignment_block:

US-08-653-294-22 x V21209_05 ..

Align seg 1/1 to: V21209_05 from: 1 to: 110000

5 ValIleLysIleAsnAsnIleArgIleValVal 15
 ::::::::::::::| ::::::::::::::| ::::::::::::::| ::::::::::::::| ::::::::::::::|

82909 ATTATTAAATCAAAATCTCCGAATCGTTGTA 82941

seq_name: N_Geneseq_36:V21209_07

seq_documentation_block:

Continuation (8 of 17) of V21209 from base 700001 (*Methanococcus jannaschii* circular
 WP Sequence split into 17 fragments LOCUS V21209 Accession V21209

Fragment Name	Begin	End
WP V21209_00	1	110000
WP V21209_01	100001	210000
WP V21209_02	200001	310000
WP V21209_03	300001	410000
WP V21209_04	400001	510000
WP V21209_05	500001	610000
WP V21209_06	600001	710000
WP V21209_07	700001	810000
WP V21209_08	800001	910000
WP V21209_09	900001	1010000
WP V21209_10	1000001	1110000
WP V21209_11	1100001	1210000
WP V21209_12	1200001	1310000
WP V21209_13	1300001	1410000
WP V21209_14	1400001	1510000
WP V21209_15	1500001	1610000
WP V21209_16	1600001	1664976

alignment_scores:
 Quality: 41.00 Length: 16
 Ratio: 3.154 Gaps: 0
 Percent Similarity: 81.250 Percent Identity: 43.750

alignment_block:

US-08-653-294-22 x V21209_07/rev ..

0
1
2
3
4
5
6
7
8
9
A
B
C
D
E
F
G
H
I
J
K
L
M
N
O
P
Q
R
S
T
U
V
W
X
Y
Z

LOCUS AU033795 329 bp mRNA EST 28-APR-1999
DEFINITION AU033795 Dictyostellium discoideum SL (H.Urushihara) Dictyostellium
discoideum cDNA clone SLB447, mRNA sequence.
ACCESSION AU033795

```

VERSION AU033795.1 GI:3799219
KEYWORDS EST.
SOURCE Dictyostelium discoideum.
ORGANISM Dictyostelium discoideum
REFERENCE Eukaryota; Dictyostelid; Dictyostelium.
AUTHORS 1 (bases 1 to 329)
Mori, T., Urushihara, H., Saito, T., Ugawa, Y., Mizuno, H., Yoshida, M.,
Yoshino, R., Mitra, B. N., Pi, M., Sato, T., Takemoto, K., Yasukawa, H.,
Williams, J., Maeda, M., Takeuchi, I., Ochiai, H. and Tanaka, Y.
TITLE The Dictyostelium developmental cDNA project: generation and
analysis of expressed sequence tags from the first-finger stage of
development
JOURNAL DNA Res. 5 (6), 335-340 (1998)
MEDLINE 99156227
COMMENT On Jan 19, 1998 this sequence version replaced gi:2150520.
Contact: Hideko Urushihara
Institute of Biological Sciences
University of Tsukuba
3-3-10 Ten-nodai, Tsukuba, Ibaraki 305, Japan
Email: d402hu@sakura.cc.tsukuba.ac.jp
PROJECT = 'Dictyostelium discoideum cDNA project in Japan'
POLYA-No. Location/Qualifiers
FEATURES
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        1..329
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            /strain="AX4"
            /db_xref="taxon:44689"
            /clone="SLB447"
            /dev_stage="slug"
            /dev_stage="slug"
BASE COUNT 151 a 30 c 39 g 109 t
ORIGIN
alignment_scores:
    Quality: 50.00 Length: 15
    Ratio: 3.571 Gaps: 0
    Percent Similarity: 93.333 Percent Identity: 60.000
alignment_block:
    US-08-653-294-22 x AU033795
Align seg 1/1 to: AU033795 from: 1 to: 329
2 TyrlsLeuValIleLysileAsnAsnIleArgIleValVallys 16
||||| :|||||:|||||:|||||:|||||:|||||:|||||
255 TACAATAATAATTAATAATAATAATAATAATTAAGTTTGGTAAAA 299
seq_name: gb_est21:C90397
seq_documentation_block:
    LOCUS C90397 355 bp mRNA EST 20-APR-1998
    DEFINITION C90397 Dictyostelium discoideum SS (H.Urushihara) Dictyostelium
    discoideum cDNA clone SSI355, mRNA sequence.
    ACCESSION C90397
    VERSION C90397.1 GI:3060017
    KEYWORDS EST.
    SOURCE Dictyostelium discoideum.
    ORGANISM Eukaryota; Dictyostelid; Dictyostelium.
    REFERENCE 1 (bases 1 to 355)
    AUTHORS Yoshino, R., Mori, T. and Tanaka, Y.
    TITLE Developmental cDNA in Dictyostelium discoideum
    JOURNAL Unpublished (1997)
    COMMENT On Jan 19, 1998 this sequence version replaced gi:2151525.
    Contact: Hideko Urushihara
    Institute of Biological Sciences
    University of Tsukuba
    3-3-10 Ten-nodai, Tsukuba, Ibaraki 305, Japan
    Email: d402hu@sakura.cc.tsukuba.ac.jp.
    Location/Qualifiers
    FEATURES
        source
            1..355
                /organism="Dictyostelium discoideum"
                /strain="AX4"
                /db_xref="taxon:44689"
                /clone="SSI355"
                /dev_stage="slug"
                /dev_stage="slug"
BASE COUNT 142 a 39 c 48 g 126 t
ORIGIN
alignment_scores:
    Quality: 50.00 Length: 15
    Ratio: 3.571 Gaps: 0
    Percent Similarity: 93.333 Percent Identity: 60.000
alignment_block:
    US-08-653-294-22 x C90397
Align seg 1/1 to: C90397 from: 1 to: 355
2 TyrlsLeuValIleLysileAsnAsnIleArgIleValVallys 16
||||| :|||||:|||||:|||||:|||||:|||||:|||||
307 TACAATAATAATTAATAATAATAATAATAATTAAGTTTGGTAAAA 351
seq_name: gb_est38:AW054448
seq_documentation_block:
    LOCUS AW054448 481 bp mRNA EST 23-SEP-1999
    DEFINITION 660007B12.x1 660 - Mixed stages of anther and pollen Zea mays cDNA,
    mRNA sequence.
    ACCESSION AW054448
    VERSION AW054448.1 GI:5919351
    KEYWORDS EST.
    SOURCE Zea mays.
    ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
    euphyllophytes; Spermatophyta; Magnoliophyta; Liliopsida; Poales;
    Poaceae; Zea.
    REFERENCE 1 (bases 1 to 481)
    AUTHORS Walbot, V.
    TITLE Maize ESTs from various cDNA libraries sequenced at Stanford
    University
    JOURNAL Unpublished (1999)
    COMMENT On May 18, 1998 this sequence version replaced gi:3138574.
    Contact: Walbot V
    Department of Biological Sciences
    Stanford University
    855 California Ave, Palo Alto, CA 94304, USA
    Tel: 650 723 2227
    Fax: 650 725 8221
    Email: walbot@stanford.edu
    Plate: 660007 row: B column: 12.
    Location/Qualifiers
    FEATURES
        source
            1..481
                /organism="Zea mays"
                /cultivar="Ohio43"
                /db_xref="taxon:4577"
                /clone_lib="660 - Mixed stages of anther and pollen"
                /tissue_type="whole premeiotic anthers to pollen shed"
                /dev_stage="premeiotic anthers to pollen shed"
                /lab_host="XLOLR"
                /note="Organ: anthers; Vector: Lambda Zap; Site_1: EcoRI;
                Site_2: XhoI; Anther and pollen cDNA library.
                Directionally sequenced with 5' end at the EcoRI site.
                Created by Amie Franklin."
BASE COUNT 135 a 103 c 87 g 156 t
ORIGIN
alignment_scores:
    Quality: 50.00 Length: 17
    Ratio: 3.571 Gaps: 0
    Percent Similarity: 82.353 Percent Identity: 52.941

```


Contact: Hideko Trushihara
Institute of Biological Sciences
University of Tsukuba
3-3-10 Ten-nodai, Tsukuba, Ibaraki 305, Japan
Email: d402hu@sakura.cc.tsukuba.ac.jp
PROJECT = 'Dictyostelium discoideum CDNA project'

Email: d402hu@sakura.cc.tsukuba.ac.jp
PROJECT - 'Dictyostelium discoideum cDNA project in Japan',
Location/Qualifiers

Location/Qualifiers
1. .628

BASE COUNT	242 a	84 C	94 q	208 t
BASE COUNT	242 a	84 C	94 q	208 t

[illegible]

DEFINITION
C94298 Dictyostelium discoideum SS (A. Gustin) *discoideum* cDNA clone SSK757, mRNA sequence.
C94298
ACCESSION
C94298.1 GI:3218012
VERSION

ORGANISM	SOURCE
<i>Dictyostelium discoideum</i>	Dictyostelium discoideum
<i>Dictyostelium</i>	Dictyostelium
<i>Eukaryota: Dictyosteliida: Dictyostelium</i>	Eukaryota: Dictyosteliida: Dictyostelium

REFERENCE	1. (Pages 1 to 497)
AUTHORS	Yoshino, R., Morio, T. and Tanaka, Y.
TITLE	Developmental cDNA in Dictyostelium discoideum
JOURNAL	Unpublished (1997)
COMMENT	On Jan 14, 1998 this sequence version replaced gi:1797150.

INSTITUTE OF BIOLOGICAL SCIENCES
University of Tsukuba

PROJECT = Dictyostelium discoideum cDNA project in Japan.
Email: d402huesakura.cc.tsukuba.ac.jp

```

/strain="AX4"

```

```
/clone="SSK757"
```

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"/dev_stage="slug"
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ORIGIN

alignment_scores:

Percent Similarity: 93.333 Percent Identity: 60.000

alignment_block:

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US-08-653-294-22 x C94298
Align seg 1/1 to: C94298 from: 1 to: 645

2 TyrlsLeuValIleLysIleAsnAsnIleArgIleValValLys 16
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599 TACAAATAAATAATAAATAAATAAATAAATTTTGGTAAAA 643

seq_name: gb_est21:C92217

seq_documentation_block:
LOCUS C92217 584 bp mRNA EST 12-JUL-1999
DEFINITION C92217 Dictyostelium discoideum SS (H.Urushihara) Dictyostelium
discoideum cDNA clone SSD246, mRNA sequence.
ACCESSION C92217
VERSION C92217.1 GI:3074093
KEYWORDS EST.
SOURCE Dictyostelium discoideum.
ORGANISM Eukaryota; Dictyosteliida; Dictyostelium.
REFERENCE 1 (bases 1 to 584)
AUTHORS Morio,T., Urushihara,H., Saito,T., Ugawa,Y., Mizuno,H., Yoshida,M.,
Williams,J., Maeda,M., Takeuchi,I., Ochiai,H. and Tanaka,Y.
The Dictyostelium developmental cDNA project: generation and
analysis of expressed sequence tags from the first-finger stage of
development
JOURNAL DNA Res. 5 (6), 335-340 (1998)
MEDLINE 99156227
COMMENT On May 9, 1995 this sequence version replaced gi:804216.
Contact: Hideko Urushihara
Institute of Biological Sciences
University of Tsukuba
3-3-10 Ten-nodai, Tsukuba, Ibaraki 305, Japan
Email: d402huesakura.cc.tsukuba.ac.jp
PROJECT = 'Dictyostelium discoideum cDNA project in Japan'
POLYA=NO.
FEATURES
source
Location/Qualifiers
1..584
/organism="Dictyostelium discoideum"
/strain="AX4"
/db_xref="taxon:44689"
/clone="SSD246"
/clone_lib="Dictyostelium discoideum SS (H.Urushihara)"
/dev_stage="slug"
BASE COUNT 228 a 79 c 82 g 193 t 2 others
ORIGIN

alignment_scores:
Quality: 48.00 Length: 15
Ratio: 3.692 Gaps: 0
Percent Similarity: 86.667 Percent Identity: 60.000

alignment_block:
US-08-653-294-22 x C92217
Align seg 1/1 to: C92217 from: 1 to: 584

2 TyrlsLeuValIleLysIleAsnAsnIleArgIleValValLys 16
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515 TACAAATAAATAATAAATAAATAAATAAATTTTGGTAAAA 559

seq_name: gb_gss12:AQ359868

seq_documentation_block:
LOCUS AQ359868 470 bp DNA GSS 06-MAR-1999
DEFINITION HS_5032_B1_B04 SP6E RPC111 Human Male BAC Library Homo sapiens
genomic clone Plate=608 Col=7 Row=D, genomic survey sequence.
ACCESSION AQ359868
VERSION AQ359868.1 GI:4208744
KEYWORDS GSS.
SOURCE human.

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 470)
AUTHORS Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,
Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and
Hood,L.
Sequence-tagged connectors: A sequence approach to mapping and
scanning the human genome
Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999)
JOURNAL 99380589
MEDLINE
COMMENT Contact: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3618
Fax: (206) 616-3887
Email: jwallace@u.washington.edu
Clones may be purchased from Research Genetics (info@resgen.com).
BAC end Web Server: http://www.htsc.washington.edu
Plate: 608 row: D column: 7
Seq primer: SP6
Class: BAC ends
High quality sequence stop: 470.
FEATURES
source
Location/Qualifiers
1..470
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="Plate=608 Col=7 Row=D"
/clone_lib="RPC111 Human Male BAC Library"
/sex="Male"
/cell_type="Lymphocytes"
/note="Vector: pBACE3.6; RPC111 Human Male BAC Library"
BASE COUNT 132 a 89 c 81 g 167 t 1 others
ORIGIN

alignment_scores:
Quality: 47.00 Length: 17
Ratio: 3.133 Gaps: 0
Percent Similarity: 88.235 Percent Identity: 47.059

alignment_block:
US-08-653-294-22 x AQ359868/rev
Align seg 1/1 to reverse of: AQ359868 from: 1 to: 470

1 SerTyrLysLeuValIleLysIleAsnAsnIleArgIleValValLysPh 17
||||| ::::::::::::::::::::::::::::|
353 AGTTACAAGTGGTGTGTTAAATTAATTAAGGATAATNTTCCTGTTAAAGTA 304

17 e 17
303 T 303

seq_name: gb_est43:AV336157

seq_documentation_block:
LOCUS AV336157 237 bp mRNA EST 11-NOV-1999
DEFINITION AV336157 RIKEN full-length enriched, adult male medulla oblongata
Mus musculus cDNA clone 6330582013 3', mRNA sequence.
ACCESSION AV336157
VERSION AV336157.1 GI:6376209
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 237)
AUTHORS Konno,H., Aizawa,K., Akahira,S., Akiyama,J., Carninci,P., Endo,T.,
Fukuda,S., Fukunishi,Y., Hara,A., Hayatsu,N., Hirozane,T., Hori,F.,
Ishii,Y., Ishikawa,T., Itoh,M., Izawa,M., Kadota,K., Kagawa,I.,
Kai,C., Kawai,J., Kikuchi,N., Kojima,Y., Koya,S., Kusakabe,M.,
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alignment_scores:      Length: 13
                       Quality: 46.00
                       Ratio: 3.833
                       Gaps: 0
Percent Similarity: 92.308  Percent Identity: 61.538

alignment_block:
US-08-653-294-22 x AQ818505  ..

Align seg 1/1  to: AQ818505  from: 1  to: 489

      2 TyrLysLeuValIleLysIleAsnAsnIleArgIleVal 14
      |||||
      295 TACAAACTCGTTGTGACGATCAATCATCTACGGCTAGTG 333
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GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: February 8, 2000, 04:05:41 ; Search time 133.56 Seconds
(without alignments)
1.773 Million cell updates/sec

Title: US-08-653-294-23
Perfect score: 50
Sequence: 1 REDLRTLLRY 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 188963 seqs, 23686106 residues

Total number of hits satisfying chosen parameters: 188963

Minimum DB seq length: 0
Maximum DB seq length: 1000000

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database : A_Geneseq_36.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	50	100.0	10	R41212	Peptide fragment o
2	50	100.0	10	R83075	HLA-B2702 CTL modu
3	50	100.0	10	R95423	HLA-B2705.75-84. C
4	50	100.0	10	W33785	Peptide B2705.75-8
5	50	100.0	17	R71442	Human HLA-B27-(62-
6	50	100.0	17	R71443	Human (Phe74)-HLA-
7	50	100.0	25	R41221	Peptide fragment o
8	50	100.0	25	R83091	HLA-B2702 CTL modu
9	50	100.0	25	R95417	HLA-B2705.60-84. C
10	50	100.0	337	P70590	Sequence of the hu
11	50	100.0	362	P70155	Sequence encoded b
12	44	88.0	10	W47271	Immunomodulatory p
13	44	88.0	24	R71435	Human MHC 1 alpha
14	43	86.0	10	W07524	T-cell modulating
15	43	86.0	13	W29421	Glucose transport
16	43	86.0	16	R50266	HLA B27 hypervaria
17	43	86.0	17	R71440	Human MHC 1 and HL
18	43	86.0	17	R71425	Human MHC 1 alpha
19	43	86.0	17	R71426	Human MHC 1 alpha
20	43	86.0	17	R71433	Human MHC 1 alpha
21	43	86.0	17	W32583	MHC peptide repeat
22	43	86.0	17	W32581	MHC peptide repeat
23	43	86.0	17	W29422	Glucose transport
24	43	86.0	17	W45885	Peptide membrane b
25	43	86.0	24	R71424	Human MHC 1 alpha
26	43	86.0	24	R71427	Human MHC 1 alpha
27	43	86.0	25	R20116	MHC Class I-derive
28	43	86.0	25	R69619	MHC-I peptide DK-(
29	43	86.0	25	R71420	Human MHC 1 alpha
30	43	86.0	36	W32582	MHC peptide having
31	43	86.0	36	W32078	Peptide DS-A85. Pe
32	40	80.0	10	R83095	HLA-B2702 CTL modu
33	40	80.0	10	R95426	HLA-B2702.75-84(T)
34	40	80.0	10	W33788	Peptide B2702.75-8

35 40 80.0 20 1 R92909 HLA-B2702 CTL modu
36 40 80.0 20 1 R92910 HLA-B2702 CTL modu
37 40 80.0 20 1 W33792 Peptide B2702.84-7
38 40 80.0 20 1 W33793 Peptide B2702.84-7
39 40 80.0 24 1 R71434 Human MHC 1 alpha
40 39 78.0 10 1 R83094 HLA-B2702 CTL modu
41 39 78.0 10 1 R83096 HLA-B2702 CTL modu
42 39 78.0 10 1 R95425 HLA-B2702.75-84(D)
43 39 78.0 10 1 W07513 T-cell modulating
44 39 78.0 10 1 W47267 Immunomodulatory p
45 39 78.0 10 1 W47269 Immunomodulatory p

ALIGNMENTS

RESULT 1

R41212 ID R41212 standard; peptide; 10 AA.
AC R41212;
DT 15-MAR-1994 (first entry)
DE Peptide fragment of Class I HLA peptide.
KW Human leukocyte antigen; HLA; peptide; transplantation; neoplasia;
KW Parasitic disease; cytotoxic T lymphocyte; modulation.
OS Synthetic.
PN WO9317699-A.
PD 16-SEP-1993.
PF 25-FEB-1993.
PR 02-MAR-1992; US-844716.
PA (STRD) UNIV LELAND STANFORD JUNIOR.
PI Clayberger CA, Krensky AM;
DR WPI; 93-303134/38.
PT New peptide(s) based on Class I HLA antigen domains - used for
PT modulating cytotoxic T-lymphocyte activity towards targets
PS Claim 11; Page 54; 61pp; English.
CC The peptide is used to modulate cytotoxic T-lymphocyte (CTL)
CC activity, either by inhibition or stimulation. It can be used
CC for inhibiting CTL toxicity in transplantations, for inducing CTL
CC activity in parasitic diseases and neoplasia and in studies on viral
CC infection. The peptide can also be used for identifying CTLs which
CC bind to it and removing subsets of CTLs from a T-cell composition.
CC This peptide sequence is more commonly found within larger peptide
CC compounds of not more than 30 amino acids in length.
SQ Sequence 10 AA;

Query Match 100.0%; Score 50; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.00083;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 REDLRTLLRY 10
|||||||
DB 1 REDLRTLLRY 10

RESULT 2

R83075 ID R83075 standard; peptide; 10 AA.
AC R83075;
DT 16-MAY-1996 (first entry)
DE HLA-B2702 CTL modulating peptide (B2702.75-84).
DE Cytotoxic T lymphocyte; CTL; major histocompatibility complex; MHC;
KW Immunosuppressant; graft versus host disorder; transplantation; therapy;
KW Class I MHC; HLA-B2702.
OS Synthetic.
PN WO9526979-A1.
PD 12-OCT-1995.
PF 05-APR-1995; U04349.
PR 05-APR-1994; US-222851.
PA (STRD) UNIV LELAND STANFORD JUNIOR.
PI Clayberger C, Krensky AM, Parham P;
DR WPI; 95-358582/46.
PT Extension of acceptance period of transplants from MHC unmatched

PT donor hosts - using Class I B75-84 MHC antigen of the recipient
 PS host
 CC Example 14; Page 34; 80pp; English.
 CC R83061-R83085, R83090-R83096 and R92907-R92913 represent fragments of
 CC class I major histocompatibility complex (MHC) antigens. This sequence
 CC corresponds to residues 75-84 of the alpha-1 domain of the class
 CC I MHC HLA-B*2702. These sequences can be used to extend the period of
 CC acceptance by a recipient of a transplant from an MHC unmatched donor.
 CC The peptides are administered to a patient in conjunction with a
 CC subtherapeutic amount of an immunosuppressant. This is administered to
 CC the patient for a limited period of time (compared to the lifetime
 CC administration for current treatments). The peptides particularly
 CC modulate (or inhibit) the activity of the cytotoxic T lymphocytes (CTLs)
 CC of the patient.
 CC Sequence 10 AA;
 SQ

Query Match 100.0%; Score 50; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.00083;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 REDLRTLLRY 10
 Db 1 REDLRTLLRY 10
 |||||

RESULT 3
 ID R95423 standard; peptide; 10 AA.
 AC R95423;
 DT 12-NOV-1996 (first entry)
 DE HLA-B*2705.75-84.
 KW T-cell lysate; membrane protein; mammal; heat shock protein; Hsc70; APC;
 KW B cell; calcium influx; cytotoxic T lymphocyte; CTL; differentiation;
 KW cytolysis; antigen presenting cell.
 OS Synthetic.
 PN W09513288-A1.
 PD 18-MAY-1995; U12985.
 PF 10-NOV-1994; U12985.
 PR 10-NOV-1993; US-150493.
 PA (STRD) UNIV LELAND STANFORD JUNIOR.
 PI Clayberger C, Krensky AM;
 DR WPI: 95-194027/25.
 PT Consns. comprising lymphoid surface membrane proteins - which may
 PT inhibit cytolytic activity and differentiation of CTLs.
 PS Example; Page 11; 29pp; English.
 CC R95413, and R95415-R95431 represent palindromes and fragments of
 CC human-leucocyte-associated antigens. This sequence represents the
 CC HLA-B*2705.75-84. These sequences can be used to isolate the protein p74
 CC from a T-cell lysate. p74 is a T-cell surface membrane protein
 CC associated with T-cell activation in mammalian T-cells, and is also
 CC immunologically cross reactive with the heat shock protein Hsc70. p74 is
 CC found in a limited number of cell types, but is particularly expressed on
 CC B and T cells. p74 can be isolated by lysis of a suitable cell with an
 CC amphoteric detergent, and then passed through an affinity column
 CC containing a covalently bound HLA-B*2702 palindromic peptide.
 CC Compositions comprising the extracellular fragment of p74 combined with
 CC HLA-B*2702.60-84 (see R95416), induces calcium influx, and inhibits
 CC cytotoxic T lymphocyte (CTL) differentiation or cytolysis. Candidate
 CC compounds can be screened for their effect on the cytolytic activity of
 CC T-cells, by combining them with the extracellular portion of p74 and
 CC determining the amount of binding between the candidate compound and p74.
 CC Modulation of CTL activity can be inhibited in a cellular composition
 CC containing T-cells and antigen presenting cells (APCs), by adding to the
 CC mix the extracellular portion of p74, in an amount sufficient to compete
 CC with p74 for the binding of the p74 ligand.
 CC Sequence 10 AA;
 SQ

Query Match 100.0%; Score 50; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.00083;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 REDLRTLLRY 10
 Db 1 REDLRTLLRY 10
 |||||

RESULT 4
 W33785
 ID W33785 standard; peptide; 10 AA.
 AC W33785;
 DT 19-JUN-1998 (first entry)
 DE Peptide B2705.75-84 tested for immunomodulating activity.
 KW Immunomodulating dimer; immunosuppressant drug; CTL activation;
 KW transplantation; autoimmune disease; Class I HLA-B alpha-1 domain;
 KW rejection.
 OS Synthetic.
 OS Homo sapiens.
 PN W09744351-A1.
 PD 27-NOV-1997.
 PF 22-MAY-1997; U08689.
 PR 24-MAY-1996; US-653294.
 PA (STRD) UNIV LELAND STANFORD JUNIOR.
 PI Beulow R, Clayberger C, Krensky AM;
 DR WPI: 98-086530/08.
 PT New immunomodulating dimer peptide(s) - based on a Class I HLA-B
 PT alpha-1 domain, used for preventing rejection of transplants or
 PT treating autoimmune diseases
 PS Example 1; Page 19; 41pp; English.
 CC Peptides W33784-98 and W33778-9 were assayed for their immunomodulating
 CC activity. A peptide-type compound or variant is claimed which has
 CC immunomodulating activity, including the N-terminal acylated and/or
 CC C-terminal amidated or esterified forms of up to 60 amino acids, where
 CC the peptide-type compound comprises the formula: A-B where A =
 CC (R aa76-77L) (aa79-84) or (aa84-79) (Laa77-76R); aa76 = E or V; aa77 =
 CC D, S or N; aa79 = R or G; aa80 = I or N; aa81, aa84 = a hydrophobic
 CC small amino acid; aa82 = R or L; aa83 = G or R; and aa represents amino
 CC acid. The sequence in the brackets may optionally be absent or truncated
 CC at any peptide type bond within the brackets. The compounds comprise
 CC amino acid sequences related to a Class I HLA-B alpha domain (positions
 CC 79-84). They can be used to inhibit cytotoxic T-lymphocytes (CTL) from
 CC undesirably attacking cells in a host or in vitro. They can also be
 CC used in combination with antigenic peptides or proteins of interest to
 CC activate CTLs. They can also inhibit the proliferation of T cells in
 CC response to anti-CD3. The peptide can be used for preventing rejection
 CC of transplants or for treating autoimmune diseases, e.g. diabetes.
 CC rheumatoid arthritis and lupus erythematosus. The products can also be
 CC used for detection and diagnosis.
 SQ Sequence 10 AA;

Query Match 100.0%; Score 50; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.00083;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 REDLRTLLRY 10
 Db 1 REDLRTLLRY 10
 |||||

RESULT 5
 R71442
 ID R71442 standard; peptide; 17 AA.
 AC R71442;
 DT 12-OCT-1995 (first entry)
 DE Human HLA-B*27-(62-85) antigen derived peptide.
 KW Human HLA-B*27-(62-85) antigen derived peptide; cell receptor;
 KW interaction modulation; arthritis; neoplasias; lupus erythematosus.
 OS Homo sapiens.
 PN W09505189-A.
 PD 23-FEB-1995.
 PF 12-AUG-1994; U09189.
 PR 12-AUG-1993; US-103416.
 PA (REGC) UNIV CALIFORNIA.

PI Goldstein A, Goodenow RS, Olsson L;
 DR WPI: 95-098577/13.
 PT Regulating cell surface receptor response - by modulating
 PT interaction between MHC class I antigen and the cell surface
 PT receptor
 PS Example 4; Page 45; 103pp; English.
 CC R71443 are human major histocompatibility complex class I
 CC (MHC 1) alpha 1 domain and HLA derived peptides and fusion peptides.
 CC They were used to modulate interactions between MHC 1/HLA and cell
 CC surface receptors. Via competitive inhibition the peptides diminish
 CC the receptors response. This feature may be useful for the treatment
 CC of neoplasias, lupus erythematosus and arthritis.
 SQ Sequence 17 AA;

Query Match 100.0%; Score 50; DB 1; Length 17;
 Best Local Similarity 100.0%; Pred. No. 0.0014; Mismatches 0; Indels 0; Gaps 0;
 Matches 10; Conservative 0;

OY 1 REDRLTLRY 10
 Db 7 REDRLTLRY 16
 |||||

RESULT 6
 ID R71443 standard; peptide; 17 AA.
 AC R71443;
 DT 12-OCT-1995 (first entry)
 DE Human [Phe74]-HLA-B27-(62-85) antigen derived peptide.
 KW Human [Phe74]-HLA-B27-(62-85) antigen derived peptide; cell receptor;
 KW interaction modulation; arthritis; neoplasias; lupus erythematosus.
 OS Homo sapiens.
 PN WO9505189-A.
 PD 23-FEB-1995.
 PF 12-AUG-1994; U09189.
 PR 12-AUG-1993; US-105416.
 PA (REGC) UNIV CALIFORNIA.
 PI Goldstein A, Goodenow RS, Olsson L;
 DR WPI: 95-098577/13.
 PT Regulating cell surface receptor response - by modulating
 PT interaction between MHC class I antigen and the cell surface
 PT receptor
 PS Example 4; Page 45; 103pp; English.
 CC R71439-R71443 are human major histocompatibility complex class 1
 CC (MHC 1) alpha 1 domain and HLA derived peptides and fusion peptides.
 CC They were used to modulate interactions between MHC 1/HLA and cell
 CC surface receptors. Via competitive inhibition the peptides diminish
 CC the receptors response. This feature may be useful for the treatment
 CC of neoplasias, lupus erythematosus and arthritis.
 SQ Sequence 17 AA;

Query Match 100.0%; Score 50; DB 1; Length 17;
 Best Local Similarity 100.0%; Pred. No. 0.0014;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 REDRLTLRY 10
 Db 7 REDRLTLRY 16
 |||||

RESULT 7
 ID R41221 standard; peptide; 25 AA.
 AC R41221;
 DT 15-MAR-1994 (first entry)
 DE Peptide fragment of HLA-B2705 antigen.
 KW Human leukocyte antigen; HLA; peptide; transplantation; neoplasia;
 KW parasitic disease; cytotoxic T lymphocyte; modulation.
 OS Synthetic.
 PN WO9317699-A.
 PD 16-SEP-1993.

PF 25-FEB-1993; U01758.
 PR 02-MAR-1992; US-844716.
 PA (STRD) UNIV LELAND STANFORD JUNIOR.
 PI Clayberger CA, Krensky AM,
 DR WPI: 93-303134/38.
 PT New peptide(s) based on Class I HLA antigen domains - used for
 PT modulating cytotoxic T-lymphocyte activity towards targets
 PS Example 13; Page 39; 61pp; English.
 CC The peptide is used to modulate cytotoxic T-lymphocyte (CTL)
 CC activity, either by inhibition or stimulation. It can be used for
 CC inhibiting CTL toxicity in transplantations, for inducing CTL
 CC activity in parasitic diseases and neoplasia and in studies on viral
 CC infection. The peptide can also be used for identifying CTLs which
 CC bind to it and removing subsets of CTLs from a T-cell composition.
 CC This peptide is derived from the HLA-B2705 antigen and corresponds
 CC to the amino acid positions 60-84 of that antigen.
 SQ Sequence 25 AA;

Query Match 100.0%; Score 50; DB 1; Length 25;
 Best Local Similarity 100.0%; Pred. No. 0.0022;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 REDRLTLRY 10
 Db 16 REDRLTLRY 25
 |||||

RESULT 8
 ID R83091 standard; peptide; 25 AA.
 AC R83091;
 DT 16-MAY-1996 (first entry)
 DE HLA-B2702 CTL modulating peptide (B2702.60-84).
 KW Cytotoxic T lymphocyte; CTL; major histocompatibility complex; MHC;
 KW immunosuppressant; graft versus host disorder; transplantation; therapy;
 KW class I MHC; HLA-B2702.
 OS Synthetic.
 PN WO9526979-A.
 PD 12-OCT-1995.
 PF 05-APR-1995; U04349.
 PR 05-APR-1994; US-222851.
 PA (STRD) UNIV LELAND STANFORD JUNIOR.
 PI Clayberger C, Krensky AM, Parham P;
 DR WPI: 95-358582/46.
 PT Extension of acceptance period of transplants from MHC unmatched
 PT donor hosts - using Class I B75-84 MHC antigen of the recipient
 PT host
 PS Example 13; Page 32; 80pp; English.
 CC R83061-R83085, R83090-R83096 and R92907-R92913 represent fragments of
 CC class I major histocompatibility complex (MHC) antigens. This sequence
 CC corresponds to residues 60-84 of the alpha-1 domain of the class I MHC
 CC HLA-B2702. These sequences can be used to extend the period of
 CC acceptance by a recipient of a transplant from an MHC unmatched donor.
 CC The peptides are administered to a patient in conjunction with
 CC a subtherapeutic amount of an immunosuppressant. This is administered to
 CC the patient for a limited period of time (compared to the lifetime
 CC administration for current treatments). The peptides particularly
 CC modulate (or inhibit) the activity of the cytotoxic T lymphocytes (CTLs)
 CC of the patient.
 SQ Sequence 25 AA;

Query Match 100.0%; Score 50; DB 1; Length 25;
 Best Local Similarity 100.0%; Pred. No. 0.0022;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 REDRLTLRY 10
 Db 16 REDRLTLRY 25
 |||||

RESULT 9

R95417
ID R95417 standard; peptide; 25 AA.
AC R95417;
DT 12-NOV-1996 (first entry)
DE HLA-B2705.60-84.
KW HLA; p74; alpha1-helix; human-leucocyte-associated antigen; inhibitor;
KW T-cell lysate; membrane protein; mammal; heat shock protein; Hsc70; APC;
KW B cell; calcium influx; cytotoxic T lymphocyte; CTL; differentiation;
KW cytolysis; antigen presenting cell.
OS Synthetic.
PN WO9513288-A1.
PD 18-MAY-1995.
PF 10-NOV-1994; UI2985.
PR 10-NOV-1993; US-150493.
PA (STRD) UNIV LELAND STANFORD JUNIOR.
PI Clayberger C, Krensky AM;
DR WPI: 95-194027/25.
PT Compns. comprising lymphoid surface membrane proteins - which may
PT inhibit cytolytic activity and differentiation of CTLs.
PS Example; Page 9; 29pp; English.
CC R95413, and R95415-R95431 represent palindromes and fragments of
CC human-leucocyte-associated antigens. This sequence represents the
CC HLA-B2705.60-84. These sequences can be used to isolate the protein p74
CC from a T-cell lysate. p74 is a T-cell surface membrane protein
CC associated with T-cell activation in mammalian T-cells, and is also
CC immunologically cross reactive with the heat shock protein Hsc70. p74 is
CC found in a limited number of cell types, but is particularly expressed on
CC B and T cells. p74 can be isolated by lysis of a suitable cell with an
CC amphoteric detergent, and then passed through an affinity column
CC containing a covalently bound HLA-B2702 palindromic peptide.
CC Compositions comprising the extracellular fragment of p74 combined with
CC HLA-B2702.60-84 (see R95416), induces calcium influx, and inhibits
CC cytotoxic T lymphocyte (CTL) differentiation or cytolysis. Candidate
CC compounds can be screened for their effect on the cytolytic activity of
CC T-cells, by combining them with the extracellular portion of p74 and
CC determining the amount of binding between the candidate compound and p74.
CC Modulation of CTL activity can be inhibited in a cellular composition
CC containing T-cells and antigen presenting cells (APCs), by adding to the
CC mix the extracellular portion of p74, in an amount sufficient to compete
CC with p74 for the binding of the p74 ligand.
SQ Sequence 25 AA;

Query Match 100.0%; Score 50; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.0022;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 REDLRTLLRY 10
DB 16 REDLRTLLRY 25
|||||

RESULT 10
P70590
ID P70590 standard; protein; 337 AA.
AC P70590;
DT 10-APR-1991 (first entry)
DE Sequence of the human histocompatibility antigen HLA B27.
KW Rheumatic disorder; genetic screening; diagnosis;
KW ankylosing spondylitis.
OS Homo sapiens.
PN DE3542024-A.
PD 04-JUN-1987.
PF 28-NOV-1985; 542024.
PR 28-NOV-1985; DE-542024.
PR 21-DEC-1985; DE-545576.
PA (BEHW) BEHRINGERWERKE AG.
PI Riethmuller G, Meo T, Weiss E, Szots H;
DR WPI: 87-157893/23.
DR N-PSDB: N70935.
PT DNA coding for antigen HLA B27 - and diagnostic reagents contg.
PT such DNA, antigen or antibody
PS Disclosure; Page 5; 5pp; German.

CC The DNA may be used as a hybridisation probe for detecting the HLA
CC B27 gene, eg for assessing susceptibility to rheumatic disorders
CC such as ankylosis spondylitis, or may be used to transform cells
CC for prodn. of HLA B27. The HLA B27 may be used to detect HLA B27
CC antibody in human serum, or to produce mono- or polyclonal HLA B27
CC antibodies for use in immunoassay.
SQ Sequence 337 AA;

Query Match 100.0%; Score 50; DB 1; Length 337;
Best Local Similarity 100.0%; Pred. No. 0.033;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 REDLRTLLRY 10
DB 75 REDLRTLLRY 84
|||||

RESULT 11
P70155
ID P70155 standard; protein; 362 AA.
AC P70155;
DT 10-MAR-1993 (revised)
DT 03-APR-1991 (first entry)
DE Sequence encoded by genomic DNA encoding human histocompatibility
DE antigen HLA-B 27.
KW Ankylosing spondylitis; rheumatic disorder; diagnosis.
OS Homo sapiens.
PN EP-226069-A.
PD 24-JUN-1987.
PF 21-NOV-1986; 116139.
PR 01-JAN-1985; DE-542024.
PR 21-DEC-1985; DE-545576.
PA (BEHW) BEHRINGERWERKE AG.
PI Szots H, Weiss E, Dorner C, Lang M, Meo T, Riethmuller G;
DR WPI: 87-171469/25.
DR N-PSDB: N70225.
PT DNA coding for human histocompatibility antigen HLA-B 27 - useful
PT for diagnosis and antigen and antibody prodn.
PS Disclosure; p6; 13pp; German.
CC The DNA may be used to detect the HLA-B 27 gene (opt. mutated) in
CC human genetic material. The HLA-B 27 may be used to detect anti-HLA-
CC B 27 antibodies in human serum. The antibodies may be used to
CC determine HLA-B 27 levels in human serum, eg for diagnosis of
CC rheumatic disorders, esp. ankylosing spondylitis.
SQ Sequence 362 AA;

Query Match 100.0%; Score 50; DB 1; Length 362;
Best Local Similarity 100.0%; Pred. No. 0.035;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 REDLRTLLRY 10
DB 99 REDLRTLLRY 108
|||||

RESULT 12
W47271
ID W47271 standard; peptide; 10 AA.
AC W47271;
DT 22-MAY-1998 (first entry)
DE Immunomodulatory peptide.
KW Immunomodulator; Class I HLA-B alpha-1 domain; inhibition;
KW transplant rejection; treatment; autoimmune disease.
OS Homo sapiens.
OS Synthetic.
FH Key
FH Key Location/Qualifiers
FT Misc_difference 1..10 /note= "at least one of the amino acids is the
FT D-isomer
PN WO9744052-A1.
PD 27-NOV-1997.

1-3 CN, 1-3 SH, 1-3 sulphinyl, 1-3 sulphonyl,
 1-3 sulphoxyl, 1-3 OH, 1-3 COOH, 1-3 haloalkyl,
 1-3 NR6R7, 1-3 alkylene-NR6R7 and 1 or 2 oxo;
 R1=H; R2=OH.

US5516642-A.
 PN 14-MAY-1996.
 PD 16-NOV-1992; 976872.
 PF 16-NOV-1992; US-976872.
 PR 16-NOV-1992; US-976872.
 PA (BRIM) BRISTOL-MYERS SQUIBB CO.
 PI Mapelli C, Meyers CA;
 DR WPI; 96-251003/25.
 FT New glucose transport enhancing poly:peptide compounds - derived from
 PT major histocompatibility complex Class I antigen, used for treating
 PT diabetes mellitus or as diagnostic reagent.
 PS Claim 1: Columns 11-12; 6pp; English.
 CC The present sequence represents the generic formula of new glucose
 CC transport enhancing peptides, derived from the major histocompatibility
 CC complex (MHC) Class I antigen. They can be used for treating diabetes
 CC mellitus and in screening for compounds with a similar mode of
 CC action. They enhance or reduce the physiological response of a
 CC cell as a result of binding to certain cellular components, such as
 CC receptors, transporters, receptor-bound ligands or other membrane-bound
 CC components. Typically, the peptides (Optionally covalently bound to
 CC insulin or its functional segment) enhance glucose uptake in a
 CC cell. They may also be used diagnostically as a ligand to determine the
 CC presence of the cellular components described above. These peptides have
 CC increased potency and stability in bioassay buffers compared with known
 CC MHC Class I-derived peptides. They can be radioiodinated with gel
 CC retention of activity, and are not subject to aggregation and gel
 CC formation.
 SQ Sequence 13 AA;

Query Match 86.08; Score 43; DB 1; Length 13;
 Best Local Similarity 90.08; Pred. NO. 0.024;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 REDLRTLLRY 10
 | | | | | | | |
 Db 3 RVDLRTLLRY 12

Search completed: February 8, 2000, 04:05:42
 Job time: 9359 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: February 7, 2000, 18:04:36 ; Search time 111.22 seconds
(without alignments)
4.241 Million cell updates/sec

Title: US-08-653-294-23
Perfect score: 50
Sequence: 1 REDLRTLRY 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 142080 seqs, 47169319 residues

Total number of hits satisfying chosen parameters: 142080

Minimum DB seq length: 0

Maximum DB seq length: 1000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : PIR_62.*

1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	50	100.0	338	2	MHC HLA-B27-HS - h
2	50	100.0	362	1	HLHUB2
3	50	100.0	362	2	MHC class I histoc
4	50	100.0	362	2	MHC class I histoc
5	50	100.0	362	2	MHC class I histoc
6	50	100.0	362	2	human lymphocyte a
7	45	90.0	137	2	MHC HLA-B27d - hum
8	44	88.0	362	2	class I histocompa
9	43	86.0	328	2	MHC class I histoc
10	43	86.0	362	2	MHC H-2K transplan
11	43	86.0	368	2	MHC H-2D-k protein
12	40	80.0	355	2	MHC H-2K-w28 prote
13	40	80.0	362	2	HLA-B alpha-chain
14	40	80.0	362	2	class I histocompa
15	40	80.0	362	2	MHC class I histoc
16	40	80.0	362	2	MHC HLA-B44.2 chai
17	39	78.0	362	2	MHC class I histoc
18	38	76.0	218	2	MHC class I lympho
19	38	76.0	298	1	MHC class I HLA-J
20	37	74.0	367	2	MHC class I histoc
21	37	74.0	426	2	hypothetical prote
22	37	74.0	1613	2	reverse gyrase (in
23	36	72.0	388	2	MHC class I histoc
24	36	72.0	337	2	H-2D cell surface
25	36	72.0	361	2	MHC class I protei
26	36	72.0	362	2	class I histocompa
27	36	72.0	362	2	class I histocompa
28	36	72.0	362	2	class I histocompa
29	36	72.0	369	1	MHC class I histoc
30	36	72.0	369	2	MHC class I antige

31 36 72.0 521 2 T16692
32 36 72.0 930 2 B72537
33 35 70.0 227 2 T10510
34 35 70.0 284 2 A45840
35 35 70.0 359 1 HLHUB4
36 35 70.0 692 2 E70571
37 35 70.0 1215 2 B72029
38 35 70.0 4644 1 A38905
39 34 68.0 157 2 G71729
40 34 68.0 273 2 T38509
41 34 68.0 274 2 I54483
42 34 68.0 315 2 A35452
43 34 68.0 319 2 G70373
44 34 68.0 354 2 I59308
45 34 68.0 354 2 I80168

hypothetical prote
hypothetical prote
cbbv protein - Rho
MHC class I histoc
MHC class I histoc
probable thrs prot
swi/snf family hel
dynein heavy chain
hypothetical prote
MHC class I histoc
MHC HLA-B38 chain
aldehyde reductase
Mg(2+) and Co(2+)
class I histocompa
class I histocompa

ALIGNMENTS

RESULT 1

I56116
MHC HLA-B27-HS - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 23-Jul-1999
C:Accession: I56116
R:Choo, S.Y.; Fan, L.A.; Hansen, J.A.

J. Immunol. 147, 174-180, 1991
A:Title: A novel HLA-B27 allele maps B27 allospecificity to the region around positio
A:Reference number: I56116; MUID:91268545
A:Accession: I56116
A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA
A:Residues: 1-338 <RES>

A:Cross-references: GB:M62852; NID:g187760; PIDN:AAA59647.1; PID:g187761
C:Superfamily: class I histocompatibility antigen; immunoglobulin homology

Query Match 100.0%; Score 50; DB 2; Length 338;

Best Local Similarity 100.0%; Pred. No. 0.039;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 REDLRTLRY 10

Db 75 REDLRTLRY 84

RESULT 2

HLHUB2

MHC class I histocompatibility antigen HLA-B27 alpha chain precursor - human
C:Species: Homo sapiens (man)
C:Date: 13-Aug-1986 #sequence_revision 28-Apr-1995 #text_change 22-Jun-1999
C:Accession: S07441; A25092; B25092; A94087; S44180; S44942; A90493; B24741; I55965;
R:Weiss, E.H.; Kuon, W.; Doerner, C.; Lang, M.; Risthmueller, G.
Immunobiology 170, 367-380, 1985

A:Title: Organization, sequence and expression of the HLA-B27 gene: a molecular appro
A:Reference number: S07441; MUID:86138405
A:Accession: S07441

A:Molecule type: DNA

A:Residues: 1-362 <WEI>

A:Cross-references: EMBL:X03945

A:Note: the authors translated the codon GAC for residue 61 as Ala and the codon CAG
A:Note: this allele is designated B*27052 (formerly 27W)

R:Seemann, G.H.A.; Rein, R.S.; Brown, C.S.; Ploegh, H.L.

EMBO J. 5, 547-552, 1986

A:Title: Gene conversion-like mechanisms may generate polymorphism in human class I g

A:Reference number: A91061; MUID:86220133

A:Accession: A25092

A:Molecule type: DNA

A:Residues: 1-362 <SEE>

A:Cross-references: GB:X03665; NID:g32250; PIDN:CAA27302.1; PID:g871297

A:Note: this allele is designated B*27051 (formerly 27W)

A:Accession: B25092

A:Molecule type: DNA
A:Residues: 1-100,'N','102-103','IA','106-362 <SE>
A:Cross-references: GB:X03664; NID:Q32238; PIDN:CAA27301.1; PID:g871296
A:Note: this allele is designated B*2702 (formerly 27K)
R:Zoeets, H.; Riettmueller, G.; Weiss, E.; Meo, T.
Proc. Natl. Acad. Sci. U.S.A. 83, 1428-1432, 1986
A:Title: Complete sequence of HLA-B*27 cDNA identified through the characterization of s
A:Reference number: A94087; MUID:86149317
A:Accession: A94087
A:Molecule type: mRNA
A:Residues: 25-205,'V','207-362 <SZO>
A:Cross-references: GB:M12678
A:Note: this allele is designated B*27052 (formerly 27W)
R:Vilches, C.
submitted to the EMBL Data Library, June 1993
A:Reference number: S34180
A:Accession: S34180
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-100,'S','102-137','D','139','Y','141-175','E','177-362 <VIL>
A:Cross-references: EMBL:X73578
A:Note: this allele is designated B*2706
R:D'Amato, M.; Sorrentino, R.
submitted to the EMBL Data Library, May 1994
A:Description: Identification of a novel HLA-B*27 subtype by restriction analysis of a c
A:Reference number: S44942
A:Accession: S44942
A:Molecule type: mRNA
A:Residues: 1-139,'H','141-362 <DAM>
A:Cross-references: EMBL:Z33453; NID:g486652; PIDN:CAA83876.1; PID:g486653
R:Esquerria, A.; Bragado, R.; Vega, M.A.; Strominger, J.L.; Woody, J.; Lopez de Castro, J
Biochemistry 24, 1733-1741, 1985
A:Title: Primary structure of papain-solubilized human histocompatibility antigen HLA-B*2
A:Reference number: A90493; MUID:85226361
A:Accession: A90493
A:Molecule type: protein
A:Residues: 25-265,'E','267-295 <EZQ>
R:Vega, M.A.; Esquerria, A.; Rojo, S.; Aparicio, P.; Bragado, R.; Lopez de Castro, J.A.
Proc. Natl. Acad. Sci. U.S.A. 82, 7394-7398, 1985
A:Title: Structural analysis of an HLA-B*27 functional variant: identification of residue
A:Reference number: A94070; MUID:86042671
A:Accession: B24741
A:Molecule type: protein
A:Residues: 86-100,'N','102-103','IA','106-107:171-181 <VEG>
R:Coppin, H.L.; McDevitt, H.O.
J. Immunol. 137, 2168-2172, 1986
A:Title: Absence of polymorphism between HLA-B*27 genomic exon sequences isolated from no
A:Reference number: I55965; MUID:87009855
A:Accession: I55965
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 25-298 <RES>
A:Cross-references: GB:M14013; NID:g187743; PIDN:AAA59643.1; PID:g187744
R:Blasczyk, R.; Weber, M.; Salama, A.
submitted to the EMBL Data Library, January 1995
A:Reference number: S52291
A:Accession: S52291
A:Molecule type: DNA
A:Residues: 116-192 <BLA>
A:Cross-references: EMBL:X83737
C:Comment: This allele for HLA-B correlates with the development of ankylosing spondylit
C:Genetics:
A:Gene: GDB:HLA-B
A:Cross-references: GDB:120048; OMIM:142830
A:Map position: 6p21.3-6p21.3
C:Superfamily: class I histocompatibility antigen; immunoglobulin homology
F:1-24/Domain: intracellular #status predicted <SIG>
F:1-24/Domain: signal sequence #status predicted <SIG>
F:25-362/Product: class I histocompatibility antigen HLA-B*27 alpha chain #status predict
F:25-307/Domain: extracellular #status predicted <EXI>
F:25-114/Domain: alpha-1 <EXI>
F:115-206/Domain: alpha-2 <EX2>

F:220-285/Domain: immunoglobulin homology <IMM>
F:308-331/Domain: transmembrane #status predicted <TM>
F:332-362/Domain: intracellular #status predicted <INT>
F:110/Binding site: carbohydrate (Asn) (covalent) #status experimental
F:125-188/227-283/Disulfide bonds: #status experimental
Query Match 100.0%; Score 50; DB 1; Length 362;
Best Local Similarity 100.0%; Pred. No. 0.042; 0; Indels 0; Gaps 0;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 REDLRTLLRY 10
|||||
Db 99 REDLRTLLRY 108
RESULT 3
MHC class I histocompatibility antigen HLA-B*37 alpha chain precursor - human
C:Species: Homo sapiens (man)
C:Date: 16-Nov-1990 #sequence_revision 13-Jan-1993 #text_change 23-Jul-1999
C:Accession: C35997
R:Ennis, P.D.; Zemmour, J.; Salter, R.D.; Parham, P.
Proc. Natl. Acad. Sci. U.S.A. 87, 2833-2837, 1990
A:Title: Rapid cloning of HLA-A,B cDNA by using the polymerase chain reaction: freque
A:Reference number: A35997; MUID:90207291
A:Accession: C35997
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-362 <ENN>
A:Cross-references: GB:M32320; NID:g187792; PIDN:AAA36233.1; PID:g307224
C:Genetics:
A:Gene: GDB:HLA-B
A:Cross-references: GDB:120048; OMIM:142830
A:Map position: 6p21.3-6p21.3
C:Superfamily: class I histocompatibility antigen; immunoglobulin homology
C:Keywords: transmembrane protein
F:220-285/Domain: immunoglobulin homology <IMM>
Query Match 100.0%; Score 50; DB 2; Length 362;
Best Local Similarity 100.0%; Pred. No. 0.042; 0; Indels 0; Gaps 0;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 REDLRTLLRY 10
|||||
Db 99 REDLRTLLRY 108
RESULT 4
MHC class I histocompatibility antigen HLA-B*47 precursor - human
C:Species: Homo sapiens (man)
C:Date: 07-Jun-1996 #sequence_revision 07-Jun-1996 #text_change 23-Jul-1999
C:Accession: I68724
R:Zemmour, J.; Ennis, P.D.; Parham, P.; Dupont, B.
Immunogenetics 27, 281-287, 1988
A:Title: Comparison of the structure of HLA-B*47 to HLA-B*13 and its relationship to 2
A:Reference number: I54442; MUID:88152906
A:Accession: I68724
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-362 <ENN>
A:Cross-references: GB:M19756; NID:g184171; PIDN:AAA52664.1; PID:g386776
C:Superfamily: class I histocompatibility antigen; immunoglobulin homology
Query Match 100.0%; Score 50; DB 2; Length 362;
Best Local Similarity 100.0%; Pred. No. 0.042; 0; Indels 0; Gaps 0;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 REDLRTLLRY 10
|||||

Db 99 REDLRTLLRY 108

RESULT 5

I37485

human lymphocyte antigen HLA-B*27 - human

C:Species: Homo sapiens (man)

C>Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 23-Jul-1999

C:Accession: I37485

R:Del Porto, P.; D'Amato, M.; Florillo, M.T.; Tuosto, L.; Piccolella, E.; Sorrentino, R.

J. Immunol. 153: 3093-3100, 1994

A>Title: Identification of a novel HLA-B*27 subtype by restriction analysis of a cytotoxic

A:Reference number: I37485; MUID:94375872

A:Accession: I37485

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-362 <RES>

A:Cross-references: EMBL:Z33453; NID:g486652; PIDN:CAA83876.1; PID:g486653

C:Superfamily: class I histocompatibility antigen; immunoglobulin homology

Query Match 100.0%; Score 50; DB 2; Length 362;

Best Local Similarity 100.0%; Pred. No. 0.042; Mismatches 0; Indels 0; Gaps 0;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 REDLRTLLRY 10

|||||

Db 99 REDLRTLLRY 108

RESULT 6

I34289

MHC HLA-B*27d - human

C:Species: Homo sapiens (man)

C>Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 23-Jul-1999

C:Accession: I34289

R:Choo, S.Y.; St. John, T.; Orr, H.T.; Hansen, J.A.

Hum. Immunol. 21: 209-219, 1988

A>Title: Molecular analysis of the variant alloantigen HLA-B*27d (HLA-B*2703) identifies

A:Reference number: I34289; MUID:88227491

A:Accession: I34289

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-362 <RES>

A:Cross-references: GB:M54883; NID:g187663; PIDN:AAA59616.1; PID:g187664

C:Genetics:

A:Gene: GDB:HLA-B

A:Cross-references: GDB:120048; OMIM:142830

A:Map position: 6p21.3-6p21.3

A:Introns: 25/1; 115/1; 207/1; 299/1; 338/1; 349/1

C:Superfamily: class I histocompatibility antigen; immunoglobulin homology

Query Match

Best Local Similarity 100.0%; Score 50; DB 2; Length 362;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 REDLRTLLRY 10

|||||

Db 99 REDLRTLLRY 108

RESULT 7

I80174

class I histocompatibility antigen - chimpanzee (fragment)

C:Species: Pan troglodytes (chimpanzee)

C>Date: 24-May-1996 #sequence_revision 24-May-1996 #text_change 23-Jul-1999

C:Accession: I80174

R:McAdam, S.N.; Boyson, J.E.; Liu, X.; Garber, T.L.; Hughes, A.L.; Bontrop, R.E.; Watkins

Proc. Natl. Acad. Sci. U.S.A. 91: 5893-5897, 1994

A>Title: A uniquely high level of recombination at the HLA-B locus.

A:Reference number: I59308; MUID:94286544

A:Accession: I80174

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-137 <RES>

A:Cross-references: EMBL:U05585; NID:g454787; PIDN:AAA50188.1; PID:g454788

C:Superfamily: class I histocompatibility antigen; immunoglobulin homology

Query Match

Best Local Similarity 90.0%; Score 45; DB 2; Length 137;

Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 REDLRTLLRY 10

|||||

Db 40 RENLRTLLRY 49

RESULT 8

I37515

MHC class I histocompatibility antigen HLA-B*2706 alpha chain precursor - human

C:Species: Homo sapiens (man)

C>Date: 04-Oct-1996 #sequence_revision 04-Oct-1996 #text_change 23-Jul-1999

C:Accession: I37515

R:Viaches, C.; de Pablo, R.; Kreisler, M.

Immunogenetics 39: 219, 1994

A>Title: Nucleotide sequence of HLA-B*2706.

A:Reference number: I37515; MUID:94102824

A:Accession: I37515

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-362 <RES>

A:Cross-references: EMBL:X73578; NID:g975658; PIDN:CAA51980.1; PID:g975659

C:Genetics:

A:Gene: GDB:HLA-B

A:Cross-references: GDB:120048; OMIM:142830

A:Map position: 6p21.3-6p21.3

C:Superfamily: class I histocompatibility antigen; immunoglobulin homology

Query Match

Best Local Similarity 88.0%; Score 44; DB 2; Length 362;

Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 REDLRTLLRY 10

|||||

Db 99 RESLRTLLRY 108

RESULT 9

I54414

MHC H-2K transplantation antigen - mouse (fragment)

C:Species: Mus musculus (house mouse)

C>Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 23-Jul-1999

C:Accession: I54414

R:Morita, T.; Delarbre, C.; Kress, M.; Kourilsky, P.; Gachelin, G.

Immunogenetics 21: 367-383, 1985

A>Title: An H-2K gene of the t-w32 mutant at the T/t complex is a close parent of an

A:Reference number: I54414; MUID:85206119

A:Accession: I54414

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-328 <RES>

A:Cross-references: GB:ML4827; NID:g199550; PIDN:AAA39656.1; PID:g387471

C:Superfamily: class I histocompatibility antigen; immunoglobulin homology

Query Match

Best Local Similarity 86.0%; Score 43; DB 2; Length 328;

Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 REDLRTLLRY 10

|||||

Db 56 RYDLRTLLRY 65

RESULT 10

I71998
MHC H-2D-k protein - mouse
C:Species: Mus musculus (house mouse)
C>Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 23-Jul-1999
C:Accession: I71998
R:Watts, S.; Vogel, J.M.; Harriman, W.D.; Itoh, T.; Staus, H.J.; Goodenow, R.S.
J. Immunol. 139, 3878-3885, 1987
A:Title: DNA sequence analysis of the C3H H-2Kk and H-2Dk loci. Evolutionary relationships
A:Reference number: I56002; MUID:88060499
A:Accession: I71998
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-362 <RES>
A:Cross-references: GB:M18524; NID:g199415; PIDN:AAAS3201.1; PID:g387453
C:Genetics:
C:Introns: 25/1; 115/1; 207/1; 338/1; 349/1; 362/1
C:Superfamily: class I histocompatibility antigen; immunoglobulin homology

Query Match 86.0%; Score 43; DB 2; Length 362;
Best Local Similarity 90.0%; Pred. No. 0.9;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 REDLRTLLRY 10
| |||||
DB 99 RVDLRTLLRY 108

RESULT 11

I68705
MHC H-2K-w28 protein - mouse
C:Species: Mus musculus (house mouse)
C>Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 23-Jul-1999
C:Accession: I68705
R:Morita, T.; Delarbre, C.; Kress, M.; Kourilsky, P.; Gachelin, G.
Immunogenetics 21, 367-383, 1995
A:Title: An H-2K gene of the t-w32 mutant at the T/t complex is a close parent of an H-2
A:Reference number: I54414; MUID:85206119
A:Accession: I68705
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-368 <RES>
A:Cross-references: GB:M14825; NID:g199552; PIDN:AAA39657.1; PID:g387472
C:Genetics:
A:Introns: 22/1; 112/1; 204/1; 296/1; 335/1; 346/1; 359/1
C:Superfamily: class I histocompatibility antigen; immunoglobulin homology

Query Match 86.0%; Score 43; DB 2; Length 368;
Best Local Similarity 90.0%; Pred. No. 0.91; 1; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 REDLRTLLRY 10
| |||||
DB 96 RVDLRTLLRY 105

RESULT 12

I37516
HLA-B alpha-chain - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 04-Oct-1996 #sequence_revision 04-Oct-1996 #text_change 23-Jul-1999
C:Accession: I37516
R:Gauchat-Feiss, D.; Breur-Vriesendorp, B.S.; Rufer, N.; Jeannet, M.; Roosnek, E.; Tiedt
Tissue Antigens 44, 261-264, 1994
A:Title: Sequencing of a novel functional HLA-B*44 subtype differing in two residues in t
A:Reference number: I37516; MUID:95176328
A:Accession: I37516
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-355 <RES>

A:Cross-references: EMBL:X75953; NID:g791007; PIDN:CAA53566.1; PID:g791008
C:Superfamily: class I histocompatibility antigen; immunoglobulin homology

Query Match 80.0%; Score 40; DB 2; Length 355;
Best Local Similarity 80.0%; Pred. No. 3.3;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 REDLRTLLRY 10
| |||||
DB 99 RENVLTALRY 108

RESULT 13

S25415
Class I histocompatibility antigen HLA-B*4403 alpha chain - human
C:Species: Homo sapiens (man)
C>Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 23-Jul-1999
C:Accession: S25415
R:Flieschhauer, K.; Kernan, N.A.; Dupont, B.; Yang, S.Y.
Tissue Antigens 37, 133-137, 1991
A:Title: The two major subtypes of HLA-B*44 differ for a single amino acid in codon 15
A:Reference number: S25415; MUID:91335451
A:Accession: S25415
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-362 <FLE>
A:Cross-references: EMBL:X64366; NID:g32178; PIDN:CAA45718.1; PID:g32179
C:Genetics:
A:Gene: GDB:HLA-B
A:Cross-references: GDB:120048; OMIM:142830
A:Map position: 6p21.3-6p21.3
C:Superfamily: class I histocompatibility antigen; immunoglobulin homology
C:Keywords: transmembrane protein
F:220-285/Domain: immunoglobulin homology <IMM>

Query Match 80.0%; Score 40; DB 2; Length 362;
Best Local Similarity 80.0%; Pred. No. 3.3;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 REDLRTLLRY 10
| |||||
DB 99 RENVLTALRY 108

RESULT 14

A45850
MHC class I histocompatibility antigen HLA-B13.1 - human
C:Species: Homo sapiens (man)
C>Date: 03-Jun-1993 #sequence_revision 03-Jun-1993 #text_change 23-Jul-1999
C:Accession: A45850
R:Rato, K.; Dupont, B.; Yang, S.Y.
Immunogenetics 29, 117-120, 1989
A:Title: Localization of nucleotide sequence which determines mongoloid subtype of HL
A:Reference number: A45850; MUID:89122134
A:Accession: A45850
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-362 <RAT>
A:Cross-references: GB:M24075; NID:g187703; PIDN:AAA59627.1; PID:g386884
C:Genetics:
A:Gene: GDB:HLA-B
A:Cross-references: GDB:120048; OMIM:142830
A:Map position: 6p21.3-6p21.3
C:Superfamily: class I histocompatibility antigen; immunoglobulin homology
F:220-285/Domain: immunoglobulin homology <IMM>

Query Match 80.0%; Score 40; DB 2; Length 362;
Best Local Similarity 80.0%; Pred. No. 3.3;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 REDLRTLLRY 10
||:|||||
Db 99 RENLRTALRY 108

RESULT 15
I61861
MHC HLA-B*44.2 chain - human
C:Species: Homo sapiens (man)
C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 23-Jul-1999
C:Accession: I61861
R:Parham, P.; Lawlor, D.A.; Lomen, C.E.; Ennis, P.D.
J. Immunol. 142, 3937-3950, 1989
A:Title: Diversity and diversification of HLA-A,B,C alleles.
A:Reference number: I36956; MUID:89235215
A:Accession: I61861
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-362 <RES>
A:Cross-references: GB:M24038; NID:G187811; PIDN:AAA59663.1; PID:G386900
C:Superfamily: class I histocompatibility antigen; immunoglobulin homology

Query Match 80.0%; Score 40; DB 2; Length 362;
Best Local Similarity 80.0%; Pred. No. 3.3;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 REDLRTLLRY 10
||:|||||
Db 99 RENLRTALRY 108

Search completed: February 7, 2000, 18:04:37
Job time: 22203 sec

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: February 8, 2000, 01:25:57 ; Search time 68.63 Seconds
(without alignments)
4.352 Million cell updates/sec

Title: US-08-653-294-23
Perfect score: 50
Sequence: 1 REDRLTLRY 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 82229 seqs, 29864866 residues

Total number of hits satisfying chosen parameters: 82229

Minimum DB seq length: 0

Maximum DB seq length: 1000000

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database : SwissProt_38.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	50	100.0	338	1B20_HUMAN	P30467 homo sapien
2	50	100.0	361	1B14_HUMAN	P03989 homo sapien
3	50	100.0	362	1B16_HUMAN	P19373 homo sapien
4	50	100.0	362	1B18_HUMAN	P10318 homo sapien
5	50	100.0	362	1B29_HUMAN	P18463 homo sapien
6	50	100.0	362	1B45_HUMAN	P30485 homo sapien
7	44	88.0	362	1B19_HUMAN	O08136 homo sapien
8	43	86.0	328	1HA1Q_MOUSE	P14428 mus musculu
9	43	86.0	362	1HA13_MOUSE	P14426 mus musculu
10	43	86.0	368	1HA1W_MOUSE	P03991 mus musculu
11	40	80.0	362	1B05_HUMAN	P30461 homo sapien
12	40	80.0	362	1B41_HUMAN	P30481 homo sapien
13	40	80.0	362	1B42_HUMAN	P30482 homo sapien
14	38	76.0	298	1HA1Y_MOUSE	P01895 mus musculu
15	38	76.0	365	1HA1Z_MOUSE	P01900 mus musculu
16	36	72.0	369	1HA1B_MOUSE	P01901 mus musculu
17	35	70.0	227	1CBY1_MOUSE	O33513 rhodobacter
18	35	70.0	359	1B40_HUMAN	P10320 homo sapien
19	35	70.0	692	1SYT_MYCTU	O06200 mycobacteri
20	35	70.0	4644	1DYHC_RAT	P38650 rattus norv
21	34	68.0	157	1Y18_RICPR	O92dx6 rickettsia
22	34	68.0	315	1ALDR_BOVIN	P16116 bos taurus
23	34	68.0	354	1GPR2_HUMAN	P46092 homo sapien
24	34	68.0	359	1B01_PANTR	P13750 pan troglod
25	34	68.0	362	1B01_GORGO	P30379 gorilla gor
26	34	68.0	362	1B02_GORGO	P30380 gorilla gor
27	34	68.0	362	1B03_GORGO	P30381 gorilla gor
28	34	68.0	362	1B15_HUMAN	P10317 homo sapien
29	34	68.0	362	1B47_HUMAN	P30487 homo sapien
30	34	68.0	362	1B49_HUMAN	P18464 homo sapien
31	34	68.0	362	1B52_HUMAN	P30489 homo sapien
32	34	68.0	362	1B53_HUMAN	P30490 homo sapien
33	34	68.0	362	1B54_HUMAN	P30491 homo sapien
34	34	68.0	362	1B60_HUMAN	P18465 homo sapien

ALIGNMENTS

RESULT 1

```

1B20_HUMAN          34 68.0 362 1 1B61_HUMAN          P30437 homo sapien
35 34 68.0 362 1 1B62_HUMAN          P10319 homo sapien
36 34 68.0 362 1 1B62_HUMAN          P01893 homo sapien
37 34 68.0 362 1 1A23_HUMAN          P30447 homo sapien
38 34 68.0 365 1 1A23_HUMAN          P05534 homo sapien
39 34 68.0 365 1 1A24_HUMAN          P50611 helicobacte
40 34 68.0 403 1 1FLGE_HELMU          P73769 synechocyst
41 34 68.0 912 1 1MUTS_SYNY3          P42345 homo sapien
42 34 68.0 2549 1 1FRAP_HUMAN          P42346 rattus norv
43 34 68.0 2549 1 1FRAP_RAT          P23734 trypanosoma
44 33 66.0 346 1 1P12_TRYBB          P54490 bacillus su
45 33 66.0 359 1 1YQGM_BACSU

AC P30467;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 01-APR-1993 (Rel. 25, Last annotation update)
DE HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-27 B*2707 ALPHA CHAIN
DE (B27-HS).
GN HLA-B OR HLAB.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Primates; Catarrhini; Homiidae; Homo.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 91268545.
RA CHOO Y.S., FAN L.A., HANSEN J.A.;
RT "A novel HLA-B*27 allele maps B27 allospecificity to the region around
RT position 70 in the alpha 1 domain."
RL J. Immunol. 147:174-180(1991).
CC -|- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
CC THE IMMUNE SYSTEM.
CC -|- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
CC MICROGLOBULIN).
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CC
CC EMBL; M62852; AAA59647.1; -.
CC HSSP; P03989; 1HSA.
CC TIM; 142830; -.
CC PROSITE; PS00290; IG_MHC; 1.
CC PFAM; PF00047; Ig; 1.
CC PFAM; PF00129; MHC_I; 1.
CC MHC I; Transmembrane; Glycoprotein.
CC DOMAIN 1 90 EXTRACELLULAR ALPHA-1.
CC DOMAIN 91 182 EXTRACELLULAR ALPHA-2.
CC DOMAIN 183 274 EXTRACELLULAR ALPHA-3.
CC DOMAIN 275 284 CONNECTING PEPTIDE.
CC TRANSMEM 285 308
CC DOMAIN 309 338 CYTOPLASMIC TAIL.
CC CARBOHYD 86 86 BY SIMILARITY.
CC DISULFID 101 164 BY SIMILARITY.
CC DISULFID 203 259 BY SIMILARITY.
CC SEQUENCE 338 AA; 37804 MW; 33FB8134 CRC32;

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Query Match 100.0%; Score 50; DB 1; Length 338;

Best Local Similarity 100.0%; Pred. No. 0.013;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 REDRLTLRY 10

|||||
75 REDRLTLRY 84

RESULT 2

DB 1B14_HUMAN STANDARD; PRT; 361 AA.
AC P03989;
DT 23-OCT-1986 (Rel. 02, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-27 ALPHA CHAIN PRECURSOR.
GN HLA-B OR HLAB.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Primates; Catarrhini; Hominidae; Homo.
[1]
RN SEQUENCE FROM N.A.
RP MEDLINE; 86138405.
RA WEISS E.H., KUON W., DOERNER C., LANG M., RIETHMUELLER G.;
RT "Organization, sequence and expression of the HLA-B27 gene: a
RT molecular approach to analyze HLA and disease associations.";
RL Immunobiology 170:367-380(1985).
[2]
RN SEQUENCE OF 25-361 FROM N.A.
RP MEDLINE; 86149317.
RX SZOETS H., RIETHMUELLER G., WEISS E., MEO T.;
RA "Complete sequence of HLA-B27 cDNA identified through the
RT characterization of structural markers unique to the HLA-A, -B, and
RT -C allelic series.";
RL Proc. Natl. Acad. Sci. U.S.A. 83:1428-1432(1986).
[3]
RN SEQUENCE OF 25-295.
RX MEDLINE; 85226361.
RA EQUEERRA A., BRAGADO R., VEGA M.A., STROMINGER J.L., WOODY J.,
RA LOPEZ DE CASTRO J.A.;
RT "Primary structure of papain-solubilized human histocompatibility
RT antigen HLA-B27.";
RL Biochemistry 24:1733-1741(1985).
[4]
RN X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS) OF 25-300.
RX MEDLINE; 92405152.
RA MADDEN D.R., GORGA J.C., STROMINGER J.L., WILEY D.C.;
RT "The three-dimensional structure of HLA-B27 at 2.1-A resolution
RT suggests a general mechanism for tight peptide binding to MHC.";
RL Cell 70:1035-1048(1992).
[5]
RN X-RAY CRYSTALLOGRAPHY.
RX MEDLINE; 92018187.
RA MADDEN D.R., GORGA J.C., STROMINGER J.L., WILEY D.C.;
RT "The structure of HLA-B27 reveals nonamer self-peptides bound in an
RT extended conformation.";
RL Nature 353:321-325(1991).
CC -!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
CC THE IMMUNE SYSTEM.
CC -!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
CC MICROGLOBULIN).
CC -!- DISEASE: THIS PROTEIN CORRELATES WITH THE DEVELOPMENT OF
CC ANKYLOSING SPONDYLITIS.
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CC -----
CC EMBL; X03945; CAA27578.1; ALT_TERM.
DR PIR; A25128; HLHUB2.
DR PIR; S07441; S07441.
DR PDB; 1HSA; 15-OCT-92.
DR MIM; 142830; -.

DR PROSITE; PS00290; IG_MHC; 1.
DR PFAM; PF00047; IG; 1.
DR PFAM; PF00129; MHC_I; 1.
KW MHC I; Transmembrane; Glycoprotein; Signal; 3D-structure.
FT SIGNAL 1 24
FT CHAIN 25 361
FT FT
FT DOMAIN 25 114
FT DOMAIN 115 206
FT DOMAIN 207 298
FT DOMAIN 299 308
FT TRANSMEM 309 332
FT DOMAIN 333 361
FT CARBOHYD 110 110
FT DISULFID 125 188
FT DISULFID 227 283
FT CONFLICT 206 206
FT CONFLICT 266 266
FT STRAND 27 38
FT TURN 39 41
FT STRAND 42 52
FT TURN 53 54
FT TURN 55 61
FT STRAND 62 63
FT STRAND 70 71
FT STRAND 74 76
FT TURN 77 78
FT HELIX 81 108
FT TURN 109 110
FT TURN 113 114
FT STRAND 118 127
FT TURN 129 130
FT STRAND 133 142
FT TURN 143 144
FT STRAND 145 150
FT TURN 152 153
FT STRAND 157 159
FT HELIX 162 173
FT TURN 174 175
FT HELIX 176 185
FT TURN 186 186
FT TURN 187 198
FT TURN 199 199
FT HELIX 200 203
FT TURN 204 204
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FT TURN 244 245
FT STRAND 246 247
FT HELIX 249 251
FT STRAND 253 254
FT STRAND 258 259
FT STRAND 265 274
FT TURN 275 276
FT TURN 278 280
FT STRAND 281 286
FT TURN 288 289
FT STRAND 294 296
SQ SEQUENCE 361 AA; 40464 MW; 802130DS CRC32;

Query Match 100.08; Score 50; DB 1; Length 361;
Best Local Similarity 100.08; Pred. No. 0.014;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 REDRLTLRY 10
|||||
DB 99 REDRLTLRY 108

RESULT 3

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1B16_HUMAN
ID 1B16_HUMAN STANDARD; PRT: 362 AA.
AC P19373;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DE HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-27 B*2703 ALPHA CHAIN
DE PRECURSOR (B-27D).
GN HLA-B OR HLAB
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Primates; Catarrhini; Hominidae; Homo.
[1]
RP SEQUENCE FROM N.A.
RX MEDLINE: 88227491.
RA CHOO S.Y., ST JOHN T., ORR H.T., HANSEN J.A.;
RT "Molecular analysis of the variant allotype HLA-B*2703 (HLA-B*2703)
RL Hum. Immunol. 21:209-219(1988).
CC -!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
CC THE IMMUNE SYSTEM.
CC -!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
CC MICROGLOBULIN).
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DR EMBL; M54883; AAA59616.1; .
DR HSSP; P03989; 1HSA.
DR MIM; 142830; .
DR PFAM; PS00290; IG_MHC; 1.
DR PFAM; PF00047; Ig; 1.
DR PFAM; PF00129; MHC_I; 1.
KW MHC I; Transmembrane; Glycoprotein; Signal.
FT SIGNAL 1 24
FT CHAIN 25 362 HLA CLASS I HISTOCOMPATIBILITY ANTIGEN,
FT DOMAIN 25 114 B-27 B*2703 ALPHA CHAIN.
FT DOMAIN 115 206 EXTRACELLULAR ALPHA-1.
FT DOMAIN 207 298 EXTRACELLULAR ALPHA-2.
FT DOMAIN 299 308 EXTRACELLULAR ALPHA-3.
FT TRANSMEM 309 332 CONNECTING PEPTIDE.
FT DOMAIN 333 362 CYTOPLASMIC TAIL.
FT CARBOHYD 110 110 BY SIMILARITY.
FT DISULFID 125 188 BY SIMILARITY.
FT DISULFID 227 283 BY SIMILARITY.
SQ SEQUENCE 362 AA; 40402 MW; 7261C3AB CRC32;

Query Match 100.0%; Score 50; DB 1; Length 362;
Best Local Similarity 100.0%; Pred. No. 0.015;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 REDRLTLRY 10
Db 99 REDRLTLRY 108
|||||
99 REDRLTLRY 108

RESULT 4
1B18_HUMAN
ID 1B18_HUMAN STANDARD; PRT: 362 AA.
AC P10318;
DT 01-MAR-1989 (Rel. 10, Created)
DT 01-MAR-1989 (Rel. 10, Last sequence update)
DE HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-27 B*2705 ALPHA CHAIN
DE... PRECURSOR (B-27W) (B27.1).
GN HLA-B OR HLAB.

```

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OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Primates; Catarrhini; Hominidae; Homo.
[1]
RP SEQUENCE FROM N.A.
RX MEDLINE: 86220133.
RA SEEMANN G.H.A., REIN R.S., BROWN C.S., PLOEGH H.L.;
RT "Gene conversion-like mechanisms may generate polymorphism in human
RT class I genes."
RL EMBO J. 5:547-552(1986).
[2]
RP SEQUENCE FROM N.A.
RX MEDLINE: 86138405.
RA WEISS E.H., KUON W., DOERNER C., LANG M., RIETHMUELLER G.;
RT "Organization, sequence and expression of the HLA-B27 gene: a
RT molecular approach to analyze HLA and disease associations."
RL Immunobiology 170:367-380(1985).
RN [3]
RX MEDLINE: 95148615.
RA ROGNAN D., SCAPOZZA L., FOLKERS G., DASER A.;
RT "Rational design of nonnatural peptides as high-affinity ligands for
RT the HLA-B*2705 human leukocyte antigen."
RL Proc. Natl. Acad. Sci. U.S.A. 92:753-757(1995).
CC -!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
CC THE IMMUNE SYSTEM.
CC -!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
CC MICROGLOBULIN).
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DR EMBL; X03665; CAA27302.1; .
DR EMBL; X03666; CAA27302.1; JOINED.
DR EMBL; M12967; AAA36221.1; .
DR PIR; A25092; HLHUBW.
DR PDB; IROG; 30-SEP-94.
DR PDB; IROH; 30-SEP-94.
DR PDB; IROI; 30-SEP-94.
DR PDB; IROJ; 30-SEP-94.
DR PDB; IROK; 30-SEP-94.
DR PDB; IROL; 30-SEP-94.
DR MIM; 142830; .
DR PROSITE; PS00290; IG_MHC; 1.
DR PFAM; PF00047; Ig; 1.
DR PFAM; PF00129; MHC_I; 1.
KW MHC I; Transmembrane; Glycoprotein; Signal; 3D-structure.
FT SIGNAL 1 24
FT CHAIN 25 362 HLA CLASS I HISTOCOMPATIBILITY ANTIGEN,
FT DOMAIN 25 114 B-27 B*2705 ALPHA CHAIN.
FT DOMAIN 115 206 EXTRACELLULAR ALPHA-1.
FT DOMAIN 207 298 EXTRACELLULAR ALPHA-2.
FT DOMAIN 299 308 EXTRACELLULAR ALPHA-3.
FT TRANSMEM 309 332 CONNECTING PEPTIDE.
FT DOMAIN 333 362 CYTOPLASMIC TAIL.
FT CARBOHYD 110 110 BY SIMILARITY.
FT DISULFID 125 188 BY SIMILARITY.
FT DISULFID 227 283 BY SIMILARITY.
SQ SEQUENCE 362 AA; 40428 MW; 73243566 CRC32;

Query Match 100.0%; Score 50; DB 1; Length 362;
Best Local Similarity 100.0%; Pred. No. 0.015;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 REDRLTLRY 10
|||||
1 REDRLTLRY 10

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Db 99 REDRLTLRY 108

RESULT 5
1B29_HUMAN
ID 1B29_HUMAN STANDARD; PRT; 362 AA.
AC P18463;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 01-APR-1993 (Rel. 25, Last annotation update)
DE HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-37 B*3701 ALPHA CHAIN
DE PRECURSOR.
GN HLA-B OR HLAB.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia;
OC Eutheria; Primates; Catarrhini; Homiidae; Homo.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 88152906.
RA ZEMMOUR J., ENNIS P.D., PARHAM P., DUPONT B.;
RT "Rapid cloning of HLA-A,B cDNA by using the polymerase chain
RT reaction: frequency and nature of errors produced in amplification.";
RL Proc. Natl. Acad. Sci. U.S.A. 87:2833-2837(1990).
CC -!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
CC THE IMMUNE SYSTEM.
CC -!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
CC MICROGLOBULIN).
CC
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CC
CC EMBL; M32320; AAA36233.1; -
CC DR PIR; C35997; C35997.
CC DR HSSP; P03989; IHS.
CC DR MIM; 142830; -
CC DR PROSITE; PS00290; IG_MHC; 1.
CC DR PFAM; PF00047; ig; 1.
CC DR PFAM; PF00129; MHC_I; 1.
CC DR MHC I; Transmembrane; Glycoprotein; Signal.
CC KW SIGNAL 1 24
CC FT CHAIN 25 362 HLA CLASS I HISTOCOMPATIBILITY ANTIGEN,
CC FT DOMAIN 25 114 B-37 B*3701 ALPHA CHAIN.
CC FT DOMAIN 115 206 EXTRACELLULAR ALPHA-1.
CC FT DOMAIN 207 298 EXTRACELLULAR ALPHA-2.
CC FT DOMAIN 299 308 EXTRACELLULAR ALPHA-3.
CC FT TRANSMEM 309 332 CONNECTING PEPTIDE.
CC FT DOMAIN 333 362 CYTOPLASMIC TAIL.
CC FT CARBOHYD 110 110 BY SIMILARITY.
CC FT DISULFID 125 188 BY SIMILARITY.
CC FT DISULFID 227 283 BY SIMILARITY.
CC SQ SEQUENCE 362 AA; 40456 MW; 8C567F8E CRC32;

Query Match 100.0%; Score 50; DB 1; Length 362;
Best Local Similarity 100.0%; Pred. No. 0.015;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 REDRLTLRY 10
| | | | | | | |
Db 99 REDRLTLRY 108

RESULT 6
1B45_HUMAN
ID 1B45_HUMAN STANDARD; PRT; 362 AA.
AC P30485;
DT 01-APR-1993 (Rel. 25, Created)

Db 99 REDRLTLRY 108

Query Match 100.0%; Score 50; DB 1; Length 362;
Best Local Similarity 100.0%; Pred. No. 0.015;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 REDRLTLRY 10
| | | | | | | |
Db 99 REDRLTLRY 108

RESULT 7
1B19_HUMAN
ID 1B19_HUMAN STANDARD; PRT; 362 AA.
AC Q08136;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-27 B*2706 ALPHA CHAIN
DE PRECURSOR.
GN HLA-B OR HLAB.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia;
OC Eutheria; Primates; Catarrhini; Homiidae; Homo.
RN [1]

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RP SEQUENCE FROM N.A.
RX MEDLINE; 94102824.
RA VILCHES C., DE PABLO R., KREISLER M.;
RT "Nucleotide sequence of HLA-B*2706."
RL Immunogenetics 39:219-219(1994).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE; 96134006.
RA RUDWALT M., BOWNESS P., WORDSWORTH P.;
RT "The nucleotide sequence of HLA-B*2704 reveals a new amino acid
RT substitution in exon 4 which is also present in HLA-B*2706."
RL Immunogenetics 43:160-162(1996).
CC -!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
CC THE IMMUNE SYSTEM.
CC -!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
CC MICROGLOBULIN).
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CC -----
DR EMBL; X73578; CAAS1980.1; -.
DR EMBL; U35734; AAC50447.1; -.
DR HSSP; P03989; LHSA.
DR PROSITE; PS00290; IG_MHC; 1.
DR PFAM; PF00047; ig; 1.
DR PFAM; PF00129; MHC_I; 1.
KW MHC I; Transmembrane; Glycoprotein; Signal.
FT SIGNAL 1 24
FT CHAIN 25 362 HLA CLASS I HISTOCOMPATIBILITY ANTIGEN,
FT B-27 B*2706 ALPHA CHAIN.
FT DOMAIN 25 114 EXTRACELLULAR ALPHA-1 (BY SIMILARITY).
FT DOMAIN 115 206 EXTRACELLULAR ALPHA-2 (BY SIMILARITY).
FT DOMAIN 207 298 EXTRACELLULAR ALPHA-3 (BY SIMILARITY).
FT DOMAIN 299 308 CONNECTING PEPTIDE (BY SIMILARITY).
FT TRANSMEM 309 332 BY SIMILARITY.
FT DOMAIN 333 362 CYTOPLASMIC TAIL (BY SIMILARITY).
FT CARBOHYD 110 110 POTENTIAL.
FT DISULFID 125 188 BY SIMILARITY.
FT DISULFID 227 283 BY SIMILARITY.
FT CONFLICT 235 235 A -> G (IN REF. 1).
FT SEQUENCE 362 AA; 40456 MW; 0D402027 CRC32;
SQ
Query Match 88.0%; Score 44; DB 1; Length 362;
Best Local Similarity 90.0%; Pred. No. 0.22;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 REDRLTLLRY 10
Db 99 RESRLTLLRY 108
|| |||||
DE H-2 CLASS I HISTOCOMPATIBILITY ANTIGEN, K-Q ALPHA CHAIN (H-2K(Q))
DE (FRAGMENT).
DE H2-K.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 85206119.
RESULT 8
HA1Q_MOUSE STANDARD; PRT; 328 AA.
AC P14428;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 01-FEB-1996 (Rel. 33, Last annotation update)
DE H-2 CLASS I HISTOCOMPATIBILITY ANTIGEN, K-Q ALPHA CHAIN (H-2K(Q))
DE (FRAGMENT).
DE H2-K.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 85206119.

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RA MORITA T., DELARBRE C., KRESS M., KOURILSKY P., GACHELIN G.;
RT "An H-2K gene of the tw32 mutant at the T/t complex is a close parent
RT of an H-2K gene."
RL Immunogenetics 21:367-383(1985).
CC -!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
CC THE IMMUNE SYSTEM.
CC -!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
CC MICROGLOBULIN).
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; M14827; AAA39656.1; -.
DR HSSP; P01901; 2CRB.
DR MGD; MGI:95904; H2-K.
DR PROSITE; PS00290; IG_MHC; 1.
DR PFAM; PF00047; ig; 1.
DR PFAM; PF00129; MHC_I; 1.
KW MHC I; Transmembrane; Glycoprotein.
FT NON_TER 1 1
FT DOMAIN <1 71 EXTRACELLULAR ALPHA-1.
FT DOMAIN 72 163 EXTRACELLULAR ALPHA-2.
FT DOMAIN 164 255 EXTRACELLULAR ALPHA-3.
FT DOMAIN 256 265 CONNECTING PEPTIDE.
FT TRANSMEM 266 289
FT DOMAIN 290 328 CYTOPLASMIC TAIL.
FT DISULFID 82 145 BY SIMILARITY.
FT DISULFID 184 240 BY SIMILARITY.
FT CARBOHYD 67 67 POTENTIAL.
FT CARBOHYD 157 157 POTENTIAL.
FT SEQUENCE 328 AA; 36855 MW; 3845B867 CRC32;
SQ
Query Match 86.0%; Score 43; DB 1; Length 328;
Best Local Similarity 90.0%; Pred. No. 0.31;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 REDRLTLLRY 10
Db 56 RVDLRTLLRY 65
| | | | | | | |
DE H-2 CLASS I HISTOCOMPATIBILITY ANTIGEN, D-K ALPHA CHAIN PRECURSOR
DE (H-2D(K)).
DE H2-D.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-C3H;
RX MEDLINE; 88060499.
RA WATTS S., VOGEL J.M., HARRIMAN W.D., ITOH T., STAUSS H.J.,
RA GOODENOW R.S.;
RT "DNA sequence analysis of the C3H H-2Kk and H-2Dk loci. Evolutionary
RT relationships to H-2 genes from four other mouse strains."
RL J. Immunol. 139:3878-3885(1987).
CC -!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
CC THE IMMUNE SYSTEM.
CC -!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
CC MICROGLOBULIN).
CC -----

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EMBL; M18524; AA53201.1; -
 HSP; P01901; 2CRB.
 MGD; MGI:95896; H2-D.
 PROSITE; PS00290; IG_MHC; 1.
 PFAM; PF00047; Ig; 1.
 PFAM; PF00129; MHC_I; 1.
 MHC I; Transmembrane; Glycoprotein; Signal.
 SIGNAL 1 24
 CHAIN 25 362
 H-2 CLASS I HISTOCOMPATIBILITY ANTIGEN,
 D-K ALPHA CHAIN.
 DOMAIN 25 114
 DOMAIN 115 206
 DOMAIN 207 298
 DOMAIN 299 306
 TRANSMEM 307 333
 DOMAIN 334 362
 DOMAIN 125 188
 DISULFID 227 283
 DISULFID 110 110
 CARBOHYD 200 200
 CARBOHYD 280 280
 SEQUENCE 362 AA; 40620 MW; 7A34877E CRC32;

Query Match 86.0%; Score 43; DB 1; Length 362;
 Best Local Similarity 90.0%; Pred. No. 0.34; 1; Indels 0; Gaps 0;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 REDLRTLLRY 10
 DB 99 RVDLRTLLRY 108

RESULT 10
 HAIW_MOUSE
 ID HAIW_MOUSE STANDARD; PRT; 368 AA.
 AC P03991; P03990;
 DT 23-OCT-1986 (Rel. 02, Created)
 DT 01-JAN-1990 (Rel. 13, Last sequence update)
 DT 01-FEB-1996 (Rel. 33, Last annotation update)
 DE H-2 CLASS I HISTOCOMPATIBILITY ANTIGEN, K-W28 ALPHA CHAIN PRECURSOR.
 GN H2-K.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 RN Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 85206119.
 RA MORITA T., DELARRE C., KRESS M., KOURILSKY P., GACHELIN G.;
 RT "An H-2k gene of the tw32 mutant at the T/t complex is a close parent
 of an H-2k gene.";
 RL Nature 306:602-604(1983).
 RL Immunogenetics 21:367-383(1985).
 RP SEQUENCE OF 258-368 FROM N.A.
 RC STRAIN-SWR;
 RX MEDLINE; 84068207.
 RA KRESS M., GLAROS D., KHOURY G., JAY G.;
 RT "Alternative RNA splicing in expression of the H-2k gene.";
 RL Nature 306:602-604(1983).
 CC -!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
 THE IMMUNE SYSTEM.
 CC -!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
 MICROGLOBULIN).

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EMBL; M14825; AAA39657.1; -
 EMBL; X00172; CAA24997.1; -
 PIR; A02197; A02197.
 PIR; A02196; A02196.
 HSP; P01901; 2CRB.
 MGD; MGI:95904; H2-K.
 PROSITE; PS00290; IG_MHC; 1.
 PFAM; PF00047; Ig; 1.
 PFAM; PF00129; MHC_I; 1.
 MHC I; Transmembrane; Glycoprotein; Signal.
 SIGNAL 1 21
 CHAIN 22 368
 H-2 CLASS I HISTOCOMPATIBILITY ANTIGEN,
 K-W28 ALPHA CHAIN.
 DOMAIN 22 111
 DOMAIN 112 203
 DOMAIN 204 295
 DOMAIN 296 305
 TRANSMEM 306 329
 DOMAIN 330 368
 DISULFID 122 185
 DISULFID 224 280
 CARBOHYD 107 107
 CARBOHYD 197 197
 SEQUENCE 368 AA; 41103 MW; E03C7D0F CRC32;

Query Match 86.0%; Score 43; DB 1; Length 368;
 Best Local Similarity 90.0%; Pred. No. 0.35; 1; Indels 0; Gaps 0;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 REDLRTLLRY 10
 DB 96 RVDLRTLLRY 105

RESULT 11
 1B05_HUMAN
 ID 1B05_HUMAN STANDARD; PRT; 362 AA.
 AC P30461;
 DT 01-APR-1993 (Rel. 25, Created)
 DT 01-APR-1993 (Rel. 25, Last sequence update)
 DT 15-JUL-1998 (Rel. 36, Last annotation update)
 DE HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B*1301 ALPHA CHAIN
 DE PRECURSOR (B13.1).
 GN HLA-B OR HLAB.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 RN Eutheria; Primates; Catarrhini; Hominidae; Homo.
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 89235215.
 RA PARHAM P., LAWZOR D.A., LOMEN C.E., ENNIS P.D.;
 RT "Diversity and diversification of HLA-A,B,C alleles.";
 RL J. Immunol. 142:3937-3950(1989).
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 88152906.
 RA ZEMMOUR J., ENNIS P.D., PARHAM P., DUPONT B.;
 RT "Comparison of the structure of HLA-B*47 to HLA-B13 and its
 relationship to 21-hydroxylase deficiency.";
 RL Immunogenetics 27:281-287(1988).
 RP SEQUENCE FROM N.A.
 RC TISSUE-BLOOD;
 RX MEDLINE; 96053518.

RA LIN L., TOKUNAGA K., NAKAJIMA F., ISHIKAWA Y., KASHIWASE K.,
 RA TANAKA H., KUMATA S., SIDELTEVA E., AKAZA T., TADOKORO K.,
 RA SHIBATA Y., CHANDANAYONG D., JUJI T.,
 RT "Both HLA-B*1301 and B*1302 exist in Asian populations and are
 RT associated with different haplotypes."
 RL Hum. Immunol. 43:51-56(1995).
 CC -!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
 CC THE IMMUNE SYSTEM.
 CC -!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
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 CC
 DR EMBL; M24041; AAA59660.1; -
 DR EMBL; M19757; AAA52657.1; -
 DR EMBL; D50291; BAA08822.1; -
 DR HSSP; P30491; IALM.
 DR MIM; 142830; -
 DR PROSITE; PS00290; IG_MHC; 1.
 DR PFAM; PF00047; Ig; 1.
 DR PFAM; PF00129; MHC_I; 1.
 KW MHC I; Transmembrane; Glycoprotein; Signal.
 FT SIGNAL 1 24
 FT CHAIN 25 362 HLA CLASS I HISTOCOMPATIBILITY ANTIGEN,
 FT B-13 B*1301 ALPHA CHAIN.
 FT DOMAIN 25 114 EXTRACELLULAR ALPHA-1.
 FT DOMAIN 115 206 EXTRACELLULAR ALPHA-2.
 FT DOMAIN 207 298 EXTRACELLULAR ALPHA-3.
 FT DOMAIN 299 309 CONNECTING PEPTIDE.
 FT TRANSMEM 310 333
 FT DOMAIN 334 362 CYTOPLASMIC TAIL.
 FT CARBOHYD 110 110 BY SIMILARITY.
 FT DISULFID 125 188 BY SIMILARITY.
 FT DISULFID 227 283 BY SIMILARITY.
 SQ SEQUENCE 362 AA; 40474 MW; 28B67875 CRC32;
 Query Match 80.0%; Score 40; DB 1; Length 362;
 Best Local Similarity 80.0%; Pred. No. 1.3;
 Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 1 REDLRTLLRY 10
 Db 99 RENLRTALRY 108
 RESULT 12
 ID 1B41_HUMAN STANDARD; PRT; 362 AA.
 AC P30481;
 DT 01-APR-1993 (Rel. 25, Created)
 DT 01-APR-1993 (Rel. 25, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, BW-44(B-12) B*4402 ALPHA CHAIN
 DE PRECURSOR (B44.2).
 GN HLA-B OR HLAB.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia;
 OC Eutheria; Primates; Catarrhini; Hominidae; Homo.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 89235215.
 RA PARHAM P., LAWLER D.A., LOMEN C.E., ENNIS P.D.;
 RT "Diversity and diversification of HLA-A,B,C alleles."
 RL J. Immunol. 142:3937-3950(1989).
 CC -!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
 CC THE IMMUNE SYSTEM.

CC -!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
 CC MICROGLOBULIN).
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 CC
 DR EMBL; M24038; AAA59663.1; -
 DR HSSP; P30491; IALM.
 DR MIM; 142830; -
 DR PROSITE; PS00290; IG_MHC; 1.
 DR PFAM; PF00047; Ig; 1.
 DR PFAM; PF00129; MHC_I; 1.
 KW MHC I; Transmembrane; Glycoprotein; Signal.
 FT SIGNAL 1 24
 FT CHAIN 25 362 HLA CLASS I HISTOCOMPATIBILITY ANTIGEN,
 FT BW-44(B-12) B*4402 ALPHA CHAIN.
 FT DOMAIN 25 114 EXTRACELLULAR ALPHA-1.
 FT DOMAIN 115 206 EXTRACELLULAR ALPHA-2.
 FT DOMAIN 207 298 EXTRACELLULAR ALPHA-3.
 FT TRANSMEM 310 333
 FT DOMAIN 334 362 CYTOPLASMIC TAIL.
 FT CARBOHYD 110 110 BY SIMILARITY.
 FT DISULFID 125 188 BY SIMILARITY.
 FT DISULFID 227 283 BY SIMILARITY.
 SQ SEQUENCE 362 AA; 40481 MW; D0AE6DD5 CRC32;
 Query Match 80.0%; Score 40; DB 1; Length 362;
 Best Local Similarity 80.0%; Pred. No. 1.3;
 Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 1 REDLRTLLRY 10
 Db 99 RENLRTALRY 108
 RESULT 13
 ID 1B42_HUMAN STANDARD; PRT; 362 AA.
 AC P30482;
 DT 01-APR-1993 (Rel. 25, Created)
 DT 01-APR-1993 (Rel. 25, Last sequence update)
 DT 15-JUL-1998 (Rel. 36, Last annotation update)
 DE HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, BW-44(B-12) B*4403 ALPHA CHAIN
 DE PRECURSOR.
 GN HLA-B OR HLAB.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia;
 OC Eutheria; Primates; Catarrhini; Hominidae; Homo.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 91335451.
 RA FLEISCHCHAUER K., KERNAN N.A., DUPONT B., YANG S.Y.;
 RT "The two major subtypes of HLA-B44 differ for a single amino acid in
 RT codon 156."
 RL Tissue Antigens 37:133-137(1991).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 96435470.
 RA ADAMS E.J., LITTLE A.M., ARNETT K.L., MCAULEY J.E., WILLIAMS R.C.,
 RA FARHAM P.;
 RT "Three new HLA-B alleles found in Mexican-Americans."
 RL Tissue Antigens 46:414-416(1995).
 CC -!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
 CC THE IMMUNE SYSTEM.
 CC -!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
 CC MICROGLOBULIN).

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CC EMBL; X64366; CAA45718.1; -;
 CC EMBL; L42282; AAB51454.1; -;
 CC EMBL; L42283; AAB51455.1; -;
 CC PIR; S25415; S25415.
 CC HSP; P30491; IAIM.
 CC MIM; 142830; -;
 CC PROSITE; PS00290; IG_MHC; 1.
 CC PFAM; PF00047; Ig; 1.
 CC PFAM; PF00129; MHC_I; 1.
 CC MHC I; Transmembrane; Glycoprotein; Signal.
 CC SIGNAL 1 24
 CC CHAIN 25 362
 CC HLA CLASS I HISTOCOMPATIBILITY ANTIGEN,
 CC BW-44(B-12) B*4403 ALPHA CHAIN.
 CC EXTRACELLULAR ALPHA-1.
 CC DOMAIN 25 114
 CC DOMAIN 115 206
 CC DOMAIN 207 298
 CC DOMAIN 299 309
 CC DOMAIN 310 333
 CC TRANSMEM 334 362
 CC CYTOPLASMIC TAIL.
 CC CARBOHYD 110 110
 CC BY SIMILARITY.
 CC DISULFID 125 188
 CC BY SIMILARITY.
 CC SEQUENCE 362 AA; 40479 MW; E72CE669 CRC32;
 SQ

Query Match 80.0%; Score 40; DB 1; Length 362;
 Best Local Similarity 80.0%; Pred. No. 1.3;
 Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 REDLTLRLY 10
 ||:|||||
 Db 99 RENLRLTALRY 108

RESULT 14
 HALY_MOUSE
 ID HALY_MOUSE STANDARD; PRT; 298 AA.
 AC P01895;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 01-JAN-1990 (Rel. 13, Last annotation update)
 DE H-2 CLASS I HISTOCOMPATIBILITY ANTIGEN, ALPHA CHAIN (CLONE PAG64)
 DE (FRAGMENT).
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia;
 CC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 RN [1]
 RP SEQUENCE OF 1-285 FROM N.A. (CLONE PAG64).
 RX MEDLINE; 84093573.
 RA BRICKELL P.M., LATCHMAN D.S., MURPHY D., WILLISON K.,
 RA RIGBY P.W.J.;
 RT "Activation of a Qa/Tla class I major histocompatibility antigen gene is a general feature of oncogenesis in the mouse."
 RL Nature 306:756-760(1983).
 RN [2]
 RP SEQUENCE OF 90-298 FROM N.A. (CLONE PH-2D-1).
 RX MEDLINE; 82013602.
 RA BRÉGERE F., ABASTADO J.P., KVIST S., RASK L., LALANNE J.-L.,
 RA GAROFF H., CAMI B., WIMAN K., LARHAMMAR D., PETERSON P.A.,
 RA GACHELIN G., KOURILSKY P., DOBERSTEIN B.;
 RT "Structure of C-terminal half of two H-2 antigens from cloned mRNA."
 RL Nature 292:78-81(1981)
 CC -!- ALTERNATIVE PRODUCTS: OF THE PRIMARY TRANSCRIPT OF THIS Qa/Tla
 CC GENE PRODUCES MRNA WITHOUT THE NUCLEOTIDES ENCODING THE SEVENTH

CC EXON (RESIDUES 286-298).
 CC -!- MISCELLANEOUS: THE ANTIGEN ENCODED BY THE PAG64 CLONE, NORMALLY
 CC EXPRESSED ONLY ON LYMPHOCYTE SUBSETS AND THYMOCYTES, IS FOUND IN
 CC INCREASED CONCENTRATIONS IN ALL TRANSFORMED CELLS TESTED, IN AN
 CC EMBRYONIC CARCINOMA CELL LINE, AND IN PLURIPOTENT EMBRYONIC CELLS.
 CC ACTIVATION OF THE GENE APPEARS TO BE A GENERAL FEATURE OF
 CC CARCINOGENESIS IN THE MOUSE. THE PAG64 CLONE, AND RELATED CDNA
 CC CLONES, HAVE IN COMMON A REPETITIVE SEQUENCE IN THEIR 3'
 CC TRANSCRIPTION UNITS THAT HAS CHARACTERISTICS OF A TRANSPOSABLE
 CC ELEMENT.
 CC -----
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 CC -----

CC EMBL; X00246; CAA25061.1; -;
 CC PIR; A02194; HLMS1.
 CC HSP; P01897; 1LD9.
 CC PROSITE; PS00290; IG_MHC; 1.
 CC PFAM; PF00047; Ig; 1.
 CC PFAM; PF00129; MHC_I; 1.
 CC MHC I; Transmembrane; Glycoprotein; Alternative splicing.
 CC NON_TER 1 1
 CC CARBOHYD 43 43
 CC BY SIMILARITY.
 CC CARBOHYD 133 133
 CC POTENTIAL.
 CC BY SIMILARITY.
 CC DISULFID 58 121
 CC BY SIMILARITY.
 CC DISULFID 160 216
 CC BY SIMILARITY.
 CC VARIANT 212 212
 CC Q -> L (IN REF. 2).
 CC VARIANT 223 223
 CC MISSING (IN REF. 2).
 CC VARIANT 285 285
 CC V -> G (IN REF. 2).
 CC SEQUENCE 298 AA; 33850 MW; 56E1DA69 CRC32;
 SQ

Query Match 76.0%; Score 38; DB 1; Length 298;
 Best Local Similarity 80.0%; Pred. No. 2.6;
 Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 REDLTLRLY 10
 | |||||
 Db 32 RVDLRLTALRY 41

RESULT 15
 HAL2_MOUSE
 ID HAL2_MOUSE STANDARD; PRT; 365 AA.
 AC P01900;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 13-AUG-1987 (Rel. 05, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE H-2 CLASS I HISTOCOMPATIBILITY ANTIGEN, D-D ALPHA CHAIN PRECURSOR
 DE (H-2D(D)).
 GN H2-D.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 CC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 83058139.
 RA MARGULIES D.H., EVANS G.A., OZATO K., CAMERINI-OTERO R.D., TANAKA K.,
 RA APPELLA E., SEIDMAN J.G.;
 RT "Expression of H-2Dd and H-2Id mouse major histocompatibility antigen
 RT genes in L cells after DNA-mediated gene transfer."
 RL J. Immunol. 130:463-470(1983).
 RN [2]
 RP REVISIONS.
 RX MEDLINE; 85235604.
 RA MARGULIES D.H., EVANS G.A., OZATO K., CAMERINI-OTERO R.D., TANAKA K.,
 RA APPELLA E., SEIDMAN J.G.;
 RT "Partial nucleotide sequence of H-2Dd major histocompatibility

RT antigen gene.";
RL J. Immunol. 135:1537-1537(1985).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE: 85140250.
RA SHER B.T., NAIRN R., COLIGAN J.E., HOOD L.E.;
RT "DNA sequence of the mouse H-2Dd transplantation antigen gene.";
RL Proc. Natl. Acad. Sci. U.S.A. 82:1175-1179(1985).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/C;
RX MEDLINE: 99086740.
RA WANG M., STEPKOWSKI S.M., HERBERT J.S., TIAN L., YU J., KAHAN B.D.;
RT "Nucleotide sequences of three H-2K and three H-2D complementary DNA
clones coding mouse class I MHC heavy chain proteins.";
RL Ann. Transplant. 1:26-31(1996).
RN [5]
RP SEQUENCE OF 25-125.
RX MEDLINE: 82046438.
RA NAIRN R., NATHENSON S.G., COLIGAN J.E.;
RT "Amino acid sequence of cyanogen bromide fragment CN-C (residues
24-98) of the mouse histocompatibility antigen H-2Dd. A comparison of
the amino-terminal 100 residues of H-2Dd, Dd, Kd, and Kb reveals
discrete areas of diversity.";
RL Biochemistry 20:4739-4745(1981).
RN [6]
RP X-RAY CRYSTALLOGRAPHY (2.4 ANGSTROMS).
RX MEDLINE: 98397257.
RA ACHOUR A., PERSSON K., HARRIS R.A., SUNDBACK J., SENTMAN C.L.,
RT LINDQVIST Y., SCHNEIDER G., KARRE K.;
RT "The crystal structure of H-2Dd MHC class I complexed with the HIV-1-
derived peptide P18-I10 at 2.4-A resolution: implications for T cell
and NK cell recognition.";
RL Immunity 9:199-208(1998).
CC -I- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
THE IMMUNE SYSTEM.
CC -I- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
MICROGLOBULIN).
CC -----
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CC -----
DR EMBL; L29190; AAA39581.1; -;
DR EMBL; U47326; AAB17604.1; -;
DR PIR; A02201; A02201.
DR PDB; 1BII; 14-OCT-98.
DR MGD; MGI:95896; H2-D.
DR PROSITE; PS00290; IG_MHC; 1.
DR PFAM; PF00047; Ig; 1.
DR PFAM; PF00129; MHC_I; 1.
KW MHC I; Transmembrane; Glycoprotein; Signal; 3D-structure.
FT SIGNAL 1 24
FT CHAIN 25 365 H-2 CLASS I HISTOCOMPATIBILITY ANTIGEN,
D-D ALPHA CHAIN.
FT DOMAIN 25 114
FT DOMAIN 115 206 EXTRACELLULAR ALPHA-1.
FT DOMAIN 207 298 EXTRACELLULAR ALPHA-2.
FT DOMAIN 299 311 EXTRACELLULAR ALPHA-3.
FT TRANSMEM 312 334 CONNECTING PEPTIDE.
FT DOMAIN 335 365 CYTOPLASMIC TAIL.
FT DISULFID 125 188 BY SIMILARITY.
FT DISULFID 227 283 BY SIMILARITY.
FT CARBOHYD 110 110 POTENTIAL.
FT CARBOHYD 200 200 POTENTIAL.
SQ SEQUENCE 365 AA; 41110 MW; 91AA5F01 CRC32;

Best Local Similarity 80.0%; Pred. No. 3.3;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 REDLRTLLRY 10
| | | | | | | |
Db 99 RVDLRTALRY 108

Search completed: February 8, 2000, 01:25:57
Job time: 1557 sec

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: February 8, 2000, 19:16:12 ; Search time 176.54 Seconds
(without alignments)
3.927 Million cell updates/sec

Title: US-08-653-294-23
Perfect score: 50
Sequence: 1 REDLRTLRLY 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 225878 seqs, 69334122 residues

Total number of hits satisfying chosen parameters: 225878

Minimum DB seq length: 0
Maximum DB seq length: 1000000

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database : SPTREMBL_12.*
1: sp_archaea.*
2: sp_bacteria.*
3: sp_fungi.*
4: sp_human.*
5: sp_invertebrate.*
6: sp_mammal.*
7: sp_mhc.*
8: sp_organelle.*
9: sp_phase.*
10: sp_plant.*
11: sp_rodent.*
12: sp_virus.*
13: sp_vertebrate.*
14: sp_unclassified.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	50	100.0	39	7 019688	019688 homo sapien
2	50	100.0	90	7 019193	019193 homo sapien
3	50	100.0	181	7 062898	062898 homo sapien
4	50	100.0	181	7 078138	078138 homo sapien
5	50	100.0	181	7 078142	078142 homo sapien
6	50	100.0	274	7 019692	019692 homo sapien
7	50	100.0	322	7 019627	019627 homo sapien
8	50	100.0	359	7 029934	029934 homo sapien
9	50	100.0	362	7 029705	029705 homo sapien
10	50	100.0	362	7 029846	029846 homo sapien
11	50	100.0	362	7 078189	078189 homo sapien
12	45	90.0	137	7 035533	035533 pan troglod
13	45	90.0	330	7 019356	019356 macaca mula
14	45	90.0	331	7 002944	002944 macaca mula
15	45	90.0	331	7 002945	002945 macaca mula
16	45	90.0	346	7 095459	095459 rattus norv
17	45	90.0	346	7 078088	078088 rattus norv
18	45	90.0	348	7 046875	046875 rattus norv
19	44	88.0	362	7 029693	029693 homo sapien
20	44	88.0	362	7 079612	079612 homo sapien

21	43	86.0	98	7 031211	031211 mus musculu
22	43	86.0	362	7 095457	095457 mus musculu
23	40	80.0	89	7 019674	019674 homo sapien
24	40	80.0	89	7 019565	019565 homo sapien
25	40	80.0	131	7 097998	097998 homo sapien
26	40	80.0	131	7 097999	097999 homo sapien
27	40	80.0	181	7 019779	019779 homo sapien
28	40	80.0	181	7 030197	030197 homo sapien
29	40	80.0	181	7 019669	019669 homo sapien
30	40	80.0	181	7 078028	078028 homo sapien
31	40	80.0	355	7 029853	029853 homo sapien
32	40	80.0	361	7 09XRVO	09XRVO pongo pygma
33	40	80.0	362	7 029637	029637 homo sapien
34	40	80.0	362	7 029935	029935 homo sapien
35	40	80.0	362	7 079524	079524 homo sapien
36	40	80.0	362	7 029850	029850 homo sapien
37	40	80.0	362	7 029661	029661 homo sapien
38	40	80.0	362	7 078180	078180 homo sapien
39	40	80.0	362	7 029933	029933 homo sapien
40	39	78.0	89	4 095956	095956 homo sapien
41	39	78.0	89	7 077959	077959 homo sapien
42	39	78.0	89	7 078077	078077 homo sapien
43	39	78.0	181	7 019555	019555 homo sapien
44	39	78.0	181	7 077933	077933 homo sapien
45	39	78.0	181	7 077935	077935 homo sapien

ALIGNMENTS

RESULT 1
019688
ID 019688 PRELIMINARY; PRT; 39 AA.
AC 019688;
DT 01-JAN-1998 (TRENBLrel. 05, Created)
DT 01-JAN-1998 (TRENBLrel. 05, Last sequence update)
DT 01-NOV-1998 (TRENBLrel. 08, Last annotation update)
DE HLA-B*27 VARIANT EXON 2 (ALPHA1 DOMAIN) (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Primates; Catarrhini; Hominidae; Homo.
RN [1]
RP SEQUENCE FROM N.A.
RA BLASZYK R., WEBER M., SALAMA A.;
RL Submitted (JAN-1995) to the EMBL/GenBank/DBJ databases.
DR EMBL; X83727; CAA58698.1; -
DR PFAM; PF00129; MHC_I; 1.
KW MHC.
FT NON_TER 1 1
FT NON_TER 39 39
SQ SEQUENCE 39 AA; 4748 MW; 6F714D4C CRC32;

Query Match 100.0%; Score 50; DB 7; Length 39;
Best Local Similarity 100.0%; Pred. No. 0.0094;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 REDLRTLRLY 10

Db 24 REDLRTLRLY 33

RESULT 2

019193
ID 019193 PRELIMINARY; PRT; 90 AA.
AC 019193;
DT 01-JAN-1998 (TRENBLrel. 05, Created)
DT 01-JAN-1998 (TRENBLrel. 05, Last sequence update)
DT 01-NOV-1998 (TRENBLrel. 08, Last annotation update)
DE HISTOCOMPATIBILITY ANTIGEN ALPHA 1 DOMAIN (FRAGMENT).
GN HLA-B*27.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;

OC Eutheria; Primates; Catarrhini; Hominidae; Homo.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 92337445.
 RA HIGGINS C.M., LUND T., SHIPLEY M.E., EBRINGER A.,
 RA SADOWSKA-WROBLEWSKA M., CRAIG R.K.;
 RT "Ankylosing spondylitis and HLA-B*27: restriction fragment length
 RT polymorphism and sequencing of an HLA-B*27 allele from a patient with
 RT ankylosing spondylitis";
 RL Ann. Rheum. Dis. 51:855-862(1992).
 DR EMBL: S39758; CAB27364.1; -;
 DR PFAM: PF00129; MHC_I; 1.
 KW MHC.
 FT NON_TER 1 1
 FT NON_TER 90 90
 SQ SEQUENCE 90 AA; 10571 MW; F22CCB4E CRC32;

Query Match 100.0%; Score 50; DB 7; Length 90;
 Best Local Similarity 100.0%; Pred. No. 0.022;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 REDLRTLLRY 10
 Db 75 REDLRTLLRY 84

RESULT 3
 ID 062898 PRELIMINARY; PRT; 181 AA.
 AC 062898;
 DT 01-AUG-1998 (TEMBLrel. 07, Created)
 DT 01-AUG-1998 (TEMBLrel. 07, Last sequence update)
 DT 01-NOV-1999 (TEMBLrel. 12, Last annotation update)
 DE MHC CLASS I ANTIGEN (FRAGMENT).
 GN HLA-B.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Eutheria; Primates; Catarrhini; Hominidae; Homo.
 RN [1]
 RP SEQUENCE FROM N.A.
 RA KOSMAN C.A., HURLEY C.K.;
 RL Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF054012; AAC32563.1; -;
 DR EMBL: AF054011; AAC32563.1; JOINED.
 DR HSP: P10318; 1ROG.
 DR PFAM: PF00129; MHC_I; 1.
 KW MHC.
 FT NON_TER 1 1
 FT NON_TER 181 181
 SQ SEQUENCE 181 AA; 21107 MW; D8E533DD CRC32;

Query Match 100.0%; Score 50; DB 7; Length 181;
 Best Local Similarity 100.0%; Pred. No. 0.045;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 REDLRTLLRY 10
 Db 74 REDLRTLLRY 83

RESULT 4
 ID 078138 PRELIMINARY; PRT; 181 AA.
 AC 078138;
 DT 01-NOV-1998 (TEMBLrel. 08, Created)
 DT 01-NOV-1998 (TEMBLrel. 08, Last sequence update)
 DT 01-NOV-1999 (TEMBLrel. 12, Last annotation update)
 DE MHC CLASS I ANTIGEN (FRAGMENT).
 GN HLA-B.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Eutheria; Primates; Catarrhini; Hominidae; Homo.

OC Eutheria; Primates; Catarrhini; Hominidae; Homo.
 RN [1]
 RP SEQUENCE FROM N.A.
 RA KOSMAN C.A., HURLEY C.K.;
 RT "Novel HLA Class I B Locus Alleles";
 RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF071770; AAC35939.1; -;
 DR EMBL: AF071769; AAC35939.1; JOINED.
 DR HSP: P10318; 1ROG.
 DR PFAM: PF00129; MHC_I; 1.
 KW MHC.
 FT NON_TER 1 1
 FT NON_TER 181 181
 SQ SEQUENCE 181 AA; 21103 MW; 8CF468CF CRC32;

Query Match 100.0%; Score 50; DB 7; Length 181;
 Best Local Similarity 100.0%; Pred. No. 0.045;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 REDLRTLLRY 10
 Db 74 REDLRTLLRY 83

RESULT 5
 ID 078142 PRELIMINARY; PRT; 181 AA.
 AC 078142;
 DT 01-NOV-1998 (TEMBLrel. 08, Created)
 DT 01-NOV-1998 (TEMBLrel. 08, Last sequence update)
 DT 01-NOV-1999 (TEMBLrel. 12, Last annotation update)
 DE MHC CLASS I ANTIGEN (FRAGMENT).
 GN HLA-B.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Eutheria; Primates; Catarrhini; Hominidae; Homo.
 RN [1]
 RP SEQUENCE FROM N.A.
 RA STEINER N.K., HURLEY C.K., KOESTER R.P.;
 RT "Novel-HLA-B allele";
 RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF072764; AAC25779.1; -;
 DR EMBL: AF072763; AAC25779.1; JOINED.
 DR HSP: P10318; 1ROG.
 DR PFAM: PF00129; MHC_I; 1.
 KW MHC.
 FT NON_TER 1 1
 FT NON_TER 181 181
 SQ SEQUENCE 181 AA; 21079 MW; 24949B0F CRC32;

Query Match 100.0%; Score 50; DB 7; Length 181;
 Best Local Similarity 100.0%; Pred. No. 0.045;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 REDLRTLLRY 10
 Db 74 REDLRTLLRY 83

RESULT 6
 ID 019692 PRELIMINARY; PRT; 274 AA.
 AC 019692;
 DT 01-JAN-1998 (TEMBLrel. 05, Created)
 DT 01-JAN-1998 (TEMBLrel. 05, Last sequence update)
 DT 01-NOV-1999 (TEMBLrel. 12, Last annotation update)
 DE MHC CLASS I HLA-B*27 M (FRAGMENT).
 GN HLA-B.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Eutheria; Primates; Catarrhini; Hominidae; Homo.

```

RN RP SEQUENCE FROM N.A.
RX MEDLINE: 87009855.
RA COPPIN H.L., MCDEVITT H.O.;
RT "Absence of polymorphism between HLA-B27 genomic exon sequences
RT isolated from normal donors and ankylosing spondylitis patients.";
RL J. Immunol. 137:2168-2172(1986).
DR EMBL; M14013; AAA59643.1; -.
DR HSSP; P10318; IROG.
DR PROSITE; PS00290; IG_MHC; 1.
DR PFAM; PF00047; Ig; 1.
DR PFAM; PF00129; MHC_I; 1.
KW MHC.
FT NON_TER 1 1
FT NON_TER 274 274
SQ SEQUENCE 274 AA; 31659 MW; 9A74A6BA CRC32;

Query Match 100.0%; Score 50; DB 7; Length 274;
Best Local Similarity 100.0%; Pred. No. 0.07;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 REDLRTLLRY 10
Db 75 REDLRTLLRY 84

RESULT 7
ID O19627 PRELIMINARY; PRT; 322 AA.
AC O19627;
DT 01-JAN-1998 (TREMBLrel. 05, Created)
DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
DT 01-NOV-1999 (TREMBLrel. 12, Last annotation update)
DE HLA-B37 (FRAGMENT).
GN B-3701.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Primates; Catarrhini; Hominidae; Homo.
RN RP SEQUENCE FROM N.A.
RA HURLEY C.K., BEI M., RODRIGUEZ S., JOHNSON A.;
RL Submitted (JUN-1994) to the EMBL/GenBank/DBJ databases.
DR EMBL; U11267; AAA19927.1; -.
DR HSSP; P30685; IA9E.
DR PROSITE; PS00290; IG_MHC; 1.
DR PFAM; PF00047; Ig; 1.
DR PFAM; PF00129; MHC_I; 1.
KW MHC.
FT NON_TER 322 322
FT NON_TER 322 322
SQ SEQUENCE 322 AA; 36626 MW; DF3B7744 CRC32;

Query Match 100.0%; Score 50; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 0.082;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 REDLRTLLRY 10
Db 99 REDLRTLLRY 108

RESULT 8
ID Q29934 PRELIMINARY; PRT; 359 AA.
AC Q29934;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-NOV-1999 (TREMBLrel. 12, Last annotation update)
DE HLA-B27 (FRAGMENT).
GN HLA-B.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;

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OC Eutheria; Primates; Catarrhini; Hominidae; Homo.
RN RP SEQUENCE FROM N.A.
RX MEDLINE: 86149317.
RA SZOTS H., RITHMULLER G., WEISS E., MEO T.;
RT "Complete sequence of HLA-B27 CDNA identified through the
RT characterization of structural markers unique to the HLA-A, -B, and -C
RT allelic series.";
RL Proc. Natl. Acad. Sci. U.S.A. 83:1428-1432(1986).
DR EMBL; M12678; AAA59614.1; -.
DR HSSP; P10318; IROG.
DR PROSITE; PS00290; IG_MHC; 1.
DR PFAM; PF00047; Ig; 1.
DR PFAM; PF00129; MHC_I; 1.
KW MHC.
FT NON_TER 1 1
FT NON_TER 359 359
SQ SEQUENCE 359 AA; 40042 MW; 069F7E64 CRC32;

Query Match 100.0%; Score 50; DB 7; Length 359;
Best Local Similarity 100.0%; Pred. No. 0.092;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 REDLRTLLRY 10
Db 96 REDLRTLLRY 105

RESULT 9
ID Q29705 PRELIMINARY; PRT; 362 AA.
AC Q29705;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-NOV-1999 (TREMBLrel. 12, Last annotation update)
DE MHC CLASS I ANTIGEN HLA-B PRECURSOR.
GN HLA-B.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Primates; Catarrhini; Hominidae; Homo.
RN RP SEQUENCE FROM N.A.
RA BALAS A., SANTOS S., VICARIO J.L.;
RL Submitted (JUL-1995) to the EMBL/GenBank/DBJ databases.
DR EMBL; U31971; AAA98506.1; -.
DR HSSP; P10318; IROG.
DR PROSITE; PS00290; IG_MHC; 1.
DR PFAM; PF00047; Ig; 1.
DR PFAM; PF00129; MHC_I; 1.
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DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-NOV-1999 (TREMBLrel. 12, Last annotation update)
DE HUMAN LYMPHOCYTE ANTIGEN HLA-B27.

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OS Homo sapiens (Human).
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 OC Eutheria; Primates; Catarrhini; Hominidae; Homo.
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 RC TISSUE=BLOOD;
 RX MEDLINE: 94375872.
 RA DEL PORTO P., D'AMATO M., FIORILLO M.T., TUOSTO L., PICCOLELLA E.,
 RA SORRENTINO R.;
 RT "Identification of a novel HLA-B*27 subtype by restriction analysis of
 RT a cytotoxic gamma delta T cell clone.";
 RL J. Immunol. 153:3093-3100(1994).
 DR EMBL: Z33453; CAA83876.1; -
 DR HSP: P10318; IROG
 DR PROSITE: PS00290; IG_MHC; 1.
 DR PFAM: PF00047; Ig; 1.
 DR PFAM: PF00129; MHC_I; 1.
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 AC 078189;
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 DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
 DT 01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
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 GN HLA-B.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Eutheria; Primates; Catarrhini; Hominidae; Homo.
 [1]
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 RA SEURYNCK K.L., BAXTER-LOWE L.A.;
 RT "B27052 w495D.";
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 DT 01-NOV-1999 (TrEMBLrel. 08, Last annotation update)
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GN HLA-B.
 OS Pan troglodytes (Chimpanzee).
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 OC Eutheria; Primates; Catarrhini; Hominidae; Pan.
 [1]
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 RC STRAIN=WODRA;
 RX MEDLINE: 94286544.
 RA MCADAM S.N., BOYSON J.E., LIU X., GARBER T.L., HUGHES A.L.,
 RA BONTROP R.E., WATKINS D.I.;
 RT "A uniquely high level of recombination at the HLA-B locus.";
 RL Proc. Natl. Acad. Sci. U.S.A. 91:5893-5897(1994).
 DR EMBL: U05585; AAA50188.1; -
 DR PFAM: PF00129; MHC_I; 1.
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 DT 01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
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 GN MAMU-AG.
 OS Macaca mulatta (Rhesus macaque).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Eutheria; Primates; Catarrhini; Cercopithecoidea; Cercopithecoinae;
 OC Macaca.
 [1]
 RN RP SEQUENCE FROM N.A.
 RC TISSUE=PLACENTA;
 RA BOYSON J.E., IWANAGA K.K., GOLOS T.G., WATKINS D.I.;
 RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
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 DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
 DT 01-NOV-1999 (TrEMBLrel. 12, Last annotation update)


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DE MHC CLASS I ANTIGEN (FRAGMENT).
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OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Primates; Catarrhini; Cercopithecoidea; Cercopithecinae;
OC Macaca.
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RA BOYSON J.E., IWANAGA K.K., GOLOS T.G., WATKINS D.I.;
RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
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DR HSSP; P30491; IALM.
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DR PFAM; PF00047; ig; 1.
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DT 01-NOV-1999 (TRENBLrel. 12, Last annotation update)
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GN MAMU-AG.
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Primates; Catarrhini; Cercopithecoidea; Cercopithecinae;
OC Macaca.
RN [1]
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RA BOYSON J.E., IWANAGA K.K., GOLOS T.G., WATKINS D.I.;
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REFERENCE 1 (bases 1 to 270)
 AUTHORS Steiner,N.K., Hurley,C.K. and Koester,R.P.
 TITLE Novel-HLA-B allele
 JOURNAL Unpublished

REFERENCE 2 (bases 1 to 270)
 AUTHORS Steiner,N.K., Hurley,C.K. and Koester,R.P.
 TITLE Direct Submission
 JOURNAL Submitted (21-JUN-1998) Microbiology and Immunology, Georgetown University Medical Center, 3970 Reservoir Road NW, Washington, DC 20007, USA

FEATURES

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 LOCUS HSB1524V1 270 bp DNA PRI 22-AUG-1998
 DEFINITION Homo sapiens isolate GN00211 MHC class I antigen HLA-B gene (B*1543 allele), exon 2.

ACCESSION AF054011
 VERSION AF054011.1 GI:2984766
 KEYWORDS
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ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 270)
 AUTHORS Kosman,C.A. and Hurley,C.K.
 TITLE Novel HLA class I B locus alleles
 JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 270)
 AUTHORS Kosman,C.A. and Hurley,C.K.
 TITLE Direct Submission
 JOURNAL Submitted (18-MAR-1998) Microbiology & Immunology, Georgetown University, 3970 Reservoir Rd. NW, Washington, DC 20007, USA

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ACCESSION AF071769
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ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 270)
 AUTHORS Kosman,C.A. and Hurley,C.K.
 TITLE Novel HLA class I B Locus Alleles
 JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 270)
 AUTHORS Kosman,C.A. and Hurley,C.K.
 TITLE Direct Submission
 JOURNAL Submitted (12-JUN-1998) Microbiology & Immunology, Georgetown University, 3970 Reservoir Rd. N.W., Washington, DC 20007, USA

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ACCESSION AF102563
 VERSION AF102563.1 GI:4704574
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 SEGMENT 1 of 2
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ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;

Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 270)
AUTHORS Kosman,C.A. and Hurley,C.K.
TITLE Novel Class I HLA-B Alleles
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 270)
AUTHORS Kosman,C.A. and Hurley,C.K.
TITLE Direct Submission
JOURNAL Submitted (28-OCT-1998) Microbiology and Immunology, Georgetown University, 3970 Reservoir Rd. N.W., Washington, DC 20007, USA

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DEFINITION Homo sapiens MHC class I antigen HLA-B gene (HLA-B*27 allele), exon 2.

ACCESSION AF110257
VERSION AF110257.1 GI:4566542

KEYWORDS

SEGMENT 2 of 3

SOURCE human.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
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REFERENCE 1 (bases 1 to 270)

Wu,J., Bassinger,S., Montoya,G.D., Yee,J., Griffith,B.B.,

Kearns,J., McKeen,M., Birkos,S., Kamoun,M. and Williams,T.M.

Identification of new HLA-B alleles in potential bone marrow donors

JOURNAL Unpublished

REFERENCE 2 (bases 1 to 270)

Wu,J., Bassinger,S., Montoya,G.D., Yee,J., Griffith,B.B.,

Kearns,J., McKeen,M., Birkos,S., Kamoun,M. and Williams,T.M.

Direct Submission

JOURNAL Submitted (30-NOV-1998) Pathology, Univ. New Mexico, 915 Camino de

Salud, NE, Albuquerque, NM 87131, USA

FEATURES Location/Qualifiers

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DEFINITION Homo sapiens MHC class I HLA-B*27052 gene, exons.

ACCESSION L76095

VERSION L76095.1 GI:1203957

KEYWORDS cell surface antigen; cell surface glycoprotein; class I gene;
integral membrane protein; major histocompatibility complex.

SOURCE Homo sapiens DNA.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 546)

AUTHORS Marcos,C.Y., Fernandez-Vina,M.A., Lazaro,A.M. and Stastny,P.

TITLE Novel HLA-B Alleles

JOURNAL Unpublished (1996)

FEATURES Location/Qualifiers

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seq_documentation_block:

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DEFINITION Human MHC class I HLA-B*27 M+ gene, exons 2-4 (introns unsequenced).

ACCESSION M14013

VERSION M14013.1 GI:187743

KEYWORDS

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SOURCE      Human DNA.
ORGANISM    Homo sapiens
REFERENCE   1 (bases 1 to 822)
AUTHORS    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
TITLE      Eutheria; Primates; Catarrhini; Hominidae; Homo.
JOURNAL    Coplin, H.L. and McDewitt, H.O.
MEDLINE    Absence of polymorphism between HLA-B*27 genomic exon sequences
            isolated from normal donors and ankylosing spondylitis patients
            J. Immunol. 137 (7), 2168-2172 (1986)
FEATURES   87009855 Location/Qualifiers
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BASE COUNT 176 a 256 c 277 g 113 t
ORIGIN

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  Percent Similarity: 100.000 Percent Identity: 100.000

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223 CGAGAGGACCTGCGGACCTGCTCGCTAC 252

seq_name: gb_prl:HSU11267

seq_documentation_block:
LOCUS      HSU11267 968 bp mRNA PRI 21-JUL-1994
DEFINITION Human HLA-B*37 (B-3701) mRNA, partial cds.
ACCESSION  U11267
VERSION     U11267.1 GI:511785
KEYWORDS
SOURCE      human.
ORGANISM    Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (sites)
AUTHORS    Hurley, C.K., Bei, M., Rodriguez, S. and Johnson, A.
TITLE      HLA-B*71
JOURNAL    Unpublished
REFERENCE   2 (bases 1 to 968)
AUTHORS    Hurley, C.K.
TITLE      Direct Submission
JOURNAL    Submitted (23-JUN-1994) Carolyn K. Hurley, Microbiology, Georgetown
            University School of Medicine, 3900 Reservoir Road, N.W.,
            Washington, D.C. 20007 USA
FEATURES   Location/Qualifiers
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BASE COUNT 196 a 310 c 314 g 148 t
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US-08-653-294-23 x HSU11267 ..
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295 CGAGAGGACCTGCGGACCTGCTCGCTAC 324

seq_name: gb_prl:HUMMHC

seq_documentation_block:
LOCUS      HUMMHC 1017 bp mRNA PRI 07-JAN-1995
DEFINITION Human MHC class I HLA-B*27-HS mRNA, 3' end.
ACCESSION  M62852
VERSION     M62852.1 GI:187760
KEYWORDS    cell surface antigen; class I gene; integral membrane protein;
            major histocompatibility complex.
SOURCE      Homo sapiens cDNA to mRNA.
ORGANISM    Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 1017)
AUTHORS    Choo, S.Y., Fan, L.A. and Hansen, J.A.
TITLE      A novel HLA-B*27 allele maps B27 allospecificity to the region
            around position 70 in the alpha 1 domain
            J. Immunol. 147 (1), 174-180 (1991)
JOURNAL
MEDLINE
FEATURES   Location/Qualifiers
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223 CGAGAGGACCTGCGGACCTGCTCCGCTAC 252

seq_name: gb_pat:A28264

seq_documentation_block: 1026 bp DNA PAT 24-MAY-1995
LOCUS A28264
DEFINITION H.sapiens mRNA for HLA-B 27 from patent EP0226069.
ACCESSION A28264
VERSION A28264.1 GI:905320

KEYWORDS
SOURCE human.

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 1026)
AUTHORS Szoets,H., Weiss,E., Doerner,C., Lang,M., Meo,T. and
Riethmuller,G.

TITLE HLA-B 27, DNA coding therefor and its utilization
JOURNAL Patent: EP 0226069-A 1 24-JUN-1987;

Riethmuller, Gert, Prof. Dr

FEATURES Location/Qualifiers

Source
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BASE COUNT 213 a 307 c 344 g 162 t

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alignment_block:

US-08-653-294-23 x A28264 ..

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223 CGAGAGGACCTGCGGACCTGCTCCGCTAC 252

seq_name: gb_pat:E01342

seq_documentation_block:

LOCUS E01342 1026 bp RNA PAT 29-SEP-1997
DEFINITION cDNA encoding C-terminal Fragment of HLA-B27.

ACCESSION E01342

VERSION E01342.1 GI:2169599

KEYWORDS JP 1987228281-A/2.

SOURCE Homo sapiens.

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 1026)

AUTHORS Hannercoore,S., Eriabeeto,W., Kurisuta,D., Maagotsuto,R., Tomaso,M.
and Geruto,R.

TITLE HLA-B27, DNA ENCODING THE SAME AND ITS USE

JOURNAL Patent: JP 1987228281-A 2 07-OCT-1987;

COMMENT BEHRINGWERKE AG

OS Human

PN JP 1987228281-A/2

PD 07-OCT-1987

PR 28-NOV-1986 JP 1986284078

PF 28-NOV-1985 DE 85 3542024, 21-DEC-1985 DE 85 3545576 PI

HANNERCOORE SUTSUETSU, ERIZABEETO WALSU, KURISUTA DERUNAA, PI

MAAGOTSUTO RANGU, TOMASO MEO, GERUTO RIITONIYURAA PC

C12N15/00,C07H21/04,C12P21/00,C12Q1/68,G01N33/577//A61K39/00, PC

C07K13/00,

PC C07K15/06,(C12P21/00,C12R1:91);

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CC topology: Linear;

CC hypothetical: No;

CC anti-sense: No;

CC fragment_type: C-Terminal Fragment;

CC *source: cell_type=Leukocyte;

FH Key

Location/Qualifiers

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HLA-B27"

FEATURES Location/Qualifiers

1..1026

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BASE COUNT 213 a 307 c 344 g 162 t

ORIGIN

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Quality: 50.00 Length: 10

Ratio: 5.000 Gaps: 0

Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:

US-08-653-294-23 x E01342 ..

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223 CGAGAGGACCTGCGGACCTGCTCCGCTAC 252

seq_name: gb_pri:HUMMHZUNIA

seq_documentation_block:

LOCUS HUMMHZUNIA 1084 bp mRNA PRI 27-SEP-1993

DEFINITION Human MHC class I (HLA-B 27052) mRNA fragment.

ACCESSION L20086

VERSION L20086.1 GI:307282

KEYWORDS class I gene; lymphocyte antigen; major histocompatibility complex.
SOURCE Homo sapiens (strain South American Amerindian) cDNA to mRNA.

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;

Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 1084)

AUTHORS

Watkins,D.I., McAdam,S.N., Liu,X., Strang,C.R., Milford,E.L.,

Levine,C.G., Garber,T.L., Dogon,A.L., Lord,C.I., Ghim,S.H.,

Troup,G.M., Hughes,A.L. and Letvin,N.L.

TITLE New recombinant HLA-B alleles in a tribe of South American

Indians indicate rapid evolution of MHC class I loci

Nature 357, 329-333 (1992)

JOURNAL

MEDLINE

92269956

FEATURES Location/Qualifiers

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  Percent Similarity: 100.000  Percent Identity: 100.000

alignment_block:
US-08-653-294-23 x HUMMHZUNIA ..
Align seg 1/1 to: HUMMHZUNIA from: 1 to: 1084

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290 CGAGAGGACCTGCGGACCTGCTCGGCTAC 319

seq_name: gb_pr2:HSU31971

seq_documentation_block:
LOCUS      HSU31971      1089 bp      mRNA      27-APR-1996
DEFINITION Human MHC class I antigen HLA-B precursor (HLA-B) mRNA, complete
cds
ACCESSION  U31971
VERSION    U31971.1  GI:1144333
KEYWORDS
SOURCE     human.
ORGANISM   Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1 (bases 1 to 1089)
AUTHORS   Balas,A., Santos,S. and Vicario,J.L.
TITLE     Serological and molecular characterization of a novel HLA-B allele
JOURNAL   Unpublished (1995)
REFERENCE  2 (bases 1 to 1089)
AUTHORS   Balas,A.
TITLE     Direct Submission
JOURNAL   Submitted (20-JUL-1995) Antonio Balas, Centro de Transfusión de
Madrid, Histocompatibilidad, Menéndez Pelayo, 65, Madrid, 28009,
Spain

FEATURES
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LOCUS      AF026218      1089 bp      mRNA      23-SEP-1998
DEFINITION Homo sapiens MHC class I antigen HLA-B (HLA-B27052 allele) mRNA,
complete cds.
ACCESSION  AF026218
VERSION    AF026218.1  GI:3643696
KEYWORDS
SOURCE     human.
ORGANISM   Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1 (bases 1 to 1089)
AUTHORS   Seurnyck,K.L. and Baxter-Lowe,L.A.
TITLE     B27052 W496D

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JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1089)
AUTHORS Seurynck,K.L. and Baxter-Lowe,L.A.
TITLE Direct Submission
JOURNAL Submitted (22-SEP-1997) Molecular Genetics, Richland Memorial
Hospital, 7 Richland Medical Park, Columbia, SC 29203, USA
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N_Genesed_36:V17143	-	36.00	119.20	48.66	853	! Human proteolipid (PLAU) cDNA.
N_Genesed_36:X13170	+	36.00	97.20	81.97	10555	! Enterococcus faecalis genome
N_Genesed_36:T62851	+	35.00	116.10	72.45	793	! Ripening banana pulp cDNA clone
N_Genesed_36:Q29167	+	34.00	121.78	34.96	270	! HLA-B*52 exon 2 alpha-1 domain
N_Genesed_36:Q01034	+	34.00	109.61	166.61	1086	! Sequence encoding HLA-B*51 anti
N_Genesed_36:Q01822	+	34.00	109.61	166.61	1086	! Sequence encoding HLA-B*52 anti
N_Genesed_36:Q05693	+	34.00	109.58	167.13	1089	! HLA-B*51 gene for production of
N_Genesed_36:Q05701	+	34.00	109.58	167.13	1089	! HLA-B*52 gene for production of
N_Genesed_36:Q01214	+	34.00	109.58	167.13	1089	! HLA-B*53 exon. HLA-B*53 gene,
N_Genesed_36:X04639	+	34.00	100.76	517.95	2985	! Nucleic acid encoding an enzym
N_Genesed_36:T62816	-	34.00	96.16	934.82	5053	! Nucleotide sequence of the spe
N_Genesed_36:V17236	-	34.00	96.16	935.24	5055	! DNA from a region of NP strain
N_Genesed_36:T00770	+	34.00	92.53	1.5e+03	7653	! Strolimus effector protein gen
N_Genesed_36:T33872	+	34.00	92.34	1.5e+03	7824	! Human RAP11 cDNA. Rapamycin bi
N_Genesed_36:T62818	+	34.00	92.20	1.6e+03	7943	! FRAP (tor1) cDNA. Selective in
N_Genesed_36:V21209_00	+	34.00	69.22	2.9e+04	110000	! Methanococcus jannaschii c
N_Genesed_36:X20248_07	-	34.00	69.22	2.9e+04	110000	! Continuation (8 of 10) of
N_Genesed_36:X13461	+	33.00	99.12	639.73	2349	! Enterococcus faecalis genome c
N_Genesed_36:T60573	+	33.00	95.83	975.01	3420	! Cercospora nicotianae cercospo
N_Genesed_36:V52088	+	32.50	98.71	673.66	1986	! Helicobacter polypeptide GHPO
N_Genesed_36:X14516	+	32.50	98.71	673.66	1986	! H. pylori GHPO 1278 gene. New
N_Genesed_36:T68022	+	32.50	98.69	675.94	1992	! H. pylori inner membrane prote
N_Genesed_36:X30428	+	32.50	98.53	689.66	2028	! H. pylori outer membrane prote
N_Genesed_36:T62846	+	32.00	125.98	20.41	71	! Human gene signature HUMGS04520
N_Genesed_36:T69627	+	32.00	108.94	181.45	498	! cDNA encoding B. napus cytosoli
N_Genesed_36:T91186	+	32.00	108.27	197.88	538	! Flea saliva protein fspN(O) cDN
N_Genesed_36:T67343	+	32.00	108.27	197.88	538	! Flea saliva protein nucleic aci
N_Genesed_36:T93328	-	32.00	102.70	404.21	1017	! DNA encoding Terebinthacete
N_Genesed_36:T03250	-	32.00	97.73	764.07	1794	! Enterobacter sp. S262 sucrose
N_Genesed_36:V22706	+	32.00	96.16	934.63	2147	! Mouse recombinase hsrEC2 gene
N_Genesed_36:Q37687	+	32.00	94.69	1.4e+03	2540	! Rat choline kinase gene. Rat c
N_Genesed_36:T63567	-	32.00	94.05	1.2e+03	2734	! Thermococcus barossii DNA poly
N_Genesed_36:V10362	-	32.00	90.17	2.0e+03	4257	! Infected cell protein number 4
N_Genesed_36:T668520	+	32.00	90.17	2.0e+03	4257	! The nucleotide sequence of the
N_Genesed_36:N91312	+	32.00	85.22	3.8e+03	7439	! pCHL1 plasmid. Synthetic oligo

LE
JE
=Delta/
0
10007.10557
ПОЛУНИ

FT intron 2450.

人 々

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FT intron 3009..3041
FT /*tag= f
FT intron 3148..3191
FT /*tag= g
PN EP-226069-A.
PD 24-JUN-1987.
PF 21-NOV-1986; 116139.
PR 01-JAN-1985; DE-542024.
PR 21-DEC-1985; DE-545576.
PA (BEHW ) BEHRINGER AG.
PI (BEHW ) Weiss E, Dorner C, Lang M, Meo T, Riethmuller G;
DR WPI: 87-171469/25.
DR P-PSDB; P70155.
DR DNA coding for human histocompatibility antigen HLA-B 27 - useful
PT for diagnosis and antigen and antibody prodn.
PS Claim 1; p6; 13pp; German.
CC THE DNA may be used to detect the HLA-B 27 gene (opt. mutated) in
CC human genetic material. The HLA-B 27 may be used to detect anti-HLA-
CC B 27 antibodies in human serum. The antibodies may be used to
CC determine HLA-B 27 levels in human serum, e.g. for diagnosis of
CC rheumatic disorders, esp. ankylosing spondylitis.
SQ Sequence 3874 BP; 751 A; 1094 C; 1171 G; 858 T;

alignment_scores:
Quality: 50.00 Length: 10
Ratio: 5.000 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
US-08-653-294-23 x N70225 ..
Align seg 1/1 to: N70225 from: 1 to: 3874

1 ArgGluAspLeuArgThrLeuLeuArgTyr 10
|||||
941 CGAGAGGACCTCGGACCTGCTCGCTAC 970

seq_name: N_Geneseq_36:T61639

seq_documentation_block:
ID T61639 standard; DNA; 6553 BP.
AC T61639;
DT 05-JUN-1997 (first entry)
DE HLA B27 consensus sequence.
KW HLA B27; seronegative spondylarthropathy; ankylosing spondylitis;
KW Reiter's syndrome; arthritis; acute anterior uveitis; diagnosis;
KW ss; ds.
OS Homo sapiens.
FH Key Location/Qualifiers
FT mrna 3968..6653
FT /*tag= a
FT /*note= "HLA-B27 3' flanking region, downstream of
FT 3' untranslated region"
FT mrna 4112..4556
FT /*tag= b
FT /*note= "3' flanking region diagnostic for genetic
FT predisposition to SNSA"
FT mrna 4270..4556
FT /*tag= b
FT /*note= "3' flanking region diagnostic for genetic
FT predisposition to SNSA"
FT misc_difference 4495
FT /*tag= d
FT /*note= "absence of cytosine at this site is
FT indicative of a predisposition to SNSA"
PN WO9709450-A1.
PD 13-MAR-1997.
PF 16-AUG-1996; U13256.
PR 01-SEP-1995; US-522942.
PA (CEDA-) CEDARS SINAI MEDICAL CENT.
PI Tyan DB;
DR WPI: 97-192924/17.

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PT Detecting pre-disposition to seronegative spondylarthropathies -
PT from the absence of a C residue at a specific position in the
PT 3'-flanking region of the HLA B27 allele
PS Claim 1; Page 52-56; 68pp; English.
CC Genetic predisposition to seronegative spondylarthropathies (SNSA)
CC is detected by determining the absence of a cytosine nucleotide in
CC the 3' flanking region (see also T61647-48) of an HLA-B gene at a
CC position corresponding to nucleotide 4495 of the HLA-B27 consensus
CC sequence given in T61639. Probes and primers (see also T61640-46)
CC based on this region can be used in diagnostic assays to detect the
CC genetic predisposition to SNSA, and permit the distinction of B27+
CC individuals who are resistant to SNSA from B27+ normal individuals
CC who are susceptible (but as yet unaffected) to such diseases.
SQ Sequence 6553 BP; 1443 A; 1619 C; 2017 G; 1474 T;

alignment_scores:
Quality: 50.00 Length: 10
Ratio: 5.000 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
US-08-653-294-23 x T61639 ..
Align seg 1/1 to: T61639 from: 1 to: 6553

1 ArgGluAspLeuArgThrLeuLeuArgTyr 10
|||||
1102 CGAGAGGACCTCGGACCTGCTCGCTAC 1131

seq_name: N_Geneseq_36:V35645

seq_documentation_block:
ID V35645 standard; DNA; 2386 BP.
AC V35645;
DT 08-SEP-1998 (first entry)
DE Cladosporium oxysporum glucose oxidase encoding DNA.
KW Glucose oxidase; Cladosporium oxysporum; enzyme; bread improver;
KW antimicrobial agent; toothpaste; detergent; stain removal;
KW dough additive; hydrogen peroxide generator; ss.
OS Cladosporium oxysporum.
FH Key Location/Qualifiers
FT 5'UTR 1..350
FT /*tag= a
FT CDS 351..2192
FT /*tag= b
FT /*product= "glucose oxidase"
FT sig_peptide 351..419
FT /*tag= c
FT /*note= "predicted signal sequence"
FT mat_peptide 420..2189
FT /*tag= d
FT 3'UTR 2190..2386
FT /*tag= e
PN WO9820136-A1.
PD 14-MAY-1998.
PF 03-NOV-1997; U20174.
PR 07-NOV-1996; US-746257.
PR (NOVO ) NOVO NORDISK BIOTECH INC.
PA (NOVO ) NOVO NORDISK AS.
PI Berka RM, Cherry JR, Halkier T;
DR WPI: 98-286952/25.
DR P-PSDB; W60593.
DR New nucleic acid encoding glucose oxidase active at acidic pH, from
PT Cladosporidium - and related vectors and host cells, producing
PT enzyme useful as bread improver, antimicrobial additive for
PT toothpaste, etc. and hydrogen peroxide generator in detergents
PS Claim 4; Fig 2A-B; 83pp; English.
CC This DNA encodes a Cladosporium oxysporum glucose oxidase. Host cells
CC containing a construct comprising the glucose oxidase encoding nucleic
CC acid sequence with regulatory sequences are used to produce recombinant
CC glucose oxidase. Preferred fragments of the nucleic acid are present in
CC pGOX4A and pGOX6A, contained in E. coli deposited as NRRL B-21628 and

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CC B-21629. The host cells are particularly Fusarium. The recombinant
CC glucose oxidase is useful as dough additive to improve the gluten
CC quality. It can be used as additive for toothpaste (particularly used
CC with a thiocyanate and lactoperoxidase to generate antimicrobial
CC oxythiocyanate anion), mouthwash, denture cleaners, soaps, hair and body
CC care products. It can be added to cleaning solutions for contact lenses
CC as bleach or as an antibacterial agent. It is also useful as a hydrogen
CC peroxide generator in laundry and dishwashing detergents, particularly
CC for stain removal.
SQ Sequence 2386 BP; 583 A; 707 C; 581 G; 515 T;

alignment_scores:
Quality: 37.00 Length: 9
Ratio: 4.625 Gaps: 0
Percent Similarity: 88.889 Percent Identity: 88.889

alignment_block:

US-08-653-294-23 x V35645 ..

Align seg 1/1 to: V35645 from: 1 to: 2386

1 ArgGluAspLeuArgThrLeuLeuArg 9
|||||
605 CGTGAGGACTTACGGACAGCCCTCGA 631

seq_name: N_Geneseq_36:V21209_16

seq_documentation_block:

Continuation (17 of 17) of V21209 from base 1600001 (Methanococcus jannaschii circular
WP Sequence split into 17 fragments LOCUS V21209 Accession V21209

Fragment Name	Begin	End
WP V21209_00	1	110000
WP V21209_01	100001	210000
WP V21209_02	200001	310000
WP V21209_03	300001	410000
WP V21209_04	400001	510000
WP V21209_05	500001	610000
WP V21209_06	600001	710000
WP V21209_07	700001	810000
WP V21209_08	800001	910000
WP V21209_09	900001	1010000
WP V21209_10	1000001	1110000
WP V21209_11	1100001	1210000
WP V21209_12	1200001	1310000
WP V21209_13	1300001	1410000
WP V21209_14	1400001	1510000
WP V21209_15	1500001	1610000
WP V21209_16	1600001	1664976

alignment_scores:
Quality: 37.00 Length: 10
Ratio: 4.111 Gaps: 0
Percent Similarity: 90.000 Percent Identity: 70.000

alignment_block:

US-08-653-294-23 x V21209_16/rev ..

Align seg 1/1 to: reverse of: V21209_16 from: 1 to: 64976

1 ArgGluAspLeuArgThrLeuLeuArgTyr 10
|||||
49695 AGAGAAAATTAAGACAGTGCTAAGATAT 49666

seq_name: N_Geneseq_36:V89109

seq_documentation_block:

ID V89109 standard; cDNA: 458 BP.

AC V89109;

DT 15-FEB-1999 (first entry)

DE: EST clone B2187.

KW Human; secreted protein; expressed sequence tag; EST; haematopoiesis;

KW tissue growth; activin; inhibin; chemotaxis; chemokinesis; haemostatic;
KW receptor; ligand; thrombolytic; anti-inflammatory; cadherin; anti-tumour;
KW gene therapy; ss.
OS Homo sapiens.
PN WO9845436-A2.
PD 15-OCT-1998.
PF 10-APR-1998; U06955.
PR 10-APR-1997; US-838821.
PA (GENY) GENETICS INST INC.
PI Agostino M, Jacobs K, Lavallie ER, McCoy JM, Merberg D,
PI Racine LA, Spaulding V, Treacy M;
DR WPI; 99-070077/06.
PT New polynucleotides encoding human secreted proteins - derived from
PT e.g. human blood, kidney, foetal lung, placenta, testes, brain,
PT ovary, pituitary, retina and colon cDNA libraries.
PS Claim 1; Page 113; 618pp; English.
CC The present sequence represents a human expressed sequence tag (EST).
CC The polynucleotide, which is a secreted EST, and the encoded protein
CC are predicted to have useful biological activities which would make
CC them suitable for treating, preventing or ameliorating medical
CC conditions in humans and animals, although no supporting data is
CC given. Suggested activities include nutritional activity, immune
CC stimulating or suppressing activity, haematopoiesis regulating
CC activity, tissue growth activity, activin/inhibin activity,
CC chemotactic/chemokinetic activity, haemostatic and thrombolytic
CC activity, receptor/ligand activity, anti-inflammatory activity,
CC cadherin/tumour invasion suppressor activity, tumour inhibition
CC activity. The polynucleotide may also be useful for gene therapy.
SQ Sequence 458 BP; 152 A; 70 C; 74 G; 162 T;

alignment_scores:

Quality: 36.00 Length: 9
Ratio: 4.000 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 66.667

alignment_block:

US-08-653-294-23 x V89109/rev ..

Align seg 1/1 to: reverse of: V89109 from: 1 to: 458

2 GluAspLeuArgThrLeuLeuArgTyr 10

|||||
358 GAAGACATTAAATACATTAAAGATAC 332

seq_name: N_Geneseq_36:V17143

seq_documentation_block:

ID V17143 standard; cDNA: 853 BP.

AC V17143;

DT 07-JUL-1998 (first entry)

DE Human proteolipid (PLHu) CDNA.

KW Human proteolipid; PLHu; exocytosis; membrane trafficking;

KW rat plasmolipin; chemokine; inflammation; ss.

OS Homo sapiens.

FH Key

Location/Qualifiers

FT CDS

FT 19..480

/tag= a

/product= "Human proteolipid"

PN WO9804691-A1.

PD 05-FEB-1998.

PF 21-JUL-1997; U12734.

PR 26-JUL-1996; US-695736.

PA (INCY-) INCYTE PHARM INC.

PI Au-Young J, Bandman O, Goli SK, Hillman JL;

DR WPI; 98-130683/12.

DR P-PSDB; W5217.

PT Human proteolipid PLHu - used to accelerate diagnosis and proper

PT treatment of diseases and conditions associated with abnormal

PT membrane trafficking

PS Claim 4; Fig 1A-1B; 53pp; English.

CC The present sequence is of a human proteolipid (PLHu) cDNA which

CC was partially isolated as Incyte clone 640699 derived from a human breast

CC CDNA library. The invention provides PLHu cDNA for expression of PLHu
 CC protein. Homology of PLHu protein to rat plasmalipin indicates its
 CC involvement in exocytosis. Exocytosis facilitated by PLHu may influence
 CC membrane trafficking within the cell and could affect the release of
 CC chemokines involved in cell migration, proteases which are active in
 CC inflammation or other similar activities involving endothelial cells,
 CC fibroblasts, etc. The invention also claims for antibodies against
 CC PLHu which can be used for e.g. in diagnostic tests to accelerate
 CC diagnosis and proper treatment of conditions associated with abnormal
 CC membrane trafficking.
 SQ Sequence 853 BP; 233 A; 187 C; 162 G; 271 T;

alignment_scores:
 Quality: 36.00 Length: 9
 Ratio: 4.000 Gaps: 0
 Percent Similarity: 100.000 Percent Identity: 66.667

alignment_block:

US-08-653-294-23 x V17143/rev ..

Align seg 1/1 to reverse of: V17143 from: 1 to: 853

2 GluAspLeuArgThrLeuLeuArgTyr 10
 |||||:|||||:|||||:|||||
 709 GAAGACATTATACATTATTAAGATAC 683

seq_name: N_Geneseq_36:X13170

seq_documentation_block:

ID X13170 standard; DNA; 10555 BP.
 AC X13170;
 DT 19-MAR-1999 (first entry)
 DE Enterococcus faecalis genome contig SEQ ID NO:233.
 KW Enterococcus faecalis; contig; detection; Enterococcal infection;
 KW vaccine; attenuation; computer readable medium; ds.
 OS Enterococcus faecalis.
 PN WO980555-A2.
 PD 12-NOV-1998.
 PF 04-MAY-1998; U08985.
 PR 14-NOV-1997; US-066009.
 PR 06-MAY-1997; US-044031.
 PR 16-MAY-1997; US-046655.
 PA (HUMA-) HUMAN GENOME SCI INC.
 PI Barash SC, Dillon PJ, Kunsch CA;
 DR WPI: 99-045171/04.

PT New isolated Enterococcus faecalis polynucleotides and polypeptides
 PT - used to develop products for the detection of Enterococcus and for
 PT use in vaccines for prevention or attenuation of Enterococcus
 PT infection.
 PS Claim 1: Page 1164-1169; 2084pp; English.
 CC A computer readable medium has been developed which has recorded on it
 CC 982 nucleotide sequences isolated from the Enterococcus faecalis genome.
 CC X12938 to X13919 represent these nucleotide sequences which are primary
 CC nucleotide sequences, also known as contigs. The computer-based system
 CC can identify fragments of the Enterococcus faecalis genome with
 CC commercial importance. The products can be used to detect the presence
 CC of Enterococcus faecalis in samples. They can also be used for
 CC diagnosing Enterococcal infection in an animal and monitoring
 CC progression of disease, and for identifying agents which can be used to
 CC modulate the growth or pathogenicity of Enterococcus faecalis, or
 CC another related organism, in vivo or in vitro. In particular the
 CC polypeptides encoded by the Enterococcus faecalis nucleotide sequences
 CC can be used in vaccines to prevent or attenuate an Enterococcal
 CC infection.
 SQ Sequence 10555 BP; 2903 A; 2453 C; 1793 G; 3396 T;

alignment_scores:
 Quality: 36.00 Length: 9
 Ratio: 4.500 Gaps: 0
 Percent Similarity: 88.889 Percent Identity: 77.778

alignment_block:

US-08-653-294-23 x X13170 ..

Align seg 1/1 to: X13170 from: 1 to: 10555

2 GluAspLeuArgThrLeuLeuArgTyr 10
 :|||:|||||:|||||:|||||
 5890 CAAGATTTAAGGAAGTTGTTGCGTTAT 5916

seq_name: N_Geneseq_36:V28651

seq_documentation_block:

ID V28651 standard; cDNA; 793 BP.
 AC V28651;
 DT 29-JUL-1998 (first entry)
 DE Ripening banana pulp cDNA clone U-0131 SEQ ID NO:9.
 KW Banana; ripening; pulp; Musa acuminata cv. Grand Nain; fruit;
 KW genetic control; tissue senescence; ss.
 OS Musa acuminata.
 PN WO9811228-A2.
 PD 19-MAR-1998.
 PF 08-SEP-1997; G02424.
 PR 25-APR-1997; GB-008366.
 PR 10-SEP-1996; GB-018862.
 PA (ZENE) ZENECA LTD.
 PI Bird CR, Medina-Suarez RDJ, Seymour GB;
 DR WPI: 98-207389/18.
 PT Modulation of ripening or tissue senescence in bananas - comprises
 PT use of DNA isolated from ripening banana pulp to produce genetically
 PT modified fruit
 PS Claim 1: Page 23-24; 72pp; English.
 CC The present sequence represents a cDNA clone isolated from ripening
 CC banana pulp. 57 clones were isolated and are given in V28643 to V28699.
 CC The cDNA clone sequence can be used in a method of modulating ripening
 CC or tissue senescence process in plants of the genus Musa. The method
 CC comprises: (a) inserting into the plant material at least 1 of the 57
 CC sequences (as above); (b) regenerating the plant material, and (c)
 CC selecting from the transformed regenerants, plants with modulated
 CC ripening or tissue senescence characteristics. Also described in the
 CC present invention are: (1) plants, their progeny, seed and material
 CC obtained from the plants, produced by the above method; (2) a vector
 CC functional in plants comprising a promoter region which is operably in
 CC plant cells, a polynucleotide sequence as defined above, and a
 CC transcription termination sequence; and (3) a method of controlling
 CC plant pathogens comprising the application of anti-pathogenic agent to
 CC plants of (1).
 SQ Sequence 793 BP; 161 A; 275 C; 199 G; 137 T;

alignment_scores:

Quality: 35.00 Length: 10
 Ratio: 4.375 Gaps: 0
 Percent Similarity: 80.000 Percent Identity: 70.000

alignment_block:

US-08-653-294-23 x V28651 ..

Align seg 1/1 to: V28651 from: 1 to: 793

1 ArgGluAspLeuArgThrLeuLeuArgTyr 10
 ||| ||| |||||:|||||:|||||
 626 CGCCAGATNAAGAACCTCTCGCTTT 655

seq_name: N_Geneseq_36:Q29167

seq_documentation_block:

ID Q29167 standard; DNA; 270 BP.
 AC Q29167;
 DT 09-MAR-1993 (first entry)
 DE HLA-B*52 exon 2 alpha-1 domain.
 KW Human leukocyte antigen; transgenic; germ cells; somatic cells;
 KW expression; ss.
 PN J04091731-A.

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PD 25-MAR-1992.
PF 03-AUG-1990; 207329.
PA (OLYU ) OLYMPUS OPTICAL CO.
DR WPI; 92-342893/42.
PT Transgenic non-human mammalian HLA-Bw 52 gene - useful for
PT analysis of expression of gene structure, and prodn. of
PT mouse model of human disease
PS Disclosure: Fig 1: 8pp; Japanese.
CC The sequence shows the exon 2 alpha-1 domain of the human leukocyte
CC antigen-Bw 52 gene. The complete gene may be introduced into non-
CC human mammals, pref. rat or mouse, or their ancestors at the primary
CC developmental biological step via transplantation into the zygote or
CC embryo to generate transgenic non-human mammals incorporating the
CC HLA-Bw 52 gene in both their germ cells and somatic cells. Transgenic
CC non-human mammals contg. HLA-Bw 52 are useful for the analysis of
CC expression of the gene, its structure, and prodn. of mouse models of
CC human disease. See also Q29166-72.
SQ Sequence 270 BP; 59 A; 88 C; 86 G; 37 T;

alignment_scores:
  Quality: 34.00 Length: 10
  Ratio: 4.250 Gaps: 0
  Percent Similarity: 80.000 Percent Identity: 70.000
alignment_block:
US-08-653-294-23 x Q29167 ..
Align seg 1/1 to: Q29167 from: 1 to: 270

1 ArgGluAspLeuArgThrLeuLeuArgTyr 10
|||||:||||| |||||
222 CGAGAGAACCTGCGGATCGCGCTCGCTAC 251

seq_name: N_Geneseq_36:Q01834
seq_documentation_block:
ID Q01834 standard; DNA; 1086 BP.
AC Q01834;
DT 19-MAR-1991 (first entry)
DE Sequence encoding HLA-B51 antigen.
KW Probe: HLA class I DNA; immunogen; ss.
OS Homo sapiens.
PN EP354580-A.
PD 14-FEB-1990.
PF 10-AUG-1989.
PR 11-AUG-1988; JP-200758.
PA (OLYU) Olympus Optical Co., Ltd.
PI Kano K, Takiguchi;
DR WPI; 90-046289/07.
DR P-PSDB; R03142.
PT New DNA for class 1 human leukocyte antigens and derived probes and
PT transformed cells, useful for DNA typing, as immunogens etc.
PS Claim 1; Page 11; 23pp; English.
CC The HLA class I DNA can be used a source of probes for use in DNA
CC typing. Transformed cells, which are useful as immunogens, can be
CC obtained by introducing these DNAs into eucaryotic cells.
SQ Sequence 1086 BP; 224 A; 334 C; 356 G; 172 T;

alignment_scores:
  Quality: 34.00 Length: 10
  Ratio: 4.250 Gaps: 0
  Percent Similarity: 80.000 Percent Identity: 70.000
alignment_block:
US-08-653-294-23 x Q01834 ..
Align seg 1/1 to: Q01834 from: 1 to: 1086

1 ArgGluAspLeuArgThrLeuLeuArgTyr 10
|||||:||||| |||||
294 CGAGAGAACCTGCGGATCGCGCTCGCTAC 323

seq_name: N_Geneseq_36:Q01822
seq_documentation_block:
ID Q01822 standard; DNA; 1086 BP.
AC Q01822;
DT 19-MAY-1991 (first entry)
DE Sequence encoding HLA-Bw52 antigen.
KW Probe: HLA class I DNA; immunogen; ss.
OS Homo sapiens.
PN EP-354580-A.
PD 14-FEB-1990.
PF 10-AUG-1989.
PR 11-AUG-1988; JP-200758.
PA (OLYU) Olympus Optical Co., Ltd.
PI Kano K, Takiguchi;
DR WPI; 90-046289/07.
DR P-PSDB; R03142.
PT New DNA for class 1 human leukocyte antigens and derived probes and
PT transformed cells, useful for DNA typing, as immunogens etc.
PS Claim 2; pp11-12; 23pp; English.
CC The HLA class I DNA can be used a source of probes for use in DNA
CC typing. Transformed cells, which are useful as immunogens, can be
CC obtained by introducing these DNAs into eucaryotic cells.
SQ Sequence 1086 BP; 223 A; 335 C; 358 G; 170 T;

alignment_scores:
  Quality: 34.00 Length: 10
  Ratio: 4.250 Gaps: 0
  Percent Similarity: 80.000 Percent Identity: 70.000
alignment_block:
US-08-653-294-23 x Q01822 ..
Align seg 1/1 to: Q01822 from: 1 to: 1086

1 ArgGluAspLeuArgThrLeuLeuArgTyr 10
|||||:||||| |||||
294 CGAGAGAACCTGCGGATCGCGCTCGCTAC 323

seq_name: N_Geneseq_36:Q05693
seq_documentation_block:
ID Q05693 standard; DNA; 1089 BP.
AC Q05693;
DT 03-JAN-1991 (first entry)
DE HLA-B51 gene for production of monoclonal antibodies.
KW Allotype specific monoclonal anti-HLA antibodies; hybridomas;
KW transgenic animals; HLA-B51 gene; ss.
FH Key Location/Qualifiers
FT exon 1..73
FT FT /tag= a
FT FT /number=1
FT exon 74..343
FT FT /tag= b
FT FT /number=2
FT FT /note="alpha 1-domain"
FT exon 344..619
FT FT /tag= c
FT FT /number=3
FT FT /note="alpha 2-domain"
FT intron 620..895
FT FT /tag= d
FT FT /number=4
FT FT /note="alpha 3-domain"
FT exon 896..1012
FT FT /tag= e
FT FT /number=5
FT exon 1013..1042

```

[illegible]

```

FT exon /*tag= f /number=6 1043..1089
FT FT /*tag= g /number=7
PN EP-383183-A.
PD 22-AUG-1990.
PF 07-FEB-1990; 102424.
PR 08-FEB-1989; JP-029313.
PA (OLYU ) OLYMPUS OPTICAL KK.
PI Takiguchi M;
DR WPI; 90-255479/34.
PT Allotype specific monoclonal anti- HLA antibodies prodn. - using
PT hybridomas derived from transgenic animals carrying HLA gene and
PT immunised with HLA antigen of different allotype
PS Disclosure; Fig 1 A-G; 20pp; English.
CC The human HLA-Bw52 gene was introduced into mouse L cells and
CC then these cells used to immunise one of the transgenic mice
CC (See Q05693).
CC The spleen lymphocytes were fused with myeloma cells (P3x63-Ag8.653).
CC Hybridomas producing antibodies were selected.
SQ Sequence 1089 BP; 224 A; 335 C; 357 G; 173 T;

alignment_scores:
Quality: 34.00 Length: 10
Ratio: 4.250 Gaps: 0
Percent Similarity: 80.000 Percent Identity: 70.000

alignment_block:
US-08-653-294-23 x Q05693 ..
Align seg 1/1 to: Q05693 from: 1 to: 1089
1 ArgGluAspLeuArgThrLeuLeuArgTyr 10
|||||:::||||| |||||
295 CGAGAGAACCTGGATCGCCTCGGTAC 324

seq_name: N_Geneseq_36:Q05701

seq_documentation_block:
ID ID Q05701 standard; DNA; 1089 BP.
AC Q12114.
DT 29-AUG-1991 (first entry)
DE HLA-Bw53 exon.
KW Human leukocyte antigen; probe; major histocompatibility complex;
KW MHC; class I; ss.
OS Homo sapiens.
FH Key Location/Qualifiers
FT cds 1..1089 /*tag= a
FT J03112487-A.
PN 14-MAY-1991.
PD 14-MAY-1991.
PF 22-SEP-1989; 247697.
PR 22-SEP-1989; JP-247697.
PA (OLYU ) OLYMPUS OPTICAL KK.
DR WPI; 91-182991/25.
DR P-PSDB; R12463.
PT HLA-Bw53 gene, DNA probe and transformant cells - used for
PT immunisation, identifying specificity of antiserum etc.
PS Claim 1; Page 1; lipp; Japanese.
CC Probes comprising part of the sequence can be used to identify
CC Class I genes. The DNA can be expressed for immunisation of
CC animals and prodn. of monoclonal antibodies specific for the
CC HLA-Bw53 antigen. See also J03112485 and J03112486.
SQ Sequence 1089 BP; 222 A; 337 C; 356 G; 174 T;

alignment_scores:
Quality: 34.00 Length: 10
Ratio: 4.250 Gaps: 0
Percent Similarity: 80.000 Percent Identity: 70.000

alignment_block:
US-08-653-294-23 x Q12114 ..

```


Align seg 1/1 to: Q12114 from: 1 to: 1089

1 ArgGluAspLeuArgThrLeuLeuArgTyr 10

|||||:|||||

295 CGAGAGAACCTGCGGATCGGCTCCGCTAC 324

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OM of: US-08-653-294-23 to: EST:* out_format : pfs

Date: Feb 8, 2000 6:22 AM

About: Results were produced by the GenCore software, version 4.5,
Copyright (c) 1993-2000 CompuGen Ltd.

Command line parameters:

-MODEM=framet.p2n.model -DEV=xlp
-O=/cgl1/USPTO.spool/US08653294/runat_04022000_160700_15770/app_query.fasta.2
-DB=EST -Qfmt=fastap -SUFFIX=rst -GAPOP=12.000 -GAPEXT=4.500
-MINMATCH=0.100 -LOOPCL=0.000 -LOOPEXT=0.000 -GAPOP=6.000
-GAPEXT=0.050 -XGAPOP=10.000 -YGAPEXT=0.500 -FGAPOP=6.000
-FGAEXT=7.000 -YGAPOP=10.000 -YGAPEXT=0.500 -DELOP=6.000
-DELEXT=7.000 -START=1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALLIGN=200 -THR SCORE=pct -ALIGN=15 -MODE=LOCAL
-OUTFMT=pfs -NORM=ext -MINLEN=0 -MAXLEN=100000 -USER=US08653294
-NCPU=6 -ICPU=3 -NO_XLPXY -WAIT -THREADS=1

Search information block:

Query: US-08-653-294-23

Query length: 10

Database: EST:*

Database sequences: 4538634

Database length: 1887831982

Search time (sec): 7600.090000

score_list:

Sequence	Strd	Orig	zScore	Escore	Len	Documentation
gb_est38:AL036690	+	50.00	190.64	0.0747	171	AL036690 DKFZP564D2463.r1.564
gb_gss8:AO039738	+	44.00	160.21	3.70	380	CIT-HSP-2317E17.TF CIT
gb_gss13:AA040598	-	44.00	159.11	4.26	430	HS_5089.B1.C10.SP6E.RP
gb_est20:AA879637	+	43.00	157.12	5.50	347	AA879637 vs38B05.r1.Stratagene
gb_est16:AA596937	+	43.00	154.70	7.51	456	AA596937 vs41A04.r1.Barstead
gb_est44:AA592217	+	43.00	154.47	12.11	694	AA592217 vs15E03.r1.Barstead
gb_est46:AA208428	+	43.00	150.97	17.33	468	AA208428 uc60C03.x1.NCI.CGAP.Ma
gb_est29:AA155688	+	40.00	148.40	16.83	249	AA155688 UI-R-C2p-ro-d-11-0-UI
gb_est23:AA124815	+	40.00	143.89	30.04	414	AA124815 am5606.x1.Johnston
gb_gss5:AAQ79881	-	40.00	142.63	35.30	477	AAQ79881 HS_2338.B1.A11.MR.CIT
gb_est25:AA1268994	+	40.00	142.14	37.58	504	AA1268994 g367H01.x1.NCI.CGAP.RP
gb_gss15:AA0600634	-	40.00	141.25	42.12	557	AA0600634 HS_5376.B1.C12.T7A.RP
gb_gss8:AA054993	-	40.00	141.03	43.32	571	AA054993 CIT-HSP-2338B21.TR.CIT
gb_est9:AA124047	+	39.00	144.58	27.47	247	AA124047 mq22b11.r1.Barstead
gb_est34:AA178735	+	39.00	142.83	34.41	301	AA178735 u13110.y1.Sugano
gb_est6:AA14823	+	39.00	138.96	56.47	465	AA14823 mb35d10.r1.Soaress mouse
gb_est37:AA1996409	+	39.00	138.59	59.24	485	AA1996409 701667055.A.thaliana
gb_est11:AA269637	+	39.00	137.74	66.11	534	AA269637 vs61C10.r1.Soaress
gb_est36:AA1892890	+	39.00	137.39	69.08	555	AA1892890 mq22b11.y1.Barstead
gb_gss12:AA0349565	+	38.00	134.63	98.48	489	AA0349565 RPI11-108N12.TJB.RP
gb_est17:AA617949	+	37.00	134.18	104.34	332	AA617949 mq22405.s1.NCI.CGAP.Lu
gb_est16:AA26511	+	37.00	131.28	151.28	460	C26511 C26511 Rice callus cDNA
gb_est36:AA1895746	+	37.00	131.26	151.66	461	AA1895746 EST265189 tomato callu
gb_gss13:AA040876	-	37.00	130.52	166.73	501	AA040876 HS_5098.B2.B04.T7A.RP
gb_gss8:AA023777	-	37.00	129.19	197.77	582	AA023777 CGR0157A Cyptosporid
gb_est36:AA1894896	+	37.00	129.09	200.48	589	AA1894896 EST264339 tomato callu
gb_est11:AA23985	+	36.00	132.95	122.13	246	283985 SSZ33985 Porcine small
gb_est35:AA1842495	+	36.00	132.74	125.52	252	AA1842495 UI-M-AM1-afy-h-08-0-UI
gb_est31:AA1708671	+	36.00	132.49	129.50	259	AA1708671 as39B04.x1.Barstead
gb_est21:AA952680	+	36.00	132.16	135.22	269	AA952680 TENS1864.T.cruzi epin
gb_est24:AA1197788	+	36.00	131.31	150.78	296	AA1197788 q149C04.x1.NCI.CGAP.Br
gb_est23:AA1158411	-	36.00	129.97	178.93	344	AA1158411 ud24807.r1.Soaress
gb_est24:AA183475	+	36.00	129.77	183.68	352	AA183475 q654B03.x1.Soaress.feta
gb_est9:AA125323	+	36.00	129.04	201.62	382	AA125323 mp80C08.r1.Soaress
gb_est30:AA1666560	+	36.00	128.79	208.25	393	AA1666560 mu14A08.x1.Soaress
gb_est15:AA502026	+	36.00	128.72	210.06	396	AA502026 nh56G12.s1.NCI.CGAP.P
gb_est19:AA764120	+	36.00	128.70	210.66	397	AA764120 v44509.x1.Soaress
gb_est30:AA1642667	+	36.00	128.68	211.27	398	AA1642667 v501F03.r1.Soaress
gb_gss13:AA044169	-	36.00	128.61	213.08	401	AA044169 GSWC0231 Trypanosoma
gb_gss6:AA0835983	+	36.00	128.52	215.50	405	AA0835983 HS_5350.A1_E03.T7A.RP
gb_gss10:AA0217176	+	36.00	128.48	216.72	407	AA0217176 HS_2139.A2_D07.T7.CIT
gb_est37:AA1957215	+	36.00	128.11	227.06	424	AA1957215 u177a10.x1.Sugano

gb_gss13:AA0431584 - 36.00 127.93 232.56 433 ! AA0431584 HS_5093.A2_C08.SP6E
gb_est25:AA1316043 + 36.00 127.87 234.39 436 ! AA1316043 u161f12.y1.Sugano
gb_est11:AA199357 - 36.00 127.83 235.62 438 ! AA199357 mu14h06.r1.Soaress

seq_name: gb_est38:AL036690

seq_documentation_block:
LOCUS AL036690 171 bp mRNA 27-SEP-1999
DEFINITION DKFZP564D2463.r1.564 (synonym: hfr2) Homo sapiens cDNA clone
DKFZP564D2463.5, mRNA sequence.

ACCESSION AL036690
VERSION AL036690.3 GI:5927859
KEYWORDS EST.
SOURCE human.

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 171)
AUTHORS Duesterhoeft,A., Lauber,J., Mewes,H.W., Gassenhuber,J. and
Wiemann,S.
TITLE EST (Duesterhoeft, et al.)
JOURNAL Unpublished (1999)
COMMENT On Jul 7, 1999 this sequence version replaced gi:5866258.
Contact: Duesterhoeft A

Am Klopferspitz 18a D-82152 Martinsried, Germany

This is the 5' sequence of the clone insert

Clone from S. Wiemann, Molecular Genome Analysis, German Cancer

Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;

sequenced by Qiagen within the cDNA sequencing consortium of the

German Genome Project.

No sl sequence available.

This clone is available at the RZPD in Berlin.

Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059

Berlin-Charlottenburg, GERMANY; Email: cloneerzpd.de.

Location/Qualifiers

source

1. 171

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="DKFZ564D2463"

/clone_1lb="564 (synonym: hfr2)"

/tissue_type="brain"

/dev_stage="fetal"

/lab_host="X1-2blue"

/note="vector: pAMP1; Site_1: NotI; Site_2: SalI"

BASE COUNT 36 a 53 c 60 g 22 t

ORIGIN

alignment_scores:

Quality: 50.00 Length: 10

Ratio: 5.000 Gaps: 0

Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:

US-08-653-294-23 x AL036690 ..

Align seg 1/1 to: AL036690 from: 1 to: 171

1 ArgGluAspLeuArgThrLeuLeuArgTyr 10

|||||

62 CGAGAGGACCTGCGACCTCGCTCGCTAC 91

seq_name: gb_gss8:AO039738

seq_documentation_block:

LOCUS AO039738 380 bp DNA GSS 11-JUL-1998

DEFINITION CIT-HSP-2317E17.TF CIT-HSP Homo sapiens genomic clone 2317E17,

genomic survey sequence.

ACCESSION AO039738

VERSION AO039738.1 GI:3305570

KEYWORDS GSS.

SOURCE human.

ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 380)
 AUTHORS Adams,M.D., Rounsley,S.D., Zhao,S., Field,C.E., Bass,S., Linher,K.,
 Golden,K., Berry,K., Granger,D., Suh,E., Wible,C., Shizuya,H.,
 Simon,M. and Venter,J.C.
 TITLE Use of a random BAC End Sequence Database for Sequence-Ready Map
 Building (1998)
 JOURNAL Unpublished (1998)
 COMMENT Other_GSSs: CIT-HSP-2317EL7.TR
 Contact: Mark Adams
 Department of Eukaryotic Genomics
 The Institute for Genomic Research
 9712 Medical Center Dr., Rockville, MD 20850, USA
 Tel: 301 838 0200
 Fax: 301 838 0208
 Email: mdadams@tigr.org
 Clones are available from Research Genetics (info@resgen.com). BAC
 end search page:
 http://www.tigr.org/cdb/humgen/bac_end_search/bac_end_search.html.
 Seq primer: M13-21
 Class: BAC ends.

FEATURES

Source Location/Qualifiers

1..380
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="2317EL7"
 /clone_lib="CIT-HSP"
 /sex="Male"
 /cell_type="Sperm"
 /note="Vector: pBelobAC11; Site_1: HindIII; Site_2:
 HindIII"

BASE COUNT 126 a 79 c 72 g 103 t

ORIGIN

alignment_scores:

Quality: 44.00 Length: 10
 Ratio: 4.889 Gaps: 0
 Percent Similarity: 90.000 Percent Identity: 90.000

alignment_block:

US-08-653-294-23 x AQ039738 ..

Align seg 1/1 to: AQ039738 from: 1 to: 380

1 ArgGluspleuArgThrLeuLeuArgTyr 10

|||||
 251 AGAAGAATCTCAGAACCCCTTTTCATAC 280

seq_name: gb_gss13:AQ440598

seq_documentation_block:

LOCUS AQ440598 430 bp DNA 31-MAR-1999
 DEFINITION HS_5089_B1_C10.SP66 RPCI-11 Human Male BAC library Homo sapiens
 genomic clone Plate-665 Col-19 Row-F, genomic survey sequence.
 ACCESSION AQ440598
 VERSION AQ440598.1 GI:4551937
 KEYWORDS GSS.
 SOURCE human.
 ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 430)

AUTHORS Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,
 Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and
 Hood,L.

TITLE Sequence-tagged connectors: A sequence approach to mapping and

scanning the human genome

JOURNAL Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999)

MEDLINE 99380589

COMMENT On Feb 19, 1999 this sequence version replaced gi:4146013.

Contact: Mahairas GG, Wallace JC, Hood L
 High Throughput Sequencing Center
 University of Washington
 401 Queen Anne Avenue North, Seattle, WA 98109, USA
 Tel: (206) 616-3618
 Fax: (206) 616-3887
 Email: jwallace@u.washington.edu
 Clones are derived from the human BAC library RPCI-11. For BAC
 library availability, please contact Pieter de Jong
 (pieter@dejong.med.buffalo.edu). Clones may be purchased from
 BACPAC Resources (http://bacpac.med.buffalo.edu/ordering_bac.htm)
 or from Resear h Genetics (info@resgen.com). BAC end Web Server:
 http://www.htsc.washington.edu
 Plate: 665 row: F column: 19
 Seq primer: SP6
 Class: BAC ends
 High quality sequence stop: 430.

FEATURES

Source

Location/Qualifiers
 1..430
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="Plate-665 Col-19 Row-F"
 /clone_lib="RPCI-11 Human Male BAC Library"
 /sex="male"
 /note="Vector: pBACe3.6; Genomic sequence of BAC ends"

BASE COUNT 122 a 81 c 84 g 142 t

ORIGIN

alignment_scores:

Quality: 44.00 Length: 10
 Ratio: 4.889 Gaps: 0
 Percent Similarity: 90.000 Percent Identity: 90.000

alignment_block:

US-08-653-294-23 x AQ440598/rev ..

Align seg 1/1 to reverse of: AQ440598 from: 1 to: 430

1 ArgGluspleuArgThrLeuLeuArgTyr 10

|||||
 177 AGAAGAATCTCAGAACCCCTTTTCATAC 148

seq_name: gb_est20:AA879637

seq_documentation_block:

LOCUS AA879637 347 bp mRNA EST 26-MAR-1998
 DEFINITION vx38b05.r1 Stratagene mouse lung 937302 Mus musculus cDNA clone
 IMAGE:1277457 5' similar to gb:X03945_cds1 HLA CLASS I
 HISTOCOMPATIBILITY ANTIGEN, B-27 ALPHA (HUMAN); gb:M27034 Mouse MHC
 class I D-region cell surface antigen (MOUSE);, mRNA sequence.

ACCESSION AA879637

VERSION AA879637.1 GI:2990342

KEYWORDS

EST.

SOURCE house mouse.

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE

AUTHORS

1 (bases 1 to 347)
 Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
 Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
 Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
 Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
 Waterston,R.

TITLE The WashU-HMI Mouse EST Project

JOURNAL Unpublished (1996)

COMMENT On Jan 9, 1998 this sequence version replaced gi:937414.

Contact: Marra M/Mouse EST Project

WashU-HMI Mouse EST Project

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800

Fax: 314 286 1810

IMAGE Consortium (info@image.llnl.gov) for further information.

MGI:581556

Trace considered overall poor quality

Seq primer: -28mi3 rev2 Et from AmerSham

High quality sequence stop: 1.

FEATURES

source

```
1. .468
/Location/Qualifiers
/organism="Mus musculus"
/strain="C3H"
/db_xref="taxon:10090"
/clone="IMAGE:1049980"
/clone_lib="Barstead mouse myotubes MPLRB5"
/cell_line="C2C12"
/lab_host="DH10B"
/note="Vector: pTT3D-Pac (Pharmacia) with a modified
polylinker; Site_1: EcoRI; Site_2: NotI; 1st strand cDNA
was primed with a Not I - oligo(dT) primer [5'
TGTTCAGTAATCGAAGTGGAGCGCCGCTTTTGTGTGTGTGTGTGTGTGT
3']; double-stranded cDNA was ligated to Eco RI adaptors
[ATTCGGATCCTTG], digested with Not I and cloned into the
Not I and Eco RI sites of the modified pT7T3 vector.
Library constructed by Bob Barstead. The C2C12 cell line
(available from ATCC, catalog # CRL-1772) differentiates
rapidly, forming contractile myotubes and producing
characteristic muscle proteins."
```

```
BASE COUNT      104 a 126 c 169 g 69 t
ORIGIN

alignment_scores:
  Quality: 43.00      Length: 10
  Ratio: 4.778       Gaps: 0
  Percent Similarity: 90.000 Percent Identity: 90.000
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alignment_block:

US-08-653-294-23 x AA592217 ..

Align seg 1/1 to: AA592217 from: 1 to: 468

1 ArgGluspleuargthrleuLeuArgTyr 10

||||| ||||||| ||||||| ||||||| |||||||

133 CGAGTGGACCTGAGGACCTGCTCCGCTAC 162

seq_name: gb_est44:AW208428

```
seq_documentation_block:
LOCUS      AW208428      694 bp      mRNA      EST      03-DEC-1999
DEFINITION u060c03.x1 NCI_CGAP_Mam1 Mus musculus cDNA clone IMAGE:2646916 3'
            similar to gb:M32320 HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-37
            B*3701 ALPHA (HUMAN); gb:M14827 Mouse MHC class I H-2K gene
            (MOUSE); mRNA sequence.
```

ACCESSION AW208428

VERSION AW208428.1 GI:5514422

KEYWORDS EST.

SOURCE house mouse.

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 694)

AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

Tumor Gene Index

JOURNAL Unpublished (1997)

COMMENT On Jun 5, 1998 this sequence version replaced gi:3188321.

Other_ESTs: u060c03.y1

Contact: Robert Strausberg, Ph.D.

Tel: (301) 496-1550

Email: Robert.Strausberg@nih.gov

Tissue procurement: Gilbert Smith, Ph.D.

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html

MGI:1027368

Seq primer: -400P from Gibco

High quality sequence stop: 420.

FEATURES

source

```
1. .694
/Location/Qualifiers
/organism="Mus musculus"
/strain="FVB/N"
/db_xref="taxon:10090"
/clone="IMAGE:2646916"
/clone_lib="NCI_CGAP_Mam1"
/tissue_type="tumor, biopsy sample"
/dev_stage="3 months, virgin"
/lab_host="DH10B"
/note="Organ: mammary; Vector: pCMV-SPORT6; Site_1: SalI;
Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT.
Library constructed by Life Technologies. Investigator
providing samples: Gilbert Smith, NIH"
```

BASE COUNT 148 a 206 c 228 g 111 t 1 others

ORIGIN

```
alignment_scores:
  Quality: 43.00      Length: 10
  Ratio: 4.778       Gaps: 0
  Percent Similarity: 90.000 Percent Identity: 90.000
```

alignment_block:

US-08-653-294-23 x AW208428 ..

Align seg 1/1 to: AW208428 from: 1 to: 694

1 ArgGluspleuargthrleuLeuArgTyr 10

||||| ||||||| ||||||| ||||||| |||||||

231 CGAGTGGACCTGAGGACCTGCTCCGCTAC 260

seq_name: gb_est29:AI556868

seq_documentation_block:

LOCUS AI556868 249 bp mRNA EST 05-JUL-1999

DEFINITION UI-R-C2p-ro-d-11-0-UI-s1 UI-R-C2p Rattus norvegicus cDNA clone

UI-R-C2p-ro-d-11-0-UI 3', mRNA sequence.

ACCESSION AI556868

VERSION AI556868.1 GI:4489231

KEYWORDS EST.

SOURCE Norway rat.

ORGANISM

Rattus norvegicus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;

Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

REFERENCE 1 (bases 1 to 249)

AUTHORS Bonaldo,M.F., Lennon,G. and Soares,M.B.

TITLE Normalization and subtraction: two approaches to facilitate gene

discovery

JOURNAL Genome Res. 6 (9), 791-806 (1996)

COMMENT 9704477

On May 18, 1998 this sequence version replaced gi:3138390.

Contact: Soares, MB

Program for Rat Gene Discovery and Mapping

University of Iowa

451 Eckstein Medical Research Building Iowa City, IA 52242, USA

Tel: 319 335 8250

Fax: 319 335 9565

Email: msoares@blue.weeg.uiowa.edu

The sequence tag present in the cDNA between the NotI site and the
oligo-dT track served to identify it as a clone from the normalized
adult 12-day-embryo library. cDNA Library Preparation: M. Fatima
Bonaldo, Ph.D. Clone distribution: clones will be available through
Research Genetics (www.resgen.com) This clone is also available
through the I.M.A.G.E. Consortium at LLNL (info@image.llnl.gov).

IMAGE ID=1790074

Seq primer: M13 Forward

COMMENT

On Jan 17, 1998 this sequence version replaced gi:1899887.

FEATURES

source
1. 249
Location/Qualifiers
/organism="Rattus norvegicus"
/strain="Sprague-Dawley"
/db_xref="taxon:10116"
/clone="UI-R-C2p-to-d-11-0-UI"
/clone.lib="UI-R-C2p"
/dev_stage="adult"
/lab_host="DH10B (Life Technologies)"
/note="Vector: pT73D-Pac (Pharmacia) with a modified polynker; Site_1: Not I; Site_2: Eco RI; The UI-R-C2p library is a subtracted library derived from the UI-R-C1 library, which is a subtracted library derived from the UI-R-C0 library. The UI-R-C0 library consisted of a mixture of individually tagged normalized libraries constructed from rat placenta, adult lung, brain, liver, kidney, heart, spleen, ovary, muscle, 8, 12 and 18-day embryo. The tag is a string of 3-5 nucleotides present between the Not I site and the oligo-dT track which allows identification of the library of origin of a clone within the mixture. The subtracted library (UI-R-C2p) was constructed as follows: PCR amplified cDNA inserts from UI-R-C1 clones from which 3' ESTs had been derived was used as a driver in a hybridization with the UI-R-C1 library in the form of single-stranded circles. The remaining single-stranded circles (subtracted library) was purified by hydroxyapatite column chromatography, converted to double-stranded circles and electroporated into DH10B bacteria (Life Technologies) to generate the UI-R-C2p library. This procedure has been previously described (Bonaldo, Lennon and Soares, Genome Research 6: 791-806, 1996)."

FEATURES

source
1. 414
Location/Qualifiers
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:1539586"
/clone.lib="Johnston frontal cortex"
/sex="male"
/tissue_type="pooled frontal lobe"
/dev_stage="adult"
/lab_host="SOLR (kanamycin resistant)"
/note="Organ: brain; Vector: Bluescript SK-; Site_1: EcoRI; Stanley Neuropathology Consortium (www.stanleylab.org) brains S-58, S-65, S-67, S-78. Random + oligo-dT primed into EcoRI site of ZAP II Vector. Mass excised. Avg insert length 1.9kb. Custom library provided by Dr. Nancy Johnston [(410) 614-3918, nlj@welchlink.welch.jhu.edu]."

BASE COUNT

80 a 140 c 136 g 58 t

ORIGIN

alignment_scores:
Quality: 40.00 Length: 10
Ratio: 4.444 Gaps: 0
Percent Similarity: 90.000 Percent Identity: 80.000

alignment_block:

US-08-653-294-23 x AI124815 ..
Align seg 1/1 to: AI124815 from: 1 to: 414

1 ArgGluAspLeuArgThrLeuLeuArgTyr 10
|||||:|||||:|||||:|||||:|||||
284 CGAGAGACCTGGCCACCGCTCGCTAC 313

seq_name: gb_gss5:AQ798581

seq_documentation_block:

LOCUS AQ798581 477 bp DNA GSS 09-AUG-1999
DEFINITION HS_2238_B1_A11_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2238 Col=21 Row=B, genomic survey sequence.
ACCESSION AQ798581
VERSION AQ798581.1 GI:5715913
KEYWORDS GSS.
SOURCE human.
ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;

Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 477)

Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,

Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and

Hood,L.

Sequence-tagged connectors: A sequence approach to mapping and

scanning the human genome

Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999)

99380589

Contact: Mahairas GG, Wallace JC, Hood L

High Throughput Sequencing Center

University of Washington

401 Queen Anne Avenue North, Seattle, WA 98109, USA

Tel: (206) 616-3618

Fax: (206) 616-3887

TITLE

JOURNAL

MEDLINE

COMMENT

POLYA-No.

Location/Qualifiers

source

1. 249

/organism="Rattus norvegicus"

/strain="Sprague-Dawley"

/db_xref="taxon:10116"

/clone="UI-R-C2p-to-d-11-0-UI"

/clone.lib="UI-R-C2p"

/dev_stage="adult"

/lab_host="DH10B (Life Technologies)"

/note="Vector: pT73D-Pac (Pharmacia) with a modified polynker; Site_1: Not I; Site_2: Eco RI; The UI-R-C2p library is a subtracted library derived from the UI-R-C1 library, which is a subtracted library derived from the UI-R-C0 library. The UI-R-C0 library consisted of a mixture of individually tagged normalized libraries constructed from rat placenta, adult lung, brain, liver, kidney, heart, spleen, ovary, muscle, 8, 12 and 18-day embryo. The tag is a string of 3-5 nucleotides present between the Not I site and the oligo-dT track which allows identification of the library of origin of a clone within the mixture. The subtracted library (UI-R-C2p) was constructed as follows: PCR amplified cDNA inserts from UI-R-C1 clones from which 3' ESTs had been derived was used as a driver in a hybridization with the UI-R-C1 library in the form of single-stranded circles. The remaining single-stranded circles (subtracted library) was purified by hydroxyapatite column chromatography, converted to double-stranded circles and electroporated into DH10B bacteria (Life Technologies) to generate the UI-R-C2p library. This procedure has been previously described (Bonaldo, Lennon and Soares, Genome Research 6: 791-806, 1996)."

BASE COUNT

67 a 31 c 78 g 73 t

ORIGIN

alignment_scores:
Quality: 40.00 Length: 8
Ratio: 5.000 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:

US-08-653-294-23 x AI556868 ..
Align seg 1/1 to: AI556868 from: 1 to: 249

3 AspLeuArgThrLeuLeuArgTyr 10
|||||:|||||:|||||:|||||:|||||
169 GACCTACGTACTTTATTAAGATAT 192

seq_name: gb_est23:AI124815

seq_documentation_block:

LOCUS AI124815 414 bp mRNA EST 11-SEP-1998
DEFINITION am56e06.xl Johnston frontal cortex Homo sapiens cDNA clone IMAGE:1539586 3', similar to gb:M24038.cdsl HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, BW-44(B-12) B*4402 (HUMAN); contains MER22.t3 TARI repetitive element ;, mRNA sequence.
ACCESSION AI124815
VERSION AI124815.1 GI:3593329
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;

Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 414)

Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S.,

Krizman,D., Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M.,

Martin,J., Moore,B., Schellenberg,K., Steptoe,M., Tan,F.,

Theising,B., White,K., Wylie,T., Waterston,K. and Wilson,R.

WashU-NCI human EST Project

Unpublished (1997)

Unpublished (1997)

Unpublished (1997)

Unpublished (1997)

Unpublished (1997)

Unpublished (1997)

Unpublished (1997)

Unpublished (1997)

Email: jwallace@u.washington.edu
 Clones may be purchased from Research Genetics (info@resgen.com).
 BAC end Web Server: <http://www.htsc.washington.edu>
 Plate: 2238 row: B column: 21
 Seq primer: M13 Reverse
 Class: BAC ends
 High quality sequence stop: 477.

Location/Qualifiers
 1..477

FEATURES
 source
 1..477
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="Plate:2238 Col-21 Row-B"
 /clone_lib="CIT Approved Human Genomic Sperm Library D"
 /sex="male"
 /note="Organ: sperm; Vector: pBelOBAC11; BAC Clones in E-Coli DH10B"

BASE COUNT 131 a 98 c 122 g 122 t 4 others

alignment_scores:
 Quality: 40.00 Length: 10
 Ratio: 4.444 Gaps: 0
 Percent Similarity: 90.000 Percent Identity: 80.000

alignment_block:

US-08-653-294-23 x A0798581/rev ..

Align seg 1/1 to reverse of: A0798581 from: 1 to: 477

1 ArgGluAspLeuArgThrLeuLeuArgTyr 10

|||||

111 AGAGAAGACTTGAGAACCTGCTATCATTC 82

seq_name: gb_est25:A1268994

seq_documentation_block:

LOCUS A1268994 504 bp mRNA EST 28-JAN-1999
 DEFINITION qj67h01.x1 NCI_CGAP_Kid3 Homo sapiens cDNA clone IMAGE:1864561 3', similar to gb:X51804 PUTATIVE RECEPTOR PROTEIN (HUMAN);, mRNA sequence.

ACCESSION A1268994
 VERSION A1268994.1 GI:3888161
 KEYWORDS EST.
 SOURCE human.

ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 504)
 NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
 National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index

JOURNAL Unpublished (1997)
 COMMENT On Jun 2, 1997 this sequence version replaced gi:2285386.
 Contact: Robert Strausberg, Ph.D.

Tel: (301) 496-1550
 Email: Robert.Strausberg@nih.gov
 Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D.
 cDNA Library Preparation: M. Bento Soares, Ph.D.
 cDNA Library Arrayed by: Greg Lennon, Ph.D.
 DNA Sequencing by: Washington University Genome Sequencing Center
 Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html

Insert Length: 594 Std Error: 0.00
 Seq primer: -400P from Gibco
 High quality sequence stop: 289.

Location/Qualifiers
 1..504
 /organism="Homo sapiens"
 /db_xref="taxon:9606"

FEATURES
 source

/clone="IMAGE:1864561"
 /clone_lib="NCI_CGAP_Kid3"
 /lab_host="DH10B"
 /note="Organ: kidney; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(df) primer, double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. mRNA source: 2 pooled kidneys. Library went through one round of normalization. Library constructed by Bento Soares and M. Fatima Bonaldo."

BASE COUNT 116 a 132 c 109 g 145 t 2 others

alignment_scores:
 Quality: 40.00 Length: 10
 Ratio: 4.444 Gaps: 0
 Percent Similarity: 90.000 Percent Identity: 80.000

alignment_block:

US-08-653-294-23 x A1268994/rev ..

Align seg 1/1 to reverse of: A1268994 from: 1 to: 504

1 ArgGluAspLeuArgThrLeuLeuArgTyr 10

|||||

413 AAAGAAGATTACGAACCTATTCCTAT 384

seq_name: gb_gss15:AQ600634

seq_documentation_block:

LOCUS AQ600634 557 bp DNA GSS 10-JUN-1999
 DEFINITION HS-5376_B1_C12_T7A RBC1-11 Human Male BAC Library Homo sapiens genomic clone Plate-952 Col-23 Row-F, genomic survey sequence.

ACCESSION AQ600634
 VERSION AQ600634.1 GI:5060628
 KEYWORDS GSS.
 SOURCE human.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 557)
 Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T., Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and Hood,L.

Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome
 Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999)
 99380589

On Feb 19, 1999 this sequence version replaced gi:4146120.

Contact: Mahairas GG, Wallace JC, Hood L

High Throughput Sequencing Center

University of Washington

401 Queen Anne Avenue North, Seattle, WA 98109, USA

Tel: (206) 616-3618

Fax: (206) 616-3887

Email: jwallace@u.washington.edu

Clones are derived from the human BAC library RBC1-11. For BAC library availability, please contact Pieter de Jong (pieterdejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/ordering_bac.htm) or from Resear h Genetics (<http://inforesgen.com>). BAC end Web Server: <http://www.htsc.washington.edu>

Plate: 952 row: F column: 23

Seq primer: T7

Class: BAC ends

High quality sequence stop: 557.

Location/Qualifiers

1..557

/organism="Homo sapiens"

/db_xref="taxon:9606"

FEATURES
 source

/clone="Plate-952 Col-23 Row-F"
/clone_lib="RPC1-11 Human Male BAC Library"
/sex="male"
/note="vector: pBACE3.6; Genomic sequence of BAC ends"

BASE COUNT 147 a 109 c 108 g 177 t 16 others

ORIGIN

alignment_scores:
Quality: 40.00 Length: 10
Ratio: 4.44 Gaps: 0
Percent Similarity: 90.000 Percent Identity: 80.000

alignment_block:

US-08-653-294-23 x A0600634/rev ..
Align seg 1/1 to reverse of: A0600634 from: 1 to: 557

1 ArgGlusLeuArgThrLeuLeuArgTyr 10
|||||
203 AGAGAGATCTCAGACCTTCTTCATAC 174

seq_name: gb_gss8:AQ054993

seq_documentation_block:
LOCUS AQ054993 571 bp DNA GSS 30-JUL-1998
DEFINITION CIT-HSP-2338B21.TF CIT-HSP Homo sapiens genomic clone 2338B21,
genomic survey sequence.

ACCESSION AQ054993
VERSION AQ054993.1 GI:3351599
KEYWORDS GSS.
SOURCE human.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE 1 (bases 1 to 571)
Adams,M.D., Rounsley,S.D., Zhao,S., Field,C.E., Bass,S., Linher,K.,
Golden,K., Berry,K., Granger,D., Suh,E., Wible,C., Shizuya,H.,
Simon,M. and Venter,J.C.
Use of a random BAC End Sequence Database for Sequence-Ready Map
Building (1998)

JOURNAL Unpublished (1998)

COMMENT Other_GSSs: CIT-HSP-2338B21.TF

Contact: Mark Adams

Department of Eukaryotic Genomics

The Institute for Genomic Research

9712 Medical Center Dr., Rockville, MD 20850, USA

Tel: 301 838 0200

Fax: 301 838 0208

Email: mdadams@tigr.org

Clones are available from Research Genetics (info@resgen.com). BAC

end search page:

http://www.tigr.org/tdb/hungen/bac_end_search/bac_end_search.html.

Seq primer: M13 Reverse

Class: BAC ends.

FEATURES Location/Qualifiers

1..571

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="2338B21"

/clone_lib="CIT-HSP"

/sex="Male"

/cell_type="Sperm"

/note="vector: pBelobAC11; Site_1: HindIII; Site_2:

HindIII"

BASE COUNT 158 a 117 c 146 g 150 t

ORIGIN

alignment_scores:
Quality: 40.00 Length: 10
Ratio: 4.44 Gaps: 0
Percent Similarity: 90.000 Percent Identity: 80.000

alignment_block:

US-08-653-294-23 x A054993/rev ..

Align seg 1/1 to reverse of: A054993 from: 1 to: 571

1 ArgGlusLeuArgThrLeuLeuArgTyr 10
|||||
127 AGAGAGACTTGAGACCTGCTATCATTC 98

seq_name: gb_est9:AA124047

seq_documentation_block:

LOCUS AA124047 247 bp mRNA EST 13-FEB-1997
DEFINITION mq22b11.r1 Barstead_MPLRB1 Mus musculus CDNA clone IMAGE:579453 5'
similar to gb:J05633 INTEGRIN BETA-5 SUBUNIT PRECURSOR (HUMAN);,
mRNA sequence.

ACCESSION AA124047
VERSION AA124047.1 GI:1682606
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 247)

AUTHORS

Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
Waterston,R.

TITLE The WashU-HMI Mouse EST Project

JOURNAL Unpublished (1996)

COMMENT On Apr 14, 1993 this sequence version replaced gi:692643.

Contact: Marra M/Mouse EST Project

WashU-HMI Mouse EST Project

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800

Fax: 314 286 1810

Email: mouseest@watson.wustl.edu

This clone is available royalty-free through LNL; contact the

IMAGE Consortium (info@image.lnl.gov) for further information.

MGI:354101

Seq primer: -28ml3 rev2 ET from Amersham

High quality sequence stop: 147.

FEATURES Location/Qualifiers

1..247

/organism="Mus musculus"

/strain="BALB/c"

/db_xref="taxon:10090"

/clone="IMAGE:579453"

/clone_lib="Barstead MPLRB1"

/sex="mixed"

/tissue_type="Kidney"

/dev_stage="6 weeks"

/lab_host="DH10B"

/note="Vector: pT73D-Pac (Pharmacia) with a modified

polylinker; Site_1: EcoRI; Site_2: NotI; 1st strand CDNA

was primed with a Not I - oligo(dT) primer [5'

TGTTACGAATCTGAAGTCGAGCGCCGCCCTTTTITTTTTTTTTTTTTT

3']; double-stranded CDNA was ligated to Eco RI adaptors

[CATGGATCGTGATCC], digested with Not I and cloned into the

Not I and Eco RI sites of the modified pT73 vector.

Library constructed by Bob Barstead."

BASE COUNT 56 a 59 c 75 g 57 t

ORIGIN

alignment_scores:
Quality: 39.00 Length: 9
Ratio: 4.333 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 88.889

alignment_block:

US-08-653-294-23 x AAL24047

Align seg 1/1 to: AAL24047 from: 1 to: 247

1 ArgGluAspLeuArgThrLeuLeuArg 9

87 CGGGAGGAGTACGGACCTTCTGCGA 113

seq_name: gb_est34:AI787375

seq_documentation_block:

LOCUS AI787375 301 bp mRNA EST 02-JUL-1999

DEFINITION u31b10.y1 Sugano mouse kidney mkia Mus musculus cDNA clone

IMAGE:1921531 5' similar to gb:J05633 INTEGRIN BETA-5 SUBUNIT

PRECURSOR (HUMAN);, mRNA sequence.

ACCESSION AI787375

VERSION AI787375.1 GI:5335091

KEYWORDS EST.

SOURCE house mouse.

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;

Eutheria; Rodentia; Sciurognathi; Muridae; Mus.

REFERENCE

AUTHORS

Maria.M., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T.,

Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y.,

Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R.,

Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R.,

Waterston,R. and Wilson,R.

The WashU-NCI Mouse EST Project 1999

Unpublished (1999)

On May 9 1996 this sequence version replaced gi:1132570.

Other_ESTs: u31b10.x1

Contact: Marra M/WashU-NCI Mouse EST Project 1999

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA

Tel: 314 286 1800

Fax: 314 286 1810

Email: mouseest@watson.wustl.edu

This clone is available royalty-free through LLNL; contact the

IMAGE Consortium (info@image.llnl.gov) for further information.

MGI:977823

Seq primer: custom primer used.

Location/Qualifiers

FEATURES

source

1..301

/organism="Mus musculus"

/strain="C57BL"

/db_xref="taxon:10090"

/clone="IMAGE:1921531"

/clone_lib="Sugano mouse kidney mkia"

/sex="female"

/dev_stage="adult"

/lab_host="DH10B"

/note="Organ: kidney; Vector: pME18S-FL3; Site_1: DraIII

(CACTGTGTG); Site_2: DraIII (CACCATGTG); 1st strand cDNA

was primed with an oligo(dT) primer

[ATGTGGCCTTTTCTTTTCTTTT]; double-stranded cDNA was

ligated to a DraIII adaptor [TGTGGCCTACTGG], digested

and cloned into distinct draIII sites of the pME18S-FL3

vector (5' site CACTGTGTG, 3' site CACCATGTG). XhoI should

be used to isolate the cDNA insert. Size selection was

performed to exclude fragments <1.5kb. Library

constructed by Dr. Sumio Sugano (University of Tokyo

Institute of Medical Science). Custom primers for

sequencing: 5' end primer CTCTGCTCTAAAGCTGCG and 3' end

primer CGACCTGCAGCTCGACACA."

BASE COUNT

ORIGIN

72 a 72 c 98 g

59 t

Length: 9

Quality: 39.00

Ratio: 4.333

Gaps: 0

Percent Similarity: 100.000 Percent Identity: 88.889

alignment_block:

US-08-653-294-23 x AI787375

Align seg 1/1 to: AI787375 from: 1 to: 301

1 ArgGluAspLeuArgThrLeuLeuArg 9

|||||

82 CGGGAGGAGTACGGACCTTCTGCGA 108

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: February 8, 2000, 04:05:42 ; Search time 133.56 Seconds
(without alignments)
1.773 Million cell updates/sec

Title: US-08-653-294-24
Perfect score: 51
Sequence: 1 RESLNLRGY 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 188963 seqs, 23686106 residues

Total number of hits satisfying chosen parameters: 188963

Minimum DB seq length: 0

Maximum DB seq length: 1000000

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database : A_Geneseq_36.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	51	100.0	10	R41209	Peptide fragment o
2	51	100.0	10	R3061	HLA-B7 CTL modul
3	51	100.0	10	W07515	T-cell modulating
4	51	100.0	10	W33786	Peptide B7.75-84 t
5	51	100.0	10	W33796	Peptide B7.75-84 t
6	51	100.0	20	R32913	HLA-B7 CTL modul
7	51	100.0	20	R95415	HLA-B7.84-75-84 Pa
8	51	100.0	20	W33790	Peptide B7.84-75/7
9	51	100.0	20	W33797	Peptide B7.84-75/7
10	51	100.0	25	R41207	Peptide fragment o
11	51	100.0	25	R3073	HLA-Bw62 CTL modul
12	51	100.0	25	R95431	HLA-B7.60-84. Comp
13	51	100.0	25	R95419	HLA-Bw62.60-84. CO
14	51	100.0	362	R12464	HLA-B35 antigen. H
15	44	86.3	25	R41206	Peptide fragment o
16	44	86.3	25	R3072	HLA-Bw46 CTL modul
17	44	86.3	25	R95418	HLA-Bw46.60-84. CO
18	44	86.3	366	R12465	HLA-C exon Cb-1. H
19	44	86.3	366	R12466	HLA-C exon Cb-2. H
20	44	86.3	366	Y07033	Breast cancer asso
21	41	80.4	274	R80911	Consensus sequence
22	37	72.5	10	W07518	T-cell modulating
23	35	68.6	22	R44112	HLA epitope. HIV G
24	35	68.6	45	R17629	HLA-alpha-1. Use o
25	35	68.6	489	R47268	Partial sequence o
26	35	68.6	489	R74305	SABP encoded by PC
27	35	68.6	489	W04316	Tobacco salicylic
28	33	64.7	793	R85199	Avenacinase-like p
29	33	64.7	850	W57445	A. thermophilum th
30	33	64.7	1130	W05178	H-lats large tumou
31	33	64.7	1201	W90345	Drosophila sp. Cos
32	32	62.7	9	R42577	HLA epitope. HIV G
33	32	62.7	425	R11329	Alpha subunit of M
34	32	62.7	624	R77674	Glucosylase from

RESULT 1

R41209
ID R41209 standard; peptide; 10 AA.
AC R41209;
DT 15-MAR-1994 (first entry)
DE Peptide fragment of Class I HLA peptide.
KW Human leukocyte antigen; HLA; peptide; transplantation; neoplasia;
KW Parasitic disease; cytotoxic T lymphocyte; modulation.
OS Synthetic.
PN W09317699-A.
PD 16-SEP-1993.
PF 25-FEB-1993; U01758.
PR 02-MAR-1992; US-844716.
PA (STRD) UNIV LELAND STANFORD JUNIOR.
PI Clayberger CA, Krensky AM;
DR WPI: 93-303134/38.
PT New peptide(s) based on Class I HLA antigen domains - used for
PT modulating cytotoxic T-lymphocyte activity towards targets
PS Claim 11; Page 54; 61pp; English.
CC The peptide is used to modulate cytotoxic T-lymphocyte (CTL)
CC activity, either by inhibition or stimulation. It can be used
CC for inhibiting CTL toxicity in transplantations, for inducing CTL
CC activity in parasitic diseases and neoplasia and in studies on viral
CC infection. The peptide can also be used for identifying CTLs which
CC bind to it and removing subsets of CTLs from a T-cell composition.
CC This peptide sequence is more commonly found within larger peptide
CC compounds of not more than 30 amino acids in length.
SQ Sequence 10 AA:

Query Match 100.0%; Score 51; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. NO. 0.00074;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 RESLNLRGY 10
| | | | | | | | | |
Db 1 RESLNLRGY 10

RESULT 2

R83061
ID R83061 standard; peptide; 10 AA.
AC R83061;
DT 15-MAY-1996 (first entry)
DE HLA-B7 CTL modulating peptide (B7.75-84).
KW Cytotoxic T lymphocyte; CTL; major histocompatibility complex; MHC;
KW Immunosuppressant; graft versus host disorder; transplantation; therapy;
KW Class I MHC; HLA-B7.
OS Synthetic.
PN W09526979-A1.
PD 12-OCT-1995.
PF 05-APR-1995; U04349.
PR 05-APR-1994; US-222851.
PA (STRD) UNIV LELAND STANFORD JUNIOR.
PI Clayberger C, Krensky AM, Farham P;
DR WPI: 95-358582/46.
PT Extension of acceptance period of transplants from MHC unmatched

35 32 62.7 685 1 W31274
36 32 62.7 785 1 R04907
37 32 62.7 854 1 P70347
38 32 62.7 865 1 R20670
39 32 62.7 865 1 R23797
40 32 62.7 868 1 R22615
41 31 60.8 10 R41211
42 31 60.8 10 W07521
43 31 60.8 93 W30133
44 31 60.8 212 R54922
45 31 60.8 286 W54071

ALIGNMENTS

Mouse frizzled-8 p
Type I interferon
Varicella-zoster v
Lipoxigenase. Prod
Rice lipoxigenase.
Varicella-zoster v
Peptide fragment o
T-cell modulating
ZAP-70 N-terminal
Cdi1 polypeptide.
Banana bunchy top

PT donor hosts - using Class I B75-84 MHC antigen of the recipient
 PT host
 PS Claim 13; Page 66; 80pp; English.
 CC This sequence represents a fragment of a class I major histocompatibility
 CC complex (MHC) antigen. This sequence corresponds to residues 75-84 of
 CC the alpha-1 domain of the class I MHC HLA-B7. This sequence, and the
 CC peptide fragments represented by R83062-R83085, R83090-R83096 and
 CC R82907-R82913 can be used to extend the period of acceptance by a
 CC recipient of a transplant from an MHC unmatched donor. The peptides are
 CC administered to a patient in conjunction with a subtherapeutic amount of
 CC an immunosuppressant. This is administered to the patient for a limited
 CC period of time (compared to the lifetime administration for current
 CC treatments). The peptides particularly modulate (or inhibit) the
 CC activity of the cytotoxic T lymphocytes (CTLs) of the patient.
 SQ Sequence 10 AA;

Query Match 100.0%; Score 51; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. NO. 0.00074;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RESLNLRGY 10
 DB 1 RESLNLRGY 10

RESULT 3
 W07515 standard; peptide; 10 AA.

AC W07515;
 DT 04-AUG-1997 (first entry)
 DE T-cell modulator; autoimmune disease; tissue destruction; alpha-domain;
 KW mammal; major histocompatibility complex; MHC class I; antigen; perforin;
 KW insulin-dependent diabetes mellitus; multiple sclerosis; inflammation;
 KW rheumatoid arthritis; psoriasis; pemphigus vulgaris; Sjogren's disease;
 KW thyroid disease; Hashimoto's thyroiditis; myasthenia gravis; granzyme;
 KW autologous target cell; cytokine release; T cell activation; therapy.
 OS Synthetic.
 PN W09635443-A1.
 PD 14-NOV-1996.
 PF 05-APR-1996; U04710.
 PR 12-MAY-1995; US-440504.
 PA (SANG-) SANGSTAT MEDICAL CORP.
 PI Buelow R.
 DR WPI; 96-518410/51.

PT Treatment of auto-immune disease by admin. of peptide(s) corresp. to
 PT major histocompatibility complex antigens - esp. for delaying onset
 PT of clinical symptoms of insulin dependent diabetes by modulating T
 PT cell mediated attack on target cells
 PS Claim 7; Page 20; 24pp; English.
 CC W07512-W07518 represent T-cell modulating peptides that can be used in
 CC the method of the invention. These sequences are based on a portion of
 CC the generic peptide corresponding to residues 70-91 of the alpha-1 domain
 CC of the major histocompatibility complex (MHC) class I antigen (see
 CC W07510). The method is for affecting the course of an autoimmune disease
 CC involving T-cell mediated destruction of tissue in mammals. These
 CC peptides are used especially to treat insulin-dependent diabetes
 CC mellitus, preferably being administered during the pre-clinical stage to
 CC delay onset of the disease. Other diseases that can be treated are
 CC multiple sclerosis, rheumatoid arthritis, psoriasis, pemphigus vulgaris,
 CC Sjogren's disease, thyroid disease, Hashimoto's thyroiditis, myasthenia
 CC gravis, etc. The peptides modulate T-cell mediated attack on autologous
 CC target cells, and may also reduce inflammation, swelling, and release of
 CC cytokines, perforins, granzymes etc. associated with T cell activation.
 SQ Sequence 10 AA;

Query Match 100.0%; Score 51; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. NO. 0.00074;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RESLNLRGY 10

DB 1 RESLNLRGY 10

RESULT 4

W33786 standard; peptide; 10 AA.

AC W33786;
 DT 19-JUN-1998 (first entry)
 DE Peptide B7.75-84 tested for immunomodulating activity.
 KW immunomodulating dimer; immunosuppressant drug; CTL activation;
 KW transplantation; autoimmune disease; Class I HLA-B alpha-1 domain;
 KW rejection.
 OS Synthetic.
 OS Homo sapiens.
 PN W09744351-A1.
 PD 27-NOV-1997.

PF 22-MAY-1997; U08689.
 PR 24-MAY-1996; US-653294.
 PA (STRD) UNIV LELAND STANFORD JUNIOR.
 PI Buelow R. Clayberger C, Krensky AM.

DR WPI; 98-08530/08.

PT New immunomodulating dimer peptide(s) - based on a Class I HLA-B
 PT alpha-1 domain, used for preventing rejection of transplants or
 PT treating autoimmune diseases
 PS Example 1; Page 19; 41pp; English.
 CC Peptides W33784-98 and W33778-9 were assayed for their immunomodulating
 CC activity. A peptide-type compound or variant is claimed which has
 CC immunomodulating activity, including the N-terminal acylated and/or
 CC C-terminal amidated or esterified forms of up to 60 amino acids, where
 CC the peptide-type compound comprises the formula: A-B, where A, B =
 CC (R aa76-77L) (aa79-84) or (aa84-79) (laa77-76R); aa76 - E or V; aa77 =
 CC D, S or N; aa79 = R or G; aa80 = I or N; aa81, aa84 = a hydrophobic or
 CC small amino acid; aa82 = R or L; aa83 = G or R; and aa represents amino
 CC acid. The sequence in the brackets may optionally be absent or truncated
 CC at any peptide type bond within the brackets. The compounds comprise
 CC amino acid sequences related to a Class I HLA-B alpha1 domain (positions
 CC 79-84). They can be used to inhibit cytotoxic T-lymphocytes (CTL) from
 CC undesirably attacking cells in a host or in vitro. They can also be
 CC used in combination with antigenic peptides or proteins of interest to
 CC activate CTLs. They can also inhibit the proliferation of T cells in
 CC response to anti-CD3. The peptide can be used for preventing rejection
 CC of transplants or for treating autoimmune diseases, e.g. diabetes,
 CC rheumatoid arthritis and lupus erythematosus. The products can also be
 CC used for detection and diagnosis.
 SQ Sequence 10 AA;

Query Match 100.0%; Score 51; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. NO. 0.00074;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RESLNLRGY 10
 DB 1 RESLNLRGY 10

RESULT 5

W33796 standard; peptide; 10 AA.

AC W33796;
 DT 19-JUN-1998 (first entry)
 DE Peptide B7.75-84 tested for immunomodulating activity.
 KW immunomodulating dimer; immunosuppressant drug; CTL activation;
 KW transplantation; autoimmune disease; Class I HLA-B alpha-1 domain;
 KW rejection.
 OS Synthetic.

OS Homo sapiens.
 PN W09744351-A1.
 PD 27-NOV-1997.

PF 22-MAY-1997; U08689.

PR 24-MAY-1996; US-653294.
 PA (STRD) UNIV LELAND STANFORD JUNIOR.

PI Beulow R, Clayberger C, Krensky AM;
 DR WPI; 98-086530/08.
 PT New immunomodulating dimer peptide(s) - based on a Class I HLA-B
 PT alpha-1 domain, used for preventing rejection of transplants or
 PT treating autoimmune diseases
 PS Example 1; Page 19; 41pp; English.
 CC Peptides W3784-98 and W3778-9 were assayed for their immunomodulating
 CC activity. A peptide-type compound or variant is claimed which has
 CC immunomodulating activity, including the N-terminal acylated and/or
 CC C-terminal amidated or esterified forms of up to 60 amino acids, where
 CC the peptide-type compound comprises the formula: A-B, where A, B =
 CC (R aa76-77L) (aa79-84) or (aa84-79) (Laa77-76R); aa76 = E or V; aa77 =
 CC D, S or R; aa79 = R or G; aa80 = I or N; aa81, aa84 = a hydrophobic or
 CC small amino acid; aa82 = R or L; aa83 = G or R; and aa represents amino
 CC acid. The sequence in the brackets may optionally be absent or truncated
 CC at any peptide type bond within the brackets. The compounds comprise
 CC amino acid sequences related to a Class I HLA-B alpha1 domain (positions
 CC 79-84). They can be used to inhibit cytotoxic T-lymphocytes (CTL) from
 CC undesirably attacking cells in a host or in vitro. They can also be
 CC used in combination with antigenic peptides or proteins of interest to
 CC activate CTLs. They can also inhibit the proliferation of T cells in
 CC response to anti-CD3. The peptide can be used for preventing rejection
 CC of transplants or for treating autoimmune diseases, e.g. diabetes,
 CC rheumatoid arthritis and lupus erythematosus. The products can also be
 CC used for detection and diagnosis.
 CC Sequence 10 AA;

Query Match 100.0%; Score 51; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.00074;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RESLNRLRGY 10
 |||||
 DB 1 RESLNRLRGY 10

RESULT 6
 ID R92913 standard; peptide; 20 AA.
 AC R92913;
 DT 16-MAY-1996 (first entry)
 DE HLA-B7 CTL modulating peptide (B7.84-75/75-84).
 KW Cytotoxic T lymphocyte; CTL; major histocompatibility complex; MHC;
 KW immunosuppressant; graft versus host disorder; transplantation; therapy;
 KW Class I MHC; HLA-B7.
 OS Synthetic.
 PN W09526979-A1.
 PD 12-OCT-1995.
 PR 05-APR-1995; U04349.
 PA (STRD) UNIV LELAND STANFORD JUNIOR.
 PI Clayberger C, Krensky AM, Farham P;
 DR WPI; 95-358582/46.
 PT Extension of acceptance period of transplants from MHC unmatched
 PT donor hosts - using Class I B75-84 MHC antigen of the recipient
 PT host
 PS Example 15; Page 36; 80pp; English.
 CC R83061-R83085, R83090-R83096 and R92907-R92913 represent fragments of
 CC class I major histocompatibility complex (MHC) antigens. This sequence
 CC is an inverted dimer of residues 75-84 of the alpha-1 domain of the class
 CC I MHC HLA-B7. These sequences can be used to extend the period of
 CC acceptance by a recipient of a transplant from an MHC unmatched donor.
 CC The peptides are administered to a patient in conjunction with a
 CC subtherapeutic amount of an immunosuppressant. This is administered to
 CC the patient for a limited period of time (compared to the lifetime
 CC administration for current treatments). The peptides particularly
 CC modulate (or inhibit) the activity of the cytotoxic T lymphocytes (CTLs)
 CC of the patient.
 CC Sequence 20 AA;

Query Match 100.0%; Score 51; DB 1; Length 20;

Best Local Similarity 100.0%; Pred. No. 0.0015;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 RESLNRLRGY 10
 |||||
 DB 11 RESLNRLRGY 20

RESULT 7
 ID R95415 standard; peptide; 20 AA.
 AC R95415;
 DT 12-NOV-1996 (first entry)
 DE HLA-B7.84-75-84 Palindrome.
 KW HLA; p74; alpha1-helix; human-leucocyte-associated antigen; inhibitor;
 KW T-cell; lysate; membrane protein; mammal; heat shock protein; Hsc70; APC;
 KW B cell; calcium influx; cytotoxic T lymphocyte; CTL; differentiation;
 KW cytolysis; antigen presenting cell.
 OS Synthetic.
 PN W09513288-A1.
 PD 18-MAY-1995.
 PR 10-NOV-1994; U12985.
 PR 10-NOV-1993; US-150493.
 PA (STRD) UNIV LELAND STANFORD JUNIOR.
 PI Clayberger C, Krensky AM;
 DR WPI; 95-194027/25.
 PT Compsns. comprising lymphoid surface membrane proteins - which may
 PT inhibit cytolytic activity and differentiation of CTLs.
 PS Example; Page 18; 29pp; English.
 CC R95413, and R95415-R95431 represent palindromes and fragments of
 CC human-leucocyte-associated antigens. This sequence represents the
 CC HLA-B7.84-75/75-84 palindrome. These sequences can be used to isolate
 CC the protein p74 from a T-cell lysate. p74 is a T-cell surface membrane
 CC protein associated with T-cell activation in mammalian T-cells, and is
 CC also immunologically cross reactive with the heat shock protein Hsc70.
 CC p74 is found in a limited number of cell types, but is particularly
 CC expressed on B and T cells. p74 can be isolated by lysis of a suitable
 CC cell with an amphoteric detergent, and then passed through an affinity
 CC column containing a covalently bound HLA-B2702 palindromic peptide.
 CC Compositions comprising the extracellular fragment of p74 combined with
 CC HLA-B2702.60-84 (see R95416), induces calcium influx, and inhibits
 CC cytotoxic T lymphocyte (CTL) differentiation or cytolysis. Candidate
 CC compounds can be screened for their effect on the cytolytic activity of
 CC T-cells, by combining them with the extracellular portion of p74 and
 CC determining the amount of binding between the candidate compound and p74.
 CC Modulation of CTL activity can be inhibited in a cellular composition
 CC containing T-cells and antigen presenting cells (APCs) by adding to the
 CC mix the extracellular portion of p74, in an amount sufficient to compete
 CC with p74 for the binding of the p74 ligand.
 CC Sequence 20 AA;

Query Match 100.0%; Score 51; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 0.0015;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RESLNRLRGY 10
 |||||
 DB 11 RESLNRLRGY 20

RESULT 8
 ID W33790 standard; peptide; 20 AA.
 AC W33790;
 DT 19-JUN-1998 (first entry)
 DE Peptide B7.84-75/75-84 tested for immunomodulating activity.
 KW Immunomodulating dimer; immunosuppressant drug; CTL activation;
 KW transplplantation; autoimmune disease; Class I HLA-B alpha-1 domain;
 KW rejection.
 OS Synthetic.
 OS Homo sapiens.
 PN W09744351-A1.

PD 27-NOV-1997.
PF 22-MAY-1997; U08689.
PR 24-MAY-1996; US-653294.
PA (STRD) UNIV LELAND STANFORD JUNIOR.
PI Beulow R, Clayberger C, Krensky AM;
DR WPI: 98-086530/08.
PT New immunomodulating dimer peptide(s) - based on a Class I HLA-B
PT alpha-1 domain, used for preventing rejection of transplants or
PT treating autoimmune diseases
PS Example 1; Page 19; 41pp; English.
CC Peptides W33784-98 and W33778-9 were assayed for their immunomodulating
CC activity. A peptide-type compound or variant is claimed which has
CC immunomodulating activity, including the N-terminal acylated and/or
CC C-terminal amidated or esterified forms of up to 60 amino acids, where
CC the peptide-type compound comprises the formula: A-B, where A, B =
CC (R aa76-77L) (aa79-84) or (aa84-79) (Laa77-76R); aa76 = E or V; aa77 =
CC D, S or N; aa79 = R or G; aa80 = I or N; aa81, aa84 = a hydrophobic or
CC small amino acid; aa82 = R or L; aa83 = G or R; and aa represents amino
CC acid. The sequence in the brackets may optionally be absent or truncated
CC at any peptide type bond within the brackets. The compounds comprise
CC amino acid sequences related to a Class I HLA-B alpha1 domain (positions
CC 79-84). They can be used to inhibit cytotoxic T-lymphocytes (CTL) from
CC undesirably attacking cells in a host or in vitro. They can also be
CC used in combination with antigenic peptides or proteins of interest to
CC activate CTLs. They can also inhibit the proliferation of T cells in
CC response to anti-CD3. The peptide can be used for preventing rejection
CC of transplants or for treating autoimmune diseases, e.g. diabetes,
CC rheumatoid arthritis and lupus erythematosus. The products can also be
CC used for detection and diagnosis.
SQ Sequence 20 AA;

Query Match 100.0%; Score 51; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.0015;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RESLNRLGY 10
Db 11 RESLNRLGY 20

RESULT 10
R41207
ID R41207 standard; peptide: 25 AA.
AC R41207;
DT 15-MAR-1994 (first entry)
DE Peptide fragment of Class I HLA peptide.
KW Human leukocyte antigen; HLA; peptide; transplantation; neoplasia;
KW parasitic disease; cytotoxic T lymphocyte; modulation.
OS Synthetic.
PN W09317699-A.
PD 16-SEP-1993.
PF 25-FEB-1993; U01758.
PR 02-MAR-1992; US-844716.
PA (STRD) UNIV LELAND STANFORD JUNIOR.
PI Clayberger CA, Krensky AM;
DR WPI: 93-303134/38.
PT New peptide(s) based on Class I HLA antigen domains - used for
PT modulating cytotoxic T-lymphocyte activity towards targets
PS Claim 10; Page 54; 61pp; English.
CC The peptide (or a fragment of at least 10 amino acids, joined at at
CC least one terminus to a sequence other than that of wild type HLA
CC antigen) is used to modulate cytotoxic T-lymphocyte (CTL) activity,
CC either by inhibition or stimulation. It can be used for
CC inhibiting CTL toxicity in transplantations, for inducing CTL
CC activity in parasitic diseases and neoplasia and in studies on viral
CC infection. The peptide can also be used for identifying CTLs which
CC bind to it and removing subsets of CTLs from a T-cell composition.
SQ Sequence 25 AA;

Query Match 100.0%; Score 51; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.0019;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RESLNRLGY 10
Db 16 RESLNRLGY 25

RESULT 11
R83073
ID R83073 standard; peptide: 25 AA.
AC R83073;
DT 16-MAY-1996 (first entry)
DE HLA-Bw62 CTL modulating peptide (Bw62.60-84).
KW Cytotoxic T lymphocyte; CTL; major histocompatibility complex; MHC;
KW immunosuppressant; graft versus host disorder; transplantation; therapy;
KW class I MHC; HLA-Bw62.
OS Synthetic.
PN W09526979-A1.
PD 12-OCT-1995.
PF 05-APR-1995; U04349.

Query Match 100.0%; Score 51; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.0015;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RESLNRLGY 10
Db 11 RESLNRLGY 20

RESULT 9
W33797
ID W33797 standard; peptide: 20 AA.
AC W33797;
DT 19-JUN-1998 (first entry)
DE Peptide B7:84-75/75-84 tested for immunomodulating activity.
KW Immunomodulating dimer; immunosuppressant drug; CTL activation;
KW transplantation; autoimmune disease; Class I HLA-B alpha-1 domain;
KW rejection.
OS Synthetic.
OS Homo sapiens.
PN W09744351-A1.
PD 27-NOV-1997.
PF 22-MAY-1997; U08689.
PR 24-MAY-1996; US-653294.
PA (STRD) UNIV LELAND STANFORD JUNIOR.
PI Beulow R, Clayberger C, Krensky AM;
DR WPI: 98-086530/08.
PT New immunomodulating dimer peptide(s) - based on a Class I HLA-B
PT alpha-1 domain, used for preventing rejection of transplants or
PT treating autoimmune diseases
PS Example 1; Page 19; 41pp; English.
CC Peptides W33784-98 and W33778-9 were assayed for their immunomodulating
CC activity. A peptide-type compound or variant is claimed which has
CC immunomodulating activity, including the N-terminal acylated and/or
CC C-terminal amidated or esterified forms of up to 60 amino acids, where
CC the peptide-type compound comprises the formula: A-B, where A, B =
CC (R aa76-77L) (aa79-84) or (aa84-79) (Laa77-76R); aa76 = E or V; aa77 =
CC D, S or N; aa79 = R or G; aa80 = I or N; aa81, aa84 = a hydrophobic or
CC small amino acid; aa82 = R or L; aa83 = G or R; and aa represents amino
CC acid. The sequence in the brackets may optionally be absent or truncated
CC at any peptide type bond within the brackets. The compounds comprise

PR 05-APR-1994; US-222851.
 PA (STRD) UNIV LELAND STANFORD JUNIOR.
 PI Clayberger C, Krensky AM, Parham P;
 DI WPI: 95-358582/46.
 PT Extension of acceptance period of transplants from MHC unmatched
 PT donor hosts - using Class I B75-84 MHC antigen of the recipient
 PT host
 PS Example 13; Page 32; 80pp; English.
 CC R83061-R83085, R83090-R83096 and R92907-R92913 represent fragments of
 CC class I major histocompatibility complex (MHC) antigens. This sequence
 CC corresponds to residues 60-84 of the alpha-1 domain of the class I MHC
 CC HLA-B*62. These sequences can be used to extend the period of acceptance
 CC by a recipient of a transplant from an MHC unmatched donor. The peptides
 CC are administered to a patient in conjunction with a subtherapeutic amount
 CC of an immunosuppressant. This is administered to the patient for a
 CC limited period of time (compared to the lifetime administration for
 CC current treatments). The peptides particularly modulate (or inhibit) the
 CC activity of the cytotoxic T lymphocytes (CTLs) of the patient.
 SQ Sequence 25 AA;

Query Match 100.0%; Score 51; DB 1; Length 25;
 Best Local Similarity 100.0%; Pred. No. 0.0019;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RESLRNLRGY 10
 DB 16 RESLRNLRGY 25
 |||||

RESULT 12

ID R95431 standard; peptide; 25 AA.
 AC R95431;
 DT 12-NOV-1996 (first entry)
 DE HLA-B*62:60-84.
 KW HLA; p74; alpha1-helix; human-leucocyte-associated antigen; inhibitor;
 KW T-cell lysate; membrane protein; mammal; heat shock protein; Hsc70; APC;
 KW B cell; calcium influx; cytotoxic T lymphocyte; CTL; differentiation;
 KW cytolysis; antigen presenting cell.
 OS Synthetic.
 PN W09513288-A1.
 PD 18-MAY-1995.
 PF 10-NOV-1994; U12985.
 PR 10-NOV-1993; US-150493.
 PA (STRD) UNIV LELAND STANFORD JUNIOR.
 PI Clayberger C, Krensky AM;
 DI WPI: 95-194027/25.
 DR Compsns. comprising lymphoid surface membrane proteins - which may
 PT inhibit cytolytic activity and differentiation of CTLs.
 PS Example; Page 12; 29pp; English.
 CC R95413, and R95415-R95431 represent palindromes and fragments of
 CC human-leucocyte-associated antigens. This sequence represents the
 CC HLA-B*62:60-84. These sequences can be used to isolate the protein p74
 CC from a T-cell lysate. p74 is a T-cell surface membrane protein
 CC associated with T-cell activation in mammalian T-cells, and is also
 CC immunologically cross reactive with the heat shock protein Hsc70. p74 is
 CC found in a limited number of cell types, but is particularly expressed on
 CC B and T cells. p74 can be isolated by lysis of a suitable cell with an
 CC amphoteric detergent, and then passed through an affinity column
 CC containing a covalently bound HLA-B2702 palindromic peptide.
 CC Compositions comprising the extracellular fragment of p74 combined with
 CC HLA-B2702:60-84 (see R95416), induces calcium influx, and inhibits
 CC cytotoxic T lymphocyte (CTL) differentiation or cytolysis. Candidate
 CC compounds can be screened for their effect on the cytolytic activity of
 CC T-cells, by combining them with the extracellular portion of p74 and
 CC determining the amount of binding between the candidate compound and p74.
 CC Modulation of CTL activity can be inhibited in a cellular composition
 CC containing T-cells and antigen presenting cells (APCs), by adding to the
 CC mix the extracellular portion of p74, in an amount sufficient to compete
 CC with p74 for the binding of the p74 ligand.

SQ Sequence 25 AA;

Query Match 100.0%; Score 51; DB 1; Length 25;
 Best Local Similarity 100.0%; Pred. No. 0.0019;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RESLRNLRGY 10
 DB 16 RESLRNLRGY 25
 |||||

RESULT 13

ID R95419 standard; peptide; 25 AA.
 AC R95419;
 DT 12-NOV-1996 (first entry)
 DE HLA-B*62:60-84.
 KW HLA; p74; alpha1-helix; human-leucocyte-associated antigen; inhibitor;
 KW T-cell lysate; membrane protein; mammal; heat shock protein; Hsc70; APC;
 KW B cell; calcium influx; cytotoxic T lymphocyte; CTL; differentiation;
 KW cytolysis; antigen presenting cell.
 OS Synthetic.
 PN W09513288-A1.
 PD 18-MAY-1995.
 PF 10-NOV-1994; U12985.
 PR 10-NOV-1993; US-150493.
 PA (STRD) UNIV LELAND STANFORD JUNIOR.
 PI Clayberger C, Krensky AM;
 DI WPI: 95-194027/25.
 DR Compsns. comprising lymphoid surface membrane proteins - which may
 PT inhibit cytolytic activity and differentiation of CTLs.
 PS Example; Page 9; 29pp; English.
 CC R95413, and R95415-R95431 represent palindromes and fragments of
 CC human-leucocyte-associated antigens. This sequence represents the
 CC HLA-B*62:60-84. These sequences can be used to isolate the protein p74
 CC from a T-cell lysate. p74 is a T-cell surface membrane protein
 CC associated with T-cell activation in mammalian T-cells, and is also
 CC immunologically cross reactive with the heat shock protein Hsc70. p74 is
 CC found in a limited number of cell types, but is particularly expressed on
 CC B and T cells. p74 can be isolated by lysis of a suitable cell with an
 CC amphoteric detergent, and then passed through an affinity column
 CC containing a covalently bound HLA-B2702 palindromic peptide.
 CC Compositions comprising the extracellular fragment of p74 combined with
 CC HLA-B2702:60-84 (see R95416), induces calcium influx, and inhibits
 CC cytotoxic T lymphocyte (CTL) differentiation or cytolysis. Candidate
 CC compounds can be screened for their effect on the cytolytic activity of
 CC T-cells, by combining them with the extracellular portion of p74 and
 CC determining the amount of binding between the candidate compound and p74.
 CC Modulation of CTL activity can be inhibited in a cellular composition
 CC containing T-cells and antigen presenting cells (APCs), by adding to the
 CC mix the extracellular portion of p74, in an amount sufficient to compete
 CC with p74 for the binding of the p74 ligand.

SQ Sequence 25 AA;

Query Match 100.0%; Score 51; DB 1; Length 25;
 Best Local Similarity 100.0%; Pred. No. 0.0019;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RESLRNLRGY 10
 DB 16 RESLRNLRGY 25
 |||||

RESULT 14

ID R12464 standard; Protein; 362 AA.
 AC R12464;
 DT 29-AUG-1991 (first entry)
 DE HLA-B*35 antigen.
 KW Human leukocyte antigen; probe; major histocompatibility complex;
 KW MHC; class I.
 OS Homo sapiens.
 PN J03112486-A.

PD 14-MAY-1991.
 PF 22-SEP-1989; 247697.
 PR 22-SEP-1989; JP-247697.
 PA (OLYU) OLYMPUS OPTICAL KK.
 DR WPI; 91-182991/25.
 DR N-PSDB; Q12115.
 PT HLA-B35 gene - used in DNA probe and transformant cells for
 PT immunising animals, for developing monoclonal antibody.
 PS Claim 1; Page 1; 11pp; Japanese.
 CC Probes comprising part of the sequence encoding this sequence can
 CC be used to identify Class I genes. The DNA can be expressed for
 CC immunisation of animals and prodn. of monoclonal antibodies
 CC specific for the HLA-B35 antigen. See also J03112485 and J03112487.
 SQ Sequence 362 AA;

Query Match 100.0%; Score 51; DB 1; Length 362;
 Best Local Similarity 100.0%; Pred. No. 0.031;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RESLNLRGY 10
 | | | | | | | | | |
 Db 99 RESLNLRGY 108

RESULT 15
 R41206
 ID R41206 standard; peptide; 25 AA.
 AC R41206;
 DT 15-MAR-1994 (first entry)
 DE Peptide fragment of Class I HLA peptide.
 KW Human leukocyte antigen; HLA; peptide; transplantation; neoplasia;
 KW parasitic disease; cytotoxic T lymphocyte; modulation.
 OS Synthetic.
 PN W09317699-A.
 PD 16-SEP-1993.
 PF 25-FEB-1993; U01758.
 PR 02-MAR-1992; US-844716.
 PA (STRD) UNIV LELAND STANFORD JUNIOR.
 PI Clayberger CA, Krensky AM;
 DR WPI; 93-303134/38.
 PT New peptide(s) based on Class I HLA antigen domains - used for
 PT modulating cytotoxic T-lymphocyte activity towards targets
 PS Claim 9; Page 53; 61pp; English.
 CC The peptide (or a fragment of at least 10 amino acids, joined at at
 CC least one terminus to a sequence other than that of wild type HLA
 CC antigen) is used to modulate cytotoxic T-lymphocyte (CTL) activity,
 CC either by inhibition or stimulation. It can be used for
 CC inhibiting CTL toxicity in transplantations, for inducing CTL
 CC activity in parasitic diseases and neoplasia and in studies on viral
 CC infection. The peptide can also be used for identifying CTLs which
 CC bind to it and removing subsets of CTLs from a T-cell composition.
 SQ Sequence 25 AA;

Query Match 86.3%; Score 44; DB 1; Length 25;
 Best Local Similarity 90.0%; Pred. No. 0.04;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RESLNLRGY 10
 | | | | | | | | | |
 Db 16 RVSLNLRGY 25

Search completed: February 8, 2000, 04:05:42
 Job time: 9359 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: February 7, 2000, 18:04:37 ; Search time 111.22 Seconds
(without alignments)
4.241 Million cell updates/sec

Title: US-08-653-294-24

Perfect score: 51

Sequence: 1 RESLNRLRGY 10

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 142080 seqs, 47169319 residues

Total number of hits satisfying chosen parameters: 142080

Minimum DB seq length: 0

Maximum DB seq length: 1000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : PIR_62:**

1: pir1:**

2: pir2:**

3: pir3:**

4: pir4:**

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	51	100.0	137	2	I38875 MHC class I antige
2	51	100.0	137	2	I38876 MHC class I antige
3	51	100.0	137	2	I38860 MHC class I antige
4	51	100.0	137	2	I38874 MHC class I antige
5	51	100.0	181	2	I59188 MHC cell surface g
6	51	100.0	270	1	HLHU40 MHC class I histoc
7	51	100.0	274	2	I68774 MHC HLA-B*39 chain
8	51	100.0	274	2	S24439 class I histocompa
9	51	100.0	300	2	I68701 cell surface antig
10	51	100.0	308	2	I36956 MHC ChIA chain - c
11	51	100.0	350	2	I68747 MHC class I lympho
12	51	100.0	350	2	I54308 MHC HLA B71 - huma
13	51	100.0	354	2	S24436 class I histocompa
14	51	100.0	354	2	S24437 class I histocompa
15	51	100.0	354	2	S24438 class I histocompa
16	51	100.0	354	2	S24440 class I histocompa
17	51	100.0	354	2	S24433 class I histocompa
18	51	100.0	358	2	S03538 class I histocompa
19	51	100.0	361	2	I54418 MHC class I histoc
20	51	100.0	362	1	HLHUB7 MHC class I histoc
21	51	100.0	362	1	S77966 MHC class I histoc
22	51	100.0	362	2	G01230 MHC class I histoc
23	51	100.0	362	2	S16789 class I histocompa
24	51	100.0	362	2	A45880 MHC class I histoc
25	51	100.0	362	2	I37519 MHC class I histoc
26	51	100.0	362	2	I37520 MHC class I histoc
27	51	100.0	362	2	I37522 MHC class I histoc
28	51	100.0	362	2	I84431 MHC HLA-B*5602 - human
29	51	100.0	362	2	I72755 HLA-B*5602 - human
30	51	100.0	362	2	I84488 lymphocyte antigen

ALIGNMENTS

RESULT 1

I38875

MHC class I antigen - human (fragment)

C:Species: Homo sapiens (man)

C:Date: 07-Jun-1996 #sequence_revision 07-Jun-1996 #text_change 23-Jul-1999

C:Accession: I38875

R:Garber, T.L.; Butler, L.M.; Trachtenberg, E.A.; Erlich, H.A.; Rickards, O.; De Stef

Immunogenetics 42, 19-27, 1995

A:Title: HLA-B alleles of the Cayapa of Ecuador: new B39 and B15 alleles.

A:Reference number: I38860; MUID:95317819

A:Accession: I38875

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-137 <RES>

A:Cross-references: EMBL:U15639; NID:9930332; PIDN:AAA74046.1; PID:9930333

C:Superfamily: class I histocompatibility antigen; immunoglobulin homology

Query Match 100.0%; Score 51; DB 2; Length 137;

Best Local Similarity 100.0%; Pred. No. 0.0045;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RESLNRLRGY 10

Db 40 RESLNRLRGY 49

RESULT 2

I38876

MHC class I antigen - human (fragment)

C:Species: Homo sapiens (man)

C:Date: 07-Jun-1996 #sequence_revision 07-Jun-1996 #text_change 23-Jul-1999

C:Accession: I38876

R:Garber, T.L.; Butler, L.M.; Trachtenberg, E.A.; Erlich, H.A.; Rickards, O.; De Stef

Immunogenetics 42, 19-27, 1995

A:Title: HLA-B alleles of the Cayapa of Ecuador: new B39 and B15 alleles.

A:Reference number: I38860; MUID:95317819

A:Accession: I38876

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-137 <RES>

A:Cross-references: EMBL:U15640; NID:9930334; PIDN:AAA74047.1; PID:9930335

C:Superfamily: class I histocompatibility antigen; immunoglobulin homology

Query Match 100.0%; Score 51; DB 2; Length 137;

Best Local Similarity 100.0%; Pred. No. 0.0045;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RESLNRLRGY 10

Db 40 RESLNRLRGY 49

HLA-B*5501 - human
HLA-B*5502 - human
HLA-B*5601 - human
MHC class I histoc
HLA-B alpha-chain
lymphocyte antigen
HLA-B*5401 - human
MHC class I protei
HLA-B*35 variant -
lymphocyte antigen
lymphocyte antigen
lymphocyte antigen
MHC HLA-B*42, HLA-
MHC HLA-B14 chain
MHC HLA-B18 chain

31 51 100.0 362 2 I72752
32 51 100.0 362 2 I72753
33 51 100.0 362 2 I72754
34 51 100.0 362 2 I38437
35 51 100.0 362 2 I37492
36 51 100.0 362 2 I54505
37 51 100.0 362 2 I56130
38 51 100.0 362 2 I36962
39 51 100.0 362 2 I37475
40 51 100.0 362 2 I56149
41 51 100.0 362 2 I59655
42 51 100.0 362 2 I59651
43 51 100.0 362 2 I61865
44 51 100.0 362 2 I61859
45 51 100.0 362 2 I61860

```

RESULT 3
I38860
MHC class I antigen - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 07-Jun-1996 #sequence_revision 07-Jun-1996 #text_change 23-Jul-1999
C:Accession: I38860
R:Garber, T.L.; Butler, L.M.; Trachtenberg, E.A.; Erlich, H.A.; Rickards, O.; De Stefani
Immunogenetics 42, 19-27, 1995
A:Title: HLA-B alleles of the Cayapa of Ecuador: new B39 and B15 alleles.
A:Reference number: I38860; MUID:95317819
A:Accession: I38860
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-137 <RES>
A:Cross-references: EMBL:U14756; NID:g930328; PIDN:AA50171.1; PID:g930329
C:Superfamily: class I histocompatibility antigen; immunoglobulin homology

Query Match 100.0%; Score 51; DB 2; Length 137;
Best Local Similarity 100.0%; Pred. No. 0.0045;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RESLNRLRGY 10
|||||
Db 40 RESLNRLRGY 49

RESULT 4
I38874
MHC class I antigen - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 07-Jun-1996 #sequence_revision 07-Jun-1996 #text_change 23-Jul-1999
C:Accession: I38874
R:Garber, T.L.; Butler, L.M.; Trachtenberg, E.A.; Erlich, H.A.; Rickards, O.; De Stefani
Immunogenetics 42, 19-27, 1995
A:Title: HLA-B alleles of the Cayapa of Ecuador: new B39 and B15 alleles.
A:Reference number: I38860; MUID:95317819
A:Accession: I38874
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-137 <RES>
A:Cross-references: EMBL:U15638; NID:g930330; PIDN:AAA74045.1; PID:g930331
C:Superfamily: class I histocompatibility antigen; immunoglobulin homology

Query Match 100.0%; Score 51; DB 2; Length 137;
Best Local Similarity 100.0%; Pred. No. 0.0045;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RESLNRLRGY 10
|||||
Db 40 RESLNRLRGY 49

RESULT 5
I59188
MHC cell surface glycoprotein - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 23-Jul-1999
C:Accession: I59188
R:Bronson, S.K.; Pei, J.; Taillon-Miller, P.; Chorney, M.J.; Geraghty, D.E.; Chaplin, D.
Proc. Natl. Acad. Sci. U.S.A. 88, 1676-1680, 1991
A:Title: Isolation and characterization of yeast artificial chromosome clones linking th
A:Reference number: I59188; MUID:91156671
A:Accession: I59188
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-181 <RES>
A:Cross-references: GB:M59841; NID:g187697; PIDN:AAA59623.1; PID:g187698
C:Genetics:
A:Gene: GDB:HLA-B
A:Cross-references: GDB:120048; OMIM:142830

Query Match 100.0%; Score 51; DB 2; Length 270;
Best Local Similarity 100.0%; Pred. No. 0.0093;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RESLNRLRGY 10
|||||
Db 75 RESLNRLRGY 84

RESULT 7
I68774
MHC HLA-B39 chain - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 07-Jun-1996 #sequence_revision 07-Jun-1996 #text_change 23-Jul-1999
C:Accession: I68774
R:Mueller, C.A.; Engler-Blum, G.; Gekeler, V.; Steiert, I.; Weiss, E.; Schmidt, H.
Immunogenetics 30, 200-207, 1989
A:Title: Genetic and serological heterogeneity of the supertypic HLA-B locus specific
A:Reference number: I54463; MUID:89379286
A:Accession: I68774
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-274 <RES>
A:Cross-references: GB:M29865; NID:g187676; PIDN:AAA36223.1; PID:g187677
C:Superfamily: class I histocompatibility antigen; immunoglobulin homology

Query Match 100.0%; Score 51; DB 2; Length 274;
Best Local Similarity 100.0%; Pred. No. 0.0095;

```

```

A:Map position: 6p21.3-6p21.3
A:Introns: 90/1
C:Superfamily: class I histocompatibility antigen; immunoglobulin homology
C:Keywords: glycoprotein

Query Match 100.0%; Score 51; DB 2; Length 181;
Best Local Similarity 100.0%; Pred. No. 0.0061;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RESLNRLRGY 10
|||||
Db 74 RESLNRLRGY 83

RESULT 6
HLH40
MHC class I histocompatibility antigen HLA-B40 alpha chain - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 28-Aug-1985 #sequence_revision 28-Aug-1985 #text_change 02-Sep-1997
C:Accession: A02186
R:Lopez de Castro, J.A.; Bragado, R.; Strong, D.M.; Strominger, J.L.
Biochemistry 22, 3961-3969, 1983
A:Title: Primary structure of papain-solubilized human histocompatibility antigen HLA
A:Reference number: A02186; MUID:84000412
A:Accession: A02186
A:Molecule type: protein
A:Residues: 1-270 <LOP>
C:Comment: Comparison of a number of class I allelic sequences (-B40 vs. -B7 and -A2
y restricted to the alpha-1 and alpha-2 domains. The most conspicuous clustering of v
ossible alloantigenic determinants of these antigens.
C:Genetics:
A:Gene: GDB:HLA-B
A:Cross-references: GDB:120048; OMIM:142830
C:Superfamily: class I histocompatibility antigen; immunoglobulin homology
F:1-90/Domain: duplication; glycoprotein; heterodimer; membrane protein; transplantation
F:91-181/Domain: alpha-1 <EX1>
F:91-181/Domain: alpha-2 <EX2>
F:195-260/Domain: immunoglobulin homology <IMV>
F:86/Binding site: carbohydrate (Asn) (covalent) #status experimental
F:101-163,202-258/disulfide bonds: #status predicted

```

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RESLRNLRGY 10

Db 75 RESLRNLRGY 84

RESULT 8

S24439

Class I histocompatibility antigen HLA-B-3901 - human (fragment)

C:Species: Homo sapiens (man)

C>Date: 22-Nov-1993 #sequence_revision 01-Nov-1996 #text_change 07-Nov-1997

C:Accession: S24439

R:Watkins, D.I.; McAdam, S.N.; Liu, X.; Strang, C.R.; Milford, E.L.; Levine, C.G.; Garbe Nature 357, 329-333, 1992

A:Title: New recombinant HLA-B alleles in a tribe of South American Amerindians indicate

A:Reference number: S24027; MUID:92269956

A:Accession: S24439

A:Molecule type: mRNA

A:Residues: 1-274 <WAT>

C:Genetics:

A:Gene: HLA-B-3901

C:Superfamily: class I histocompatibility antigen; immunoglobulin homology

C:Keywords: glycoprotein

F:1-274/Product: class I histocompatibility antigen HLA-B-3901 #status predicted <WAT>

F:1-90/Domain: alpha-1 #status predicted <EX1>

F:91-182/Domain: alpha-2 #status predicted <EX2>

F:196-261/Domain: immunoglobulin homology <IMM>

F:86/Binding site: carbohydrate (Asn) (covalent) #status predicted

F:101-164,203-259/Disulfide bonds: #status predicted

Query Match

Best Local Similarity 100.0%; Score 51; DB 2; Length 274;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RESLRNLRGY 10

Db 75 RESLRNLRGY 84

RESULT 9

I68701

cell surface antigen - human (fragment)

C:Species: Homo sapiens (man)

C>Date: 07-Jun-1996 #sequence_revision 07-Jun-1996 #text_change 23-Jul-1999

C:Accession: I68701

R:Arnot, D.; Lillie, J.W.; Auffray, C.; Kappes, D.; Strominger, J.L.

Immunogenetics 20, 237-252, 1984

A:Title: Inter-locus and intra-allelic polymorphisms of HLA class I antigen gene mRNA.

A:Reference number: I54412; MUID:84287690

A:Accession: I68701

A:Status: preliminary; translated from GB/EMBL/DBDJ

A:Molecule type: mRNA

A:Residues: 1-300 <RES>

A:Cross-references: GB:M27540; NID:g187733; PIDN:AAA59638.1; PID:g386890

C:Superfamily: class I histocompatibility antigen; immunoglobulin homology

C:Keywords: surface antigen

Query Match

Best Local Similarity 100.0%; Score 51; DB 2; Length 300;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RESLRNLRGY 10

Db 37 RESLRNLRGY 46

RESULT 10

I36956

MHC class II chain - chimpanzee (fragment)

C:Species: Pan troglodytes (chimpanzee)

C>Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 23-Jul-1999

C:Accession: I36956

R:Parham, P.; Lawlor, D.A.; Lomen, C.E.; Ennis, P.D.

J. Immunol. 142, 3937-3950, 1989

A:Title: Diversity and diversification of HLA-A,B,C alleles.

A:Reference number: I36956; MUID:89235215

A:Accession: I36956

A:Status: preliminary; translated from GB/EMBL/DBDJ

A:Molecule type: mRNA

A:Residues: 1-308 <RES>

A:Cross-references: GB:M24044; NID:g176812; PIDN:AAA53423.1; PID:g176813

C:Superfamily: class I histocompatibility antigen; immunoglobulin homology

Query Match

Best Local Similarity 100.0%; Score 51; DB 2; Length 308;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RESLRNLRGY 10

Db 45 RESLRNLRGY 54

RESULT 11

I68747

MHC class I lymphocyte antigen - human (fragment)

C:Species: Homo sapiens (man)

C>Date: 07-Jun-1996 #sequence_revision 07-Jun-1996 #text_change 23-Jul-1999

C:Accession: I68747

R:Pohla, H.; Kuon, W.; Tabaczewski, P.; Doerner, C.; Weiss, E.H.

Immunogenetics 29, 297-307, 1989

A:Title: Allelic variation in HLA-B and HLA-C sequences and the evolution of the HLA-

A:Reference number: I54457; MUID:89233295

A:Accession: I68747

A:Status: preliminary; translated from GB/EMBL/DBDJ

A:Molecule type: mRNA

A:Residues: 1-350 <RES>

A:Cross-references: GB:M28204; NID:g576472; PIDN:AAA53257.1; PID:g576473

C:Superfamily: class I histocompatibility antigen; immunoglobulin homology

Query Match

Best Local Similarity 100.0%; Score 51; DB 2; Length 350;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RESLRNLRGY 10

Db 87 RESLRNLRGY 96

RESULT 12

I54308

MHC HLA B71 - human (fragment)

C:Species: Homo sapiens (man)

C>Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 23-Jul-1999

C:Accession: I54308

R:Rodriguez, S.G.; Johnson, A.H.; Hurley, C.K.

Hum. Immunol. 37, 192-194, 1993

A:Title: Molecular characterization of HLA-B71 from an African American individual.

A:Reference number: I54308; MUID:94064392

A:Accession: I54308

A:Status: preliminary; translated from GB/EMBL/DBDJ

A:Molecule type: mRNA

A:Residues: 1-350 <RES>

A:Cross-references: GB:L07950; NID:g307236; PIDN:AAA59683.1; PID:g307237

C:Genetics:

A:Gene: GDB:HLA-B

A:Cross-references: GDB:L20048; OMIM:142830

A:Map position: 6p21.3-6p21.3

C:Superfamily: class I histocompatibility antigen; immunoglobulin homology

Query Match

Best Local Similarity 100.0%; Score 51; DB 2; Length 350;

Best Local Similarity 100.0%; Pred. No. 0.012;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RESLRNLRGY 10
|||||
DB 99 RESLRNLRGY 108

RESULT 13
S24436
class I histocompatibility antigen HLA-B-3504 precursor - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 22-Nov-1993 #sequence_revision 18-Jul-1997 #text_change 07-Nov-1997
C:Accession: S24436
R:Watkins, D.I.; McAdam, S.N.; Liu, X.; Strang, C.R.; Milford, E.L.; Levine, C.G.; Garber
Nature 357, 329-333, 1992
A:Title: New recombinant HLA-B alleles in a tribe of South American Amerindians indicate
A:Reference number: S24027; MUID:92269956
A:Accession: S24436
A:Molecule type: mRNA
A:Residues: 1-354 <WAT>
C:Genetics:
A:Gene: HLA-B-3504
C:Superfamily: class I histocompatibility antigen; immunoglobulin homology
C:Keywords: glycoprotein; transmembrane protein
F:1-17/Domain: signal sequence #status predicted <SIG>
F:17-354/Product: class I histocompatibility antigen HLA-B-3504 #status predicted <WAT>
F:17-299/Domain: extracellular #status predicted <EXT>
F:107-198/Domain: alpha-2 #status predicted <EX2>
F:212-277/Domain: immunoglobulin homology <IMM>
F:300-323/Domain: transmembrane #status predicted <TMN>
F:324-354/Domain: intracellular #status predicted <INT>
F:102/Binding site: carbohydrate (Asn) (covalent) #status predicted
F:117-180,219-275/Disulfide bonds: #status predicted

Query Match 100.0%; Score 51; DB 2; Length 354;
Best Local Similarity 100.0%; Pred. No. 0.012;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RESLRNLRGY 10
|||||
DB 91 RESLRNLRGY 100

RESULT 14
S24437
class I histocompatibility antigen HLA-B-4802 precursor - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 22-Nov-1993 #sequence_revision 18-Jul-1997 #text_change 07-Nov-1997
C:Accession: S24437
R:Watkins, D.I.; McAdam, S.N.; Liu, X.; Strang, C.R.; Milford, E.L.; Levine, C.G.; Garber
Nature 357, 329-333, 1992
A:Title: New recombinant HLA-B alleles in a tribe of South American Amerindians indicate
A:Reference number: S24027; MUID:92269956
A:Accession: S24437
A:Molecule type: mRNA
A:Residues: 1-354 <WAT>
C:Genetics:
A:Gene: HLA-B-4802
C:Superfamily: class I histocompatibility antigen; immunoglobulin homology
C:Keywords: glycoprotein; transmembrane protein
F:1-17/Domain: signal sequence #status predicted <SIG>
F:17-354/Product: class I histocompatibility antigen HLA-B-4802 #status predicted <WAT>
F:17-299/Domain: extracellular #status predicted <EXT>
F:107-198/Domain: alpha-2 #status predicted <EX2>
F:212-277/Domain: immunoglobulin homology <IMM>
F:300-323/Domain: transmembrane #status predicted <TMN>
F:324-354/Domain: intracellular #status predicted <INT>
F:102/Binding site: carbohydrate (Asn) (covalent) #status predicted
F:117-180,219-275/Disulfide bonds: #status predicted

Query Match 100.0%; Score 51; DB 2; Length 354;
Best Local Similarity 100.0%; Pred. No. 0.012;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RESLRNLRGY 10
|||||
DB 91 RESLRNLRGY 100

RESULT 15
S24438
class I histocompatibility antigen HLA-B-4801 precursor - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 22-Nov-1993 #sequence_revision 18-Jul-1997 #text_change 07-Nov-1997
C:Accession: S24438
R:Watkins, D.I.; McAdam, S.N.; Liu, X.; Strang, C.R.; Milford, E.L.; Levine, C.G.; Ga
Nature 357, 329-333, 1992
A:Title: New recombinant HLA-B alleles in a tribe of South American Amerindians indic
A:Reference number: S24027; MUID:92269956
A:Accession: S24438
A:Molecule type: mRNA
A:Residues: 1-354 <WAT>
C:Genetics:
A:Gene: HLA-B-4801
C:Superfamily: class I histocompatibility antigen; immunoglobulin homology
C:Keywords: glycoprotein; transmembrane protein
F:1-17/Domain: signal sequence #status predicted <SIG>
F:17-354/Product: class I histocompatibility antigen HLA-B-4801 #status predicted <WA
F:17-299/Domain: extracellular #status predicted <EXT>
F:107-198/Domain: alpha-2 #status predicted <EX2>
F:212-277/Domain: immunoglobulin homology <IMM>
F:300-323/Domain: transmembrane #status predicted <TMN>
F:324-354/Domain: intracellular #status predicted <INT>
F:102/Binding site: carbohydrate (Asn) (covalent) #status predicted
F:117-180,219-275/Disulfide bonds: #status predicted

Query Match 100.0%; Score 51; DB 2; Length 354;
Best Local Similarity 100.0%; Pred. No. 0.012;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RESLRNLRGY 10
|||||
DB 91 RESLRNLRGY 100

Search completed: February 7, 2000, 18:04:37
Job time: 22:03 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: February 8, 2000, 01:25:57 ; Search time 68.63 seconds
(without alignments)
4.352 Million cell updates/sec

Title: US-08-653-294-24
Perfect score: 51
Sequence: 1 RESLNRLRGY 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 82229 seqs, 29864866 residues

Total number of hits satisfying chosen parameters: 82229

Minimum DB seq length: 0

Maximum DB seq length: 1000000

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database : SwissProt_38.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	51	100.0	270	1	P01890 homo sapien
2	51	100.0	354	1	P30470 homo sapien
3	51	100.0	362	1	P16210 pan troglod
4	51	100.0	362	1	P01889 homo sapien
5	51	100.0	362	1	P13751 pan troglod
6	51	100.0	362	1	P30460 homo sapien
7	51	100.0	362	1	P30462 homo sapien
8	51	100.0	362	1	P30463 homo sapien
9	51	100.0	362	1	P30464 homo sapien
10	51	100.0	362	1	P30465 homo sapien
11	51	100.0	362	1	P30513 homo sapien
12	51	100.0	362	1	P30466 homo sapien
13	51	100.0	362	1	P30685 homo sapien
14	51	100.0	362	1	P30468 homo sapien
15	51	100.0	362	1	P30469 homo sapien
16	51	100.0	362	1	P30471 homo sapien
17	51	100.0	362	1	P30472 homo sapien
18	51	100.0	362	1	P30473 homo sapien
19	51	100.0	362	1	P30474 homo sapien
20	51	100.0	362	1	P30475 homo sapien
21	51	100.0	362	1	P30476 homo sapien
22	51	100.0	362	1	Q04826 homo sapien
23	51	100.0	362	1	P30477 homo sapien
24	51	100.0	362	1	P30478 homo sapien
25	51	100.0	362	1	P30479 homo sapien
26	51	100.0	362	1	P30480 homo sapien
27	51	100.0	362	1	P30483 homo sapien
28	51	100.0	362	1	P30486 homo sapien
29	51	100.0	362	1	P30488 homo sapien
30	51	100.0	362	1	P30492 homo sapien
31	51	100.0	362	1	P30493 homo sapien
32	51	100.0	362	1	P30494 homo sapien
33	51	100.0	362	1	P30495 homo sapien
34	51	100.0	362	1	P30496 homo sapien

35	51	100.0	362	1	1B63_HUMAN	P30498 homo sapien
36	44	86.3	342	1	1CXX_HUMAN	P10321 homo sapien
37	44	86.3	362	1	1B44_HUMAN	P30484 homo sapien
38	44	86.3	366	1	1C01_HUMAN	P30499 homo sapien
39	44	86.3	366	1	1C01_PANTR	P30686 pan troglod
40	44	86.3	366	1	1C02_HUMAN	P30500 homo sapien
41	44	86.3	366	1	1C05_HUMAN	P04222 homo sapien
42	44	86.3	366	1	1C06_HUMAN	P30503 homo sapien
43	44	86.3	366	1	1C11_HUMAN	Q28631 homo sapien
44	44	86.3	366	1	1C12_HUMAN	P30505 homo sapien
45	44	86.3	366	1	1C13_HUMAN	P30506 homo sapien

ALIGNMENTS

RESULT 1
ID 1B33_HUMAN STANDARD; PRT; 270 AA.
AC P01890;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DE 01-APR-1993 (Rel. 25, Last annotation update)
DE HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, BW-60(B-40) B*4001 ALPHA CHAIN
DE (FRAGMENT).
GN HLA-B OR HLAB.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Primates; Catarrhini; Hominidae; Homo.
RN [1]
RP SEQUENCE.
RX MEDLINE: 84000412.
RA LOPEZ DE CASTRO J.A., BRAGADO R., STRONG D.M., STROMINGER J.L.;
RT "Primary structure of papain-solubilized human histocompatibility
antigen HLA-B*40 (-Bw60). An outline of alloantigenic determinants.";
RL Biochemistry 22:3961-3969(1983).
CC -!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
THE IMMUNE SYSTEM.
CC -!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
MICROGLOBULIN).
DR PIR; A02186; HLH40.
DR HSSP; P30460; IAGB.
DR MIM; 142830;
DR PROSITE; PS00290; IG_MHC; 1.
DR PFAM; PF00047; Ig; 1.
DR PFAM; PF00129; MHC_I; 1.
KW MHC I; Glycoprotein.
FT DOMAIN 1 90
FT DOMAIN 91 181
FT DOMAIN 182 >270
FT CARBOHYD 86 86
FT DISULFID 101 163
FT DISULFID 202 258
FT NON_TER 270 270
SQ SEQUENCE 270 AA; BFE44EFF CRC32;

Query Match 100.0%; Score 51; DB 1; Length 270;
Best Local Similarity 100.0%; Pred. No. 0.0048;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RESLNRLRGY 10
DB 75 RESLNRLRGY 84
RESULT 2
ID 1B24_HUMAN STANDARD; PRT; 354 AA.
AC P30470;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)

DE HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-35 B*3504 ALPHA CHAIN
DE PRECURSOR (FRAGMENT).
GN HLA-B OR HLAB.

OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Primates; Catarrhini; Hominidae; Homo.
RN [1]
RP SEQUENCE FROM N.A.

RX MEDLINE; 92269956.
RA WATKINS D.I., MCADAM S.N., LIU X., STANG C.R., MILFORD E.L.,
RA LEVINE C.G., GABER T.L., DOON A.L., LORD C.I., GHIM S.H.,
RA TROUP G.M., HUGHES A.L., LETVIN N.L.;

"New recombinant HLA-B alleles in a tribe of South American
Amerindians indicate rapid evolution of MHC class I loci".
RL Nature 337:329-333(1992).
CC -1- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
CC THE IMMUNE SYSTEM.
CC -1- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
CC MICROGLOBULIN).
CC -----

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CC or send an email to license@isb-sib.ch).
CC -----

DR EMBL; M86403; ; NOT_ANNOTATED_CDS.
DR HSP; P30685; IAIN.
DR MIM; 142830; .

DR PROSITE; PS00290; IG_MHC; 1.
DR PFAM; PF00047; Ig; 1. 1.
DR PFAM; PF00129; MHC_I; 1.

KW MHC I; Transmembrane; Glycoprotein; Signal.
FT NON_TER 1 1
FT SIGNAL <1 16
FT CHAIN 17 354

FT DOMAIN 17 106 HLA CLASS I HISTOCOMPATIBILITY ANTIGEN,
FT DOMAIN 107 198 B-35 B*3504 ALPHA CHAIN.
FT DOMAIN 199 290 EXTRACELLULAR ALPHA-1.
FT DOMAIN 291 300 EXTRACELLULAR ALPHA-2.
FT TRANSMEM 301 324 EXTRACELLULAR ALPHA-3.
FT DOMAIN 301 324 CONNECTING PEPTIDE.
FT DOMAIN 325 354 CYTOPLASMIC TAIL.
FT CARBOHYD 102 102 BY SIMILARITY.
FT DISULFID 117 180 BY SIMILARITY.
FT DISULFID 219 275 BY SIMILARITY.

FT CARBOHYD 117 180 BY SIMILARITY.
FT DISULFID 219 275 BY SIMILARITY.
SQ SEQUENCE 354 AA; 6564795A CRC32;

Query Match 100.0%; Score 51; DB 1; Length 354;
Best Local Similarity 100.0%; Pred. No. 0.0065;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RESLNRNGY 10
Db |||||
91 RESLNRNGY 100

RESULT 3
1A02_PANTR STANDARD; PRT; 362 AA.
AC P16210;
DT 01-APR-1990 (Rel. 14, Created)

DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 01-APR-1993 (Rel. 25, Last annotation update)
DE CHLA CLASS I HISTOCOMPATIBILITY ANTIGEN, A-5 ALPHA CHAIN PRECURSOR.
OS Pan troglodytes (Chimpanzee).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Primates; Catarrhini; Hominidae; Pan.
RN [1]
RP SEQUENCE FROM N.A.

RX MEDLINE; 90201944.
RA LAWLOR D.A., WARREN E., WARD F.E., PARHAM P.;
RT "Comparison of class I MHC alleles in humans and apes.";
RL Immunol. Rev. 113:147-185(1990).
CC -1- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
CC THE IMMUNE SYSTEM.
CC -1- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
CC MICROGLOBULIN).
CC -----

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CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (see <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----

DR EMBL; M30679; AAA87971.1; .
DR HSP; P30685; IAIN.
DR PROSITE; PS00290; IG_MHC; 1.
DR PFAM; PF00047; Ig; 1. 1.
DR PFAM; PF00129; MHC_I; 1.

KW MHC I; Transmembrane; Glycoprotein; Signal.
FT SIGNAL 1 24
FT CHAIN 25 362

FT DOMAIN 25 114 CHLA CLASS I HISTOCOMPATIBILITY ANTIGEN,
FT DOMAIN 115 206 A-5 ALPHA CHAIN.
FT DOMAIN 207 298 EXTRACELLULAR ALPHA-1.
FT DOMAIN 299 308 EXTRACELLULAR ALPHA-2.
FT TRANSMEM 309 332 EXTRACELLULAR ALPHA-3.
FT DOMAIN 333 362 CONNECTING PEPTIDE.
FT DOMAIN 333 362 CYTOPLASMIC TAIL.
FT DISULFID 125 188 BY SIMILARITY.
FT DISULFID 227 283 BY SIMILARITY.
FT CARBOHYD 110 110 BY SIMILARITY.

FT CARBOHYD 110 110 BY SIMILARITY.
SQ SEQUENCE 362 AA; 40487 MW; 9756CE8A CRC32;

Query Match 100.0%; Score 51; DB 1; Length 362;
Best Local Similarity 100.0%; Pred. No. 0.0066;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RESLNRNGY 10
Db |||||
99 RESLNRNGY 108

RESULT 4
1B02_HUMAN STANDARD; PRT; 362 AA.
AC P01889;
DT 21-JUL-1986 (Rel. 01, Created)

DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-7 B*0702 ALPHA CHAIN
DE PRECURSOR (B7.2).
GN HLA-B OR HLAB.

OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Primates; Catarrhini; Hominidae; Homo.
RN [1]
RP SEQUENCE FROM N.A.

RX ENNIS P.D., ZEMMOUR J., SALTER R.D., PARHAM P.;
RT "Rapid cloning of HLA-A,B CDNA by using the polymerase chain
RL reaction: frequency and nature of errors produced in amplification.";
Proc. Natl. Acad. Sci. U.S.A. 87:2833-2837(1990).
RN [2]
RP SEQUENCE FROM N.A.

RX MEDLINE; 90315860.
RA PARHAM P., BENJAMIN R.J., CHEN B.P., CLAYBERGER C., ENNIS P.D.,
RA KRENSKY A.M., LAWLOR D.A., LITTMAN D.R., NORMENT A.M., ORR H.T.,
RA SALTER R.D., ZEMMOUR J.;

"Diversity of class I HLA molecules: functional and evolutionary interactions with T cells.";
 Cold Spring Harb. Symp. Quant. Biol. 54:529-543(1989).
 (3)
 SEQUENCE FROM N.A.
 MEDLINE: 85287366.
 RA SOOD A.K., PAN J., BIRO P.A., PEREIRA D., SRIVASTAVA R., REDDY V.B.,
 DUCURMAN B.W., WEISSMAN S.M.;
 "Structure and polymorphism of class I MHC antigen mRNA.";
 Immunogenetics 22:101-121(1985).
 (4)
 SEQUENCE FROM N.A.
 ELLERSON M.E., ZHANG L., HILDEBRAND W.H.;
 Submitted (JUN-1995) to the EMBL/GenBank/DBJ databases.
 (5)
 SEQUENCE OF 25-295.
 RP MEDLINE: 80088278.
 RA ORR H.T., LOPEZ DE CASTRO J.A., LANCET D., STROMINGER J.L.;
 "Complete amino acid sequence of a papain-solubilized human histocompatibility antigen, HLA-B*7.2. Sequence determination and search for homologies.";
 Biochemistry 18:5711-5720(1979).
 CC -!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO THE IMMUNE SYSTEM.
 CC -!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-MICROGLOBULIN).
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 CC
 DR EMBL: M32317; AAA36230.1; -;
 DR EMBL: M16102; AAA59622.1; AUT_SEQ.
 DR EMBL: U29057; AAA91229.1; -;
 DR PIR: A02185; HLHUB7.
 DR PIR: B35997; B35997.
 DR HSP: P30460; LAGB.
 DR MIM: 142830; -;
 DR PROSITE: PS00290; IG_MHC; 1.
 DR PFAM: PF00047; ig; 1.
 DR PFAM: PF00129; MHC_I; 1.
 KW MHC I; Transmembrane; Glycoprotein; Signal.
 FT SIGNAL 1 24
 FT CHAIN 25 362
 FT
 FT HLA CLASS I HISTOCOMPATIBILITY ANTIGEN,
 B-7 B*0702 ALPHA CHAIN.
 FT DOMAIN 25 114
 FT DOMAIN 115 206
 FT DOMAIN 207 298
 FT DOMAIN 299 309
 FT DOMAIN 310 333
 FT TRANSMEM 334 362
 FT CARBOHYD 110 110
 FT DISULFID 125 188
 FT DISULFID 227 283
 FT CONFLICT 15 18
 FT CONFLICT 266 266
 FT CONFLICT 268 268
 FT CONFLICT 297 297
 FT CONFLICT 314 315
 FT CONFLICT 314 315
 FT SEQUENCE 362 AA; 40460 MW; 8782ED84 CRC32;
 AALA -> GPW (IN REF. 3).
 Q -> E (IN REF. 5).
 W -> S (IN REF. 3).
 R -> G (IN REF. 3).
 GL -> RP (IN REF. 3).
 Query Match 100.0%; Score 51; DB 1; Length 362;
 Best Local Similarity 100.0%; Pred. No. 0.0066;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 RESLRNGY 10
 DB 99 RESLRNGY 108
 RESULT 6
 1B04_HUMAN STANDARD; PRT; 362 AA.
 AC P30460;

RESULT 5
 1B02_PANTR STANDARD; PRT; 362 AA.
 ID 1B02_PANTR
 AC P13751;
 DT 01-JAN-1990 (Rel. 13, Created)
 DT 01-JAN-1990 (Rel. 13, Last sequence update)
 DT 01-APR-1993 (Rel. 25, Last annotation update)
 DE CHLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-2 ALPHA CHAIN PRECURSOR.
 OS Pan troglodytes (Chimpanzee).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Eutheria; Primates; Catarrhini; Hominiidae; Pan.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 89030641.
 RA MAYER W.E., JONKER M., KLEIN D., IVANYI P., VAN SEVENTER G.,
 KLEIN J.;
 "Nucleotide sequences of chimpanzee MHC class I alleles: evidence for trans-species mode of evolution.";
 EMBO J. 7:2765-2774(1988).
 RN [2]
 RP REVISIONS.
 RA MAYER W.;
 RL Submitted (FEB-1989) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO THE IMMUNE SYSTEM.
 CC -!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-MICROGLOBULIN).
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 CC
 DR EMBL: X13116; CAA31508.1; -;
 DR PIR: S03538; S03538.
 DR HSP: P30685; IAIN.
 DR PROSITE: PS00290; IG_MHC; 1.
 DR PFAM: PF00047; ig; 1.
 DR PFAM: PF00129; MHC_I; 1.
 KW MHC I; Transmembrane; Glycoprotein; Signal.
 FT SIGNAL 1 24
 FT CHAIN 25 362
 FT
 FT HLA CLASS I HISTOCOMPATIBILITY ANTIGEN,
 B-2 ALPHA CHAIN.
 FT DOMAIN 25 114
 FT DOMAIN 115 206
 FT DOMAIN 207 298
 FT DOMAIN 299 308
 FT TRANSMEM 309 332
 FT DOMAIN 333 362
 FT DISULFID 125 188
 FT DISULFID 227 283
 FT CARBOHYD 110 110
 FT SEQUENCE 362 AA; 40488 MW; 4BF65A6C CRC32;
 Query Match 100.0%; Score 51; DB 1; Length 362;
 Best Local Similarity 100.0%; Pred. No. 0.0066;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 RESLRNGY 10
 DB 99 RESLRNGY 108
 RESULT 6
 1B04_HUMAN STANDARD; PRT; 362 AA.
 ID 1B04_HUMAN
 AC P30460;

DT 01-APR-1993 (Rel. 25, Created)
 DT 01-APR-1993 (Rel. 25, Last sequence update)
 DT 15-JUL-1998 (Rel. 36, Last annotation update)
 DE HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-8 B*0801 ALPHA CHAIN
 DE PRECURSOR.
 GN HLA-B OR HLAB.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Eutheria; Primates; Catarrhini; Hominidae; Homo.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 89235215.
 RA PARHAM P., LAWLER D.A., LOMEN C.E., ENNIS P.D.;
 RT "Diversity and diversification of HLA-A,B,C alleles.";
 RL J. Immunol. 142:3937-3950(1989).
 RN [2]
 RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS) OF 25-300.
 RX MEDLINE; 97130420.
 RA REID S.W., MCADAM S., SMITH K.J., KLENERMAN P., O'CALLAGHAN C.A.,
 RA HARLOS K., JAKOBSEN B.K., MCMICHAEL A.J., BELL J.I., STUART D.I.,
 RA JONES E.Y.;
 RT "Antagonist HIV-1 Gag peptides induce structural changes in HLA B8.";
 RL J. Exp. Med. 184:2279-2286(1996).
 CC -!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
 THE IMMUNE SYSTEM.
 CC -!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
 MICROGLOBULIN).
 CC
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 CC
 DR EMBL; M24036; AAA52662.1; .
 DR PDB; IAGB; 16-JUN-97.
 DR PDB; IAGC; 16-JUN-97.
 DR PDB; IAGD; 16-JUN-97.
 DR PDB; IAGE; 16-JUN-97.
 DR PDB; IAGF; 16-JUN-97.
 DR MIM; 142830; .
 DR PROSITE; PS00290; IG_MHC; 1.
 DR PFAM; PF00047; Ig; 1.
 DR PFAM; PF00129; MHC_I; 1.
 KW MHC I; Transmembrane; Glycoprotein; Signal; 3D-structure.
 FT SIGNAL 1 24
 FT CHAIN 25 362
 FT
 FT DOMAIN 25 114
 FT DOMAIN 115 206
 FT DOMAIN 207 298
 FT DOMAIN 299 309
 FT TRANSMEM 310 333
 FT DOMAIN 334 362
 FT CARBOHYD 110 110
 FT DISULFID 125 188
 FT DISULFID 227 283
 SQ SEQUENCE 362 AA; 40331 MW; 1467B8EB CRC32;
 Query Match 100.0%; Score 51; DB 1; Length 362;
 Best Local Similarity 100.0%; Pred. No. 0.0066;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 RESLNRLGY 10
 DB 99 RESLNRLGY 108
 RESULT 7
 1B07_HUMAN

ID 1B07_HUMAN STANDARD; PRT; 362 AA.
 AC P30452;
 DT 01-APR-1993 (Rel. 25, Created)
 DT 01-APR-1993 (Rel. 25, Last sequence update)
 DT 01-APR-1993 (Rel. 25, Last annotation update)
 DE HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-14 B*1401 ALPHA CHAIN
 DE PRECURSOR.
 GN HLA-B OR HLAB.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Eutheria; Primates; Catarrhini; Hominidae; Homo.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 89235215.
 RA PARHAM P., LAWLER D.A., LOMEN C.E., ENNIS P.D.;
 RT "Diversity and diversification of HLA-A,B,C alleles.";
 RL J. Immunol. 142:3937-3950(1989).
 CC -!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
 THE IMMUNE SYSTEM.
 CC -!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
 MICROGLOBULIN).
 CC
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 CC
 DR EMBL; M24040; AAA59661.1; .
 DR HSSP; P30460; IAGB.
 DR MIM; 142830; .
 DR PROSITE; PS00290; IG_MHC; 1.
 DR PFAM; PF00047; Ig; 1.
 DR PFAM; PF00129; MHC_I; 1.
 KW MHC I; Transmembrane; Glycoprotein; Signal.
 FT SIGNAL 1 24
 FT CHAIN 25 362
 FT
 FT DOMAIN 25 114
 FT DOMAIN 115 206
 FT DOMAIN 207 298
 FT DOMAIN 299 309
 FT TRANSMEM 310 333
 FT DOMAIN 334 362
 FT CARBOHYD 110 110
 FT DISULFID 125 188
 FT DISULFID 227 283
 SQ SEQUENCE 362 AA; 40358 MW; 9BED8199 CRC32;
 Query Match 100.0%; Score 51; DB 1; Length 362;
 Best Local Similarity 100.0%; Pred. No. 0.0066;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 RESLNRLGY 10
 DB 99 RESLNRLGY 108
 RESULT 8
 1B08_HUMAN STANDARD; PRT; 362 AA.
 AC P30463;
 DT 01-APR-1993 (Rel. 25, Created)
 DT 01-APR-1993 (Rel. 25, Last sequence update)
 DT 01-APR-1993 (Rel. 25, Last annotation update)
 DE HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B*1402 ALPHA CHAIN
 DE PRECURSOR.
 GN HLA-B OR HLAB.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Eutheria; Primates; Catarrhini; Hominidae; Homo.

OC Eutheria; Primates; Catarrhini; Hominidae; Homo.
 (1)
 RN SEQUENCE FROM N.A.
 RP MEDLINE; 89235215.
 RX PARHAM P., LAWLER D.A., LOMEN C.E., ENNIS P.D.;
 RA "Diversity and diversification of HLA-A,B,C alleles."
 RT J. Immunol. 142:3937-3950(1989).
 RL
 CC
 CC -1- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
 CC THE IMMUNE SYSTEM.
 CC
 CC -1- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
 CC MICROGLOBULIN).
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 CC
 CC EMBL; M24032; AAA59664.1; -;
 DR HSP; P30460; IAGB.
 DR MIN; 142830; -;
 DR PROSITE; PS00290; IG_MHC; 1.
 DR PFAM; PF00047; Ig; 1.
 DR PFAM; PF00129; MHC_I; 1.
 KW MHC I; Transmembrane; Glycoprotein; Signal.
 FT SIGNAL 1 24
 FT CHAIN 25 362 HLA CLASS I HISTOCOMPATIBILITY ANTIGEN,
 FT BW-65(B-14) B*1402 ALPHA CHAIN.
 FT DOMAIN 25 114 EXTRACELLULAR ALPHA-1.
 FT DOMAIN 115 206 EXTRACELLULAR ALPHA-2.
 FT DOMAIN 207 298 EXTRACELLULAR ALPHA-3.
 FT DOMAIN 299 309 CONNECTING PEPTIDE.
 FT TRANSMEM 310 333
 FT DOMAIN 334 362 CYTOPLASMIC TAIL.
 FT CARBOHYD 110 110 BY SIMILARITY.
 FT DISULFID 125 188 BY SIMILARITY.
 FT DISULFID 227 283 BY SIMILARITY.
 SQ SEQUENCE 362 AA; 40342 MW; B568AC9E CRC32;
 Query Match 100.0%; Score 51; DB 1; Length 362;
 Best Local Similarity 100.0%; Pred. No. 0.0066;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 RESLRNLRGY 10
 Db 99 RESLRNLRGY 108
 RESULT 9
 LB10_HUMAN
 ID LB10_HUMAN STANDARD; PRT; 362 AA.
 AC P30464;
 DT 01-APR-1993 (Rel. 25, Created)
 DT 01-APR-1993 (Rel. 25, Last sequence update)
 DT 15-JUL-1998 (Rel. 36, Last annotation update)
 DE HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, BW-75(B-15) B*1502 ALPHA CHAIN
 DE PRECURSOR.
 GN HLA-B OR HLAB.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Eutheria; Primates; Catarrhini; Hominidae; Homo.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 92196792.
 RA "The HLA-B*75 subtype of B15: molecular characterization and
 RT comparison with crossreacting antigens."
 RL Tissue Antigens 38:186-190(1991).
 RN [2]
 RP SEQUENCE FROM N.A.

RC TISSUE-BLOOD;
 RX MEDLINE; 96369309.
 RA LIN L., TOKUNAGA K., TANAKA H., NAKAJIMA F., IMANISHI T.,
 RA KASHIWASE K., BANNAI M., MIZUNO S., AKAZA T., TADOKORO K.,
 RA SHIBATA Y., JUJI T.;
 RT "Further molecular diversity in the HLA-B15 group."
 RL Tissue Antigens 47:265-274(1996).
 CC
 CC -1- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
 CC THE IMMUNE SYSTEM.
 CC
 CC -1- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
 CC MICROGLOBULIN).
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 CC
 CC EMBL; M75138; AAA59630.1; -;
 DR EMBL; D50293; BAA08824.1; -;
 DR HSP; P30685; IAIN.
 DR MIN; 142830; -;
 DR PROSITE; PS00290; IG_MHC; 1.
 DR PFAM; PF00047; Ig; 1.
 DR PFAM; PF00129; MHC_I; 1.
 KW MHC I; Transmembrane; Glycoprotein; Signal.
 FT SIGNAL 1 24
 FT CHAIN 25 362 HLA CLASS I HISTOCOMPATIBILITY ANTIGEN,
 FT BW-75(B-15) B*1502 ALPHA CHAIN.
 FT DOMAIN 25 114 EXTRACELLULAR ALPHA-1.
 FT DOMAIN 115 206 EXTRACELLULAR ALPHA-2.
 FT DOMAIN 207 298 EXTRACELLULAR ALPHA-3.
 FT DOMAIN 299 309 CONNECTING PEPTIDE.
 FT TRANSMEM 310 333
 FT DOMAIN 334 362 CYTOPLASMIC TAIL.
 FT CARBOHYD 110 110 BY SIMILARITY.
 FT DISULFID 125 188 BY SIMILARITY.
 FT DISULFID 227 283 BY SIMILARITY.
 SQ SEQUENCE 362 AA; 40338 MW; 8CF9ECD0 CRC32;
 Query Match 100.0%; Score 51; DB 1; Length 362;
 Best Local Similarity 100.0%; Pred. No. 0.0066;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 RESLRNLRGY 10
 Db 99 RESLRNLRGY 108
 RESULT 10
 LB11_HUMAN
 ID LB11_HUMAN STANDARD; PRT; 362 AA.
 AC P30465;
 DT 01-APR-1993 (Rel. 25, Created)
 DT 01-APR-1993 (Rel. 25, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, BW-72(BW-70) B*1503 ALPHA
 DE CHAIN PRECURSOR.
 GN HLA-B OR HLAB.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Eutheria; Primates; Catarrhini; Hominidae; Homo.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 93056508.
 RA MADRIGAL J.A., BELICH M.P., HILDEBRAND W.H., BENJAMIN R.J.,
 RA LITTLE A.-M., ZEMMOUR J., ENNIS P.D., WARD F.E., PETZL-ERLER M.L.,
 RA MARTELL R.W., DU TOIT E.D., PARHAM P.;
 RT "Distinctive HLA-A,B antigens of black populations formed by
 RT interallelic conversion."

RL J. Immunol. 149:3411-3415(1992).
 CC -!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
 CC THE IMMUNE SYSTEM.
 CC -!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
 CC MICROGLOBULIN).
 CC -----
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 CC -----
 CC EMBL: X61709; CAAM3878.1; -
 DR PIR: S16789; S16789.
 DR HSSP: P30685; IAIN.
 DR MIM: 142830; -
 DR PROSITE: PS00290; IG_MHC; 1.
 DR PFAM: PF00047; ig; 1.
 DR PFAM: PF00129; MHC_I; 1.
 KW MHC I; Transmembrane; Glycoprotein; Signal.
 FT SIGNAL 1 24
 FT CHAIN 25 362 HLA CLASS I HISTOCOMPATIBILITY ANTIGEN,
 FT BW-72(BW-70) B*1503 ALPHA CHAIN.
 FT DOMAIN 25 114 EXTRACELLULAR ALPHA-1.
 FT DOMAIN 115 206 EXTRACELLULAR ALPHA-2.
 FT DOMAIN 207 298 EXTRACELLULAR ALPHA-3.
 FT DOMAIN 299 309 CONNECTING PEPTIDE.
 FT TRANSMEM 310 333
 FT DOMAIN 334 362 CYTOPLASMIC TAIL.
 FT CARBOHYD 110 110 BY SIMILARITY.
 FT DISULFID 125 188 BY SIMILARITY.
 FT DISULFID 227 283 BY SIMILARITY.
 SQ SEQUENCE 362 AA: 40387 MW: 99D70546 CRC32;

Query Match 100.0%; Score 51; DB 1; Length 362;
 Best Local Similarity 100.0%; Pred. No. 0.0066;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RESLRNLRGY 10
 |||||
 Db 99 RESLRNLRGY 108

RESULT 11
 ID 1B12_HUMAN STANDARD; PRT; 362 AA.
 AC P30513;
 DT 01-APR-1993 (Rel. 25, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-62 B*1504 ALPHA CHAIN
 DE PRECURSOR.
 GN HLA-B OR HLAB.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Eutheria; Primates; Catarrhini; Homiidae; Homo.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 92269956.
 RA WATKINS D.I., MCADAM S.N., LIU X., STANG C.R., MILFORD E.L.,
 RA LEVINE C.G., GARBER T.L., DOGON A.L., LORD C.I., GHIM S.H.,
 RA TROUP G.M., HUGHES A.L., LEVIN N.I.
 RT "New recombinant HLA-B alleles in a tribe of South American
 RT Amerindians indicate rapid evolution of MHC class I loci."
 RL Nature 357:329-333(1992).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE-BLOOD:
 RA RAMOS M., BARBER D.F., LAYRISSE Z., DE CASTRO J.A.;
 RL Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.

CC -!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
 CC THE IMMUNE SYSTEM.
 CC -!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
 CC MICROGLOBULIN).
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 CC -----
 CC EMBL: M84382; AAA59632.1; -
 DR EMBL: U70528; AAB16918.1; -
 DR PIR: S24433; S24433.
 DR HSSP: P30685; IAIN.
 DR MIM: 142830; -
 DR PROSITE: PS00290; IG_MHC; 1.
 DR PFAM: PF00047; ig; 1.
 DR PFAM: PF00129; MHC_I; 1.
 KW MHC I; Transmembrane; Glycoprotein; Signal.
 FT SIGNAL 1 24
 FT CHAIN 25 362 HLA CLASS I HISTOCOMPATIBILITY ANTIGEN,
 FT B-62 B*1504 ALPHA CHAIN.
 FT DOMAIN 25 114 EXTRACELLULAR ALPHA-1.
 FT DOMAIN 115 206 EXTRACELLULAR ALPHA-2.
 FT DOMAIN 207 298 EXTRACELLULAR ALPHA-3.
 FT DOMAIN 299 309 CONNECTING PEPTIDE.
 FT TRANSMEM 310 333
 FT DOMAIN 334 362 CYTOPLASMIC TAIL.
 FT CARBOHYD 110 110 BY SIMILARITY.
 FT DISULFID 125 188 BY SIMILARITY.
 FT DISULFID 227 283 BY SIMILARITY.
 SQ SEQUENCE 362 AA: 40406 MW: E80FC24C CRC32;

Query Match 100.0%; Score 51; DB 1; Length 362;
 Best Local Similarity 100.0%; Pred. No. 0.0066;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RESLRNLRGY 10
 |||||
 Db 99 RESLRNLRGY 108

RESULT 12
 ID 1B13_HUMAN STANDARD; PRT; 362 AA.
 AC P30466;
 DT 01-APR-1993 (Rel. 25, Created)
 DT 01-APR-1993 (Rel. 25, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-18 B*1801 ALPHA CHAIN
 DE PRECURSOR.
 GN HLA-B OR HLAB.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Eutheria; Primates; Catarrhini; Homiidae; Homo.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 89235215.
 RA PARHAM P., LAWLER D.A., LOMEN C.E., ENNIS P.D.;
 RT "Diversity and diversification of HLA-A,B,C alleles."
 RL J. Immunol. 142:3937-3950(1989).
 CC -!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
 CC THE IMMUNE SYSTEM.
 CC -!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
 CC MICROGLOBULIN).
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 CC -----

DR EMBL; M24039; AAA59662.1; -
 DR HSSP; P30460; 1AGB.
 DR MIN; 142830; -
 DR PROSITE; PS00290; IG_MHC; 1.
 DR PFAM; PF00047; Ig; 1.
 DR PFAM; PF00129; MHC_I; 1.
 DR MHC I; Transmembrane; Glycoprotein; Signal.
 FT SIGNAL 1 24
 FT CHAIN 25 362
 FT
 FT HLA CLASS I HISTOCOMPATIBILITY ANTIGEN,
 FT B-18 B*1801 ALPHA CHAIN.
 FT EXTRACELLULAR ALPHA-1.
 FT EXTRACELLULAR ALPHA-2.
 FT EXTRACELLULAR ALPHA-3.
 FT CONNECTING PEPTIDE.
 FT
 FT CYTOPLASMIC TAIL.
 FT BY SIMILARITY.
 FT BY SIMILARITY.
 FT BY SIMILARITY.
 FT DISULFID 125 188
 FT DISULFID 227 283
 SQ SEQUENCE 362 AA; 40275 MW; 038EC3FC CRC32;

Query Match 100.0%; Score 51; DB 1; Length 362;
 Best Local Similarity 100.0%; Pred. No. 0.0066;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 RESLNRLGY 10
 |||||
 Db 99 RESLNRLGY 108

RESULT 13
 1B21_HUMAN
 ID 1B21_HUMAN STANDARD; PRT; 362 AA.
 AC P30685;
 DT 01-APR-1993 (Rel. 25, Created)
 DT 01-APR-1993 (Rel. 25, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-35 B*3501 ALPHA CHAIN
 DE PRECURSOR.
 GN HLA-B OR HLAB.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Eutheria; Primates; Catarrhini; Hominidae; Homo.
 [1]
 RP SEQUENCE FROM N.A.
 RP MEDLINE; 89339610.
 RA Ooba I., HAYASHI H., KARAKI S., TANABE M., KANO K., TAKIGUCHI M.;
 RT "The structure of HLA-B*35 suggests that it is derived from HLA-B*58
 RT by two genetic mechanisms.";
 RL Immunogenetics 30:76-80(1989).
 RN [2]
 RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF 25-300.
 RX MEDLINE; 96209671.
 RA SMITH K.J., REID S.W., STUART D.I., MCMICHAEL A.J., JONES E.Y.,
 RA BELL J.I.;
 RT "An altered position of the alpha 2 helix of MHC class I is revealed
 RT by the crystal structure of HLA-B*3501.";
 RL Immunity 4:203-214(1996).
 RN [3]
 RP X-RAY CRYSTALLOGRAPHY (3.2 ANGSTROMS).
 RA MENSSSEN R., ORTH P., ZIEGLER A., SAENGER W.;
 RL Submitted (APR-1998) to the PDB data bank.
 CC -!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
 CC THE IMMUNE SYSTEM.
 CC -!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
 CC MICROGLOBULIN).
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DR EMBL; M28115; AAA59617.1; -
 DR EMBL; M28109; AAA59617.1; JOINED.
 DR EMBL; M28110; AAA59617.1; JOINED.
 DR EMBL; M28111; AAA59617.1; JOINED.
 DR EMBL; M28112; AAA59617.1; JOINED.
 DR EMBL; M28113; AAA59617.1; JOINED.
 DR EMBL; M28114; AAA59617.1; JOINED.
 DR PIR; A45880; A45880.
 DR PDB; 1A9B; 08-APR-98.
 DR PDB; 1A9E; 18-NOV-98.
 DR PDB; 1A9E; 18-NOV-98.
 DR MIN; 142830; -
 DR PROSITE; PS00290; IG_MHC; 1.
 DR PFAM; PF00047; Ig; 1.
 DR PFAM; PF00129; MHC_I; 1.
 DR MHC I; Transmembrane; Glycoprotein; Signal; 3D-structure.
 FT SIGNAL 1 24
 FT CHAIN 25 362
 FT
 FT HLA CLASS I HISTOCOMPATIBILITY ANTIGEN,
 FT B-35 B*3501 ALPHA CHAIN.
 FT EXTRACELLULAR ALPHA-1.
 FT EXTRACELLULAR ALPHA-2.
 FT EXTRACELLULAR ALPHA-3.
 FT CONNECTING PEPTIDE.
 FT
 FT CYTOPLASMIC TAIL.
 FT BY SIMILARITY.
 FT BY SIMILARITY.
 FT DISULFID 125 188
 FT DISULFID 227 283
 SQ SEQUENCE 362 AA; 40455 MW; AEC1C675 CRC32;

Query Match 100.0%; Score 51; DB 1; Length 362;
 Best Local Similarity 100.0%; Pred. No. 0.0066;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 RESLNRLGY 10
 |||||
 Db 99 RESLNRLGY 108

RESULT 14
 1B22_HUMAN
 ID 1B22_HUMAN STANDARD; PRT; 362 AA.
 AC P30468;
 DT 01-APR-1993 (Rel. 25, Created)
 DT 01-APR-1993 (Rel. 25, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-35 B*3502 ALPHA CHAIN
 DE PRECURSOR.
 GN HLA-B OR HLAB.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Eutheria; Primates; Catarrhini; Hominidae; Homo.
 [1]
 RP SEQUENCE FROM N.A.
 RP MEDLINE; 91365651.
 RA CHERTKOFF L.P., HERRERA M., FAIBOIM L., SATZ M.L.;
 RT "Complete nucleotide sequence of a genomic clone encoding HLA-B*35
 RT isolated from a Caucasian individual of Hispanic origin.
 RT Identification of a new variant of HLA-B*35.";
 RL Hum. Immunol. 31:153-158(1991).
 CC -!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
 CC THE IMMUNE SYSTEM.
 CC -!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
 CC MICROGLOBULIN).
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DR EMBL; M63454; AAA59682.1; -
 DR HSP; P30685; IAIN.
 DR MIM; 142830; -
 DR PROSITE; PS00290; IG_MHC; 1.
 DR PFAM; PF00047; ig; 1.
 DR PFAM; PF00129; MHC_I; 1.
 KW MHC I; Transmembrane; Glycoprotein; Signal.
 FT SIGNAL 1 24
 FT CHAIN 25 362
 FT DOMAIN 25 114
 FT DOMAIN 115 206
 FT DOMAIN 207 298
 FT DOMAIN 299 308
 FT TRANSMEM 309 332
 FT DOMAIN 333 362
 FT CARBOHYD 110 110
 FT DISULFID 125 188
 FT DISULFID 227 283
 SQ SEQUENCE 362 AA; D7B5C2C9 CRC32;

Query Match 100.0%; Score 51; DB 1; Length 362;
 Best Local Similarity 100.0%; Pred. No. 0.0066;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RESLRNLRGY 10
 |||||
 Db 99 RESLRNLRGY 108

RESULT 15

1B23_HUMAN
 ID 1B23_HUMAN STANDARD; PRT; 362 AA.
 AC P30469;
 DT 01-APR-1993 (Rel. 25, Created)
 DT 01-APR-1993 (Rel. 25, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-35 B*3503 ALPHA CHAIN
 DE PRECURSOR.
 GN HLA-B OR HLAB.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Eutheria; Primates; Catarrhini; Hominidae; Homo.
 [1]
 RN SEQUENCE FROM N.A.
 RX MEDLINE; 92176651.
 RA ZEMMOUR J., LITTLE A.M., SCHENDEL D.J., PARHAM P.;
 RT "The HLA-A-B 'negative' mutant cell line CLR expresses a novel
 RT HLA-B35 allele, which also has a point mutation in the translation
 RT initiation codon."
 RL J. Immunol. 148:1941-1948(1992).
 [2]
 RN SEQUENCE FROM N.A.
 RC TISSUE-BLOOD;
 RX MEDLINE; 95279930.
 RA BECK Y., SATZ L., TAKAMIYA Y., NAKAYAMA S., LING L., ISHIIKAWA Y.,
 RA NAGAO T., UCHIDA H., TOKUNAGA K., MULLER C., JUJI T., TAKIGUCHI M.;
 RT "Polymorphism of human minor histocompatibility antigens: T cell
 RT recognition of human minor histocompatibility peptides presented by
 RT HLA-B35 subtype molecules."
 RL J. Exp. Med. 181:2037-2048(1995).
 CC -!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
 CC THE IMMUNE SYSTEM.

CC -!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
 CC MICROGLOBULIN).
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DR EMBL; M61798; AAA59684.1; -
 DR EMBL; D50299; BAA0828.1; -
 DR HSP; P30685; IAIN.
 DR MIM; 142830; -
 DR PROSITE; PS00290; IG_MHC; 1.
 DR PFAM; PF00047; ig; 1.
 DR PFAM; PF00129; MHC_I; 1.
 KW MHC I; Transmembrane; Glycoprotein; Signal.
 FT SIGNAL 1 24
 FT CHAIN 25 362
 FT DOMAIN 25 114
 FT DOMAIN 115 206
 FT DOMAIN 207 298
 FT DOMAIN 299 308
 FT TRANSMEM 309 332
 FT DOMAIN 333 362
 FT CARBOHYD 110 110
 FT DISULFID 125 188
 FT DISULFID 227 283
 SQ SEQUENCE 362 AA; 40515 MW; 4222D30A CRC32;

Query Match 100.0%; Score 51; DB 1; Length 362;
 Best Local Similarity 100.0%; Pred. No. 0.0066;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RESLRNLRGY 10
 |||||
 Db 99 RESLRNLRGY 108

Search completed: February 8, 2000, 01:25:58
 Job time: 1558 sec

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OM protein - protein search, using sw model

Run on: February 8, 2000, 19:16:13 ; Search time 176.54 Seconds
(without alignments)
3.927 Million cell updates/sec

Title: US-08-653-294-24
Perfect score: 51
Sequence: 1 RESLNRLRG 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 225878 seqs, 69334122 residues

Total number of hits satisfying chosen parameters: 225878

Minimum DB seq length: 0

Maximum DB seq length: 1000000

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database : SPTREMBL_12.*
1: sp.archaea.*
2: sp.bacteria.*
3: sp.fungi.*
4: sp.human.*
5: sp.invertebrate.*
6: sp.mammal.*
7: sp.mhc.*
8: sp.organelle.*
9: sp.phage.*
10: sp.plant.*
11: sp.rodent.*
12: sp.virus.*
13: sp.vertebrate.*
14: sp.unclassified.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	51	100.0	81	7 O19523	O19523 homo sapien
2	51	100.0	81	7 O19525	O19525 homo sapien
3	51	100.0	81	7 O19527	O19527 homo sapien
4	51	100.0	81	7 O19529	O19529 homo sapien
5	51	100.0	81	7 O19531	O19531 homo sapien
6	51	100.0	81	7 O19533	O19533 homo sapien
7	51	100.0	81	7 O19535	O19535 homo sapien
8	51	100.0	81	7 O19537	O19537 homo sapien
9	51	100.0	83	7 O19539	O19539 homo sapien
10	51	100.0	83	7 O19541	O19541 homo sapien
11	51	100.0	83	7 O19543	O19543 homo sapien
12	51	100.0	89	4 Q9Y452	Q9Y452 homo sapien
13	51	100.0	89	7 P79615	P79615 homo sapien
14	51	100.0	89	7 P79620	P79620 homo sapien
15	51	100.0	89	7 O19548	O19548 homo sapien
16	51	100.0	89	7 O19549	O19549 homo sapien
17	51	100.0	89	7 O19550	O19550 homo sapien
18	51	100.0	89	7 O19551	O19551 homo sapien
19	51	100.0	89	7 O19640	O19640 homo sapien
20	51	100.0	89	7 O77967	O77967 homo sapien

21	51	100.0	89	7	O78174	homo sapien
22	51	100.0	89	7	O19638	homo sapien
23	51	100.0	89	7	P79487	homo sapien
24	51	100.0	89	7	O19567	homo sapien
25	51	100.0	89	7	O19576	homo sapien
26	51	100.0	89	7	O19577	homo sapien
27	51	100.0	89	7	O19581	homo sapien
28	51	100.0	89	7	O19583	homo sapien
29	51	100.0	112	7	O92671	homo sapien
30	51	100.0	134	7	O29677	homo sapien
31	51	100.0	137	7	O29660	homo sapien
32	51	100.0	137	7	O29663	homo sapien
33	51	100.0	137	7	O29665	homo sapien
34	51	100.0	137	7	O29664	homo sapien
35	51	100.0	147	7	O29707	homo sapien
36	51	100.0	165	7	P79665	homo sapien
37	51	100.0	165	7	P79666	homo sapien
38	51	100.0	166	7	O19777	homo sapien
39	51	100.0	166	7	O19778	homo sapien
40	51	100.0	172	7	O19776	homo sapien
41	51	100.0	176	7	O29662	homo sapien
42	51	100.0	179	7	O29676	homo sapien
43	51	100.0	180	7	O29678	homo sapien
44	51	100.0	180	7	O77960	homo sapien
45	51	100.0	181	7	O29716	homo sapien

ALIGNMENTS

RESULT 1
O19523 PRELIMINARY; PRT; 81 AA.
AC O19523;
DT 01-JAN-1998 (TREMBLrel. 05, Created)
DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
DT 01-NOV-1998 (TREMBLrel. 08, Last annotation update)
DE MHC CLASS I ANTIGEN HLA-B (FRAGMENT).
GN HLA-B.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Primates; Catarrhini; Hominidae; Homo.
RN [1]
RP SEQUENCE FROM N.A.
RA CHANDANAYINGYONG D., SIRIKONG M., LUANGTRAKOOL K., SRINAK D.,
RA RUNGRONG E., BEJCHANDRA S.;
RL Submitted (JUL-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF014769; AAB67807.1; -
DR PFAM; PF00129; MHC_I; 1.
KW MHC.
FT NON_TER 1 1
FT NON_TER 81 81
SQ SEQUENCE 81 AA; 9405 MW; 073087CE CRC32;
Query Match 100.0%; Score 51; DB 7; Length 81;
Best Local Similarity 100.0%; Pred. No. 0.013;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 RESLNRLRG 10
Db 66 RESLNRLRG 75
RESULT 2
O19525 PRELIMINARY; PRT; 81 AA.
AC O19525;
DT 01-JAN-1998 (TREMBLrel. 05, Created)
DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
DT 01-NOV-1998 (TREMBLrel. 08, Last annotation update)
DE MHC CLASS I ANTIGEN HLA-B (FRAGMENT).
GN HLA-B.

OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Eutheria; Primates; Catarrhini; Hominidae; Homo.
 RN [1]
 RP SEQUENCE FROM N.A.
 RA CHANDANAYINGYONG D., SIRIKONG M., LUANGTRAKOOL K., SRINAK D.,
 RA RUNGROUNG E., BEJCHANDRA S.;
 RL Submitted (JUL-1997) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF014771; AAB67809.1; -
 DR PFAM; PF00129; MHC_I; 1.
 KW MHC.
 FT NON_TER 1 1
 FT NON_TER 81 81
 SQ SEQUENCE 81 AA; 9405 MW; 073087CE CRC32;

Query Match 100.0%; Score 51; DB 7; Length 81;
 Best Local Similarity 100.0%; Pred. No. 0.013;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RESLRNLRGY 10
 Db 66 RESLRNLRGY 75

RESULT 3
 O19527 ID O19527 PRELIMINARY; PRT; 81 AA.
 AC O19527;
 DT 01-JAN-1998 (TREMBLrel. 05, Created)
 DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
 DT 01-NOV-1998 (TREMBLrel. 08, Last annotation update)
 DE MHC CLASS I ANTIGEN HLA-B (FRAGMENT).
 GN HLA-B.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Eutheria; Primates; Catarrhini; Hominidae; Homo.
 RN [1]

RP SEQUENCE FROM N.A.
 RA CHANDANAYINGYONG D., SIRIKONG M., LUANGTRAKOOL K., SRINAK D.,
 RA RUNGROUNG E., BEJCHANDRA S.;
 RL Submitted (JUL-1997) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF014773; AAB67811.1; -
 DR PFAM; PF00129; MHC_I; 1.
 KW MHC.
 FT NON_TER 1 1
 FT NON_TER 81 81
 SQ SEQUENCE 81 AA; 9405 MW; 073087CE CRC32;

Query Match 100.0%; Score 51; DB 7; Length 81;
 Best Local Similarity 100.0%; Pred. No. 0.013;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RESLRNLRGY 10
 Db 66 RESLRNLRGY 75

RESULT 4
 O19529 ID O19529 PRELIMINARY; PRT; 81 AA.
 AC O19529;
 DT 01-JAN-1998 (TREMBLrel. 05, Created)
 DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
 DT 01-NOV-1998 (TREMBLrel. 08, Last annotation update)
 DE MHC CLASS I ANTIGEN HLA-B (FRAGMENT).
 GN HLA-B.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Eutheria; Primates; Catarrhini; Hominidae; Homo.
 RN [1]
 RP SEQUENCE FROM N.A.

RA CHANDANAYINGYONG D., SIRIKONG M., LUANGTRAKOOL K., SRINAK D.,
 RA RUNGROUNG E., BEJCHANDRA S.;
 RL Submitted (JUL-1997) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF014775; AAB67813.1; -
 DR PFAM; PF00129; MHC_I; 1.
 KW MHC.
 FT NON_TER 1 1
 FT NON_TER 81 81
 SQ SEQUENCE 81 AA; 9405 MW; 073087CE CRC32;

Query Match 100.0%; Score 51; DB 7; Length 81;
 Best Local Similarity 100.0%; Pred. No. 0.013;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RESLRNLRGY 10
 Db 66 RESLRNLRGY 75

RESULT 5
 O19531 ID O19531 PRELIMINARY; PRT; 81 AA.
 AC O19531;
 DT 01-JAN-1998 (TREMBLrel. 05, Created)
 DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
 DT 01-NOV-1998 (TREMBLrel. 08, Last annotation update)
 DE MHC CLASS I ANTIGEN HLA-B (FRAGMENT).
 GN HLA-B.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Eutheria; Primates; Catarrhini; Hominidae; Homo.
 RN [1]

RP SEQUENCE FROM N.A.
 RA CHANDANAYINGYONG D., SIRIKONG M., LUANGTRAKOOL K., SRINAK D.,
 RA RUNGROUNG E., BEJCHANDRA S.;
 RL Submitted (JUL-1997) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF014777; AAB67815.1; -
 DR PFAM; PF00129; MHC_I; 1.
 KW MHC.
 FT NON_TER 1 1
 FT NON_TER 81 81
 SQ SEQUENCE 81 AA; 9405 MW; 073087CE CRC32;

Query Match 100.0%; Score 51; DB 7; Length 81;
 Best Local Similarity 100.0%; Pred. No. 0.013;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RESLRNLRGY 10
 Db 66 RESLRNLRGY 75

RESULT 6
 O19533 ID O19533 PRELIMINARY; PRT; 81 AA.
 AC O19533;
 DT 01-JAN-1998 (TREMBLrel. 05, Created)
 DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
 DT 01-NOV-1998 (TREMBLrel. 08, Last annotation update)
 DE MHC CLASS I ANTIGEN HLA-B (FRAGMENT).
 GN HLA-B.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Eutheria; Primates; Catarrhini; Hominidae; Homo.
 RN [1]
 RP SEQUENCE FROM N.A.
 RA CHANDANAYINGYONG D., SIRIKONG M., LUANGTRAKOOL K., SRINAK D.,
 RA RUNGROUNG E., BEJCHANDRA S.;
 RL Submitted (JUL-1997) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF014779; AAB67817.1; -
 DR PFAM; PF00129; MHC_I; 1.

KW MHC.
FT NON_TER 1 1
FT NON_TER 81 81
SQ SEQUENCE 81 AA; 9405 MW; 073087CE CRC32;

Query Match 100.0%; Score 51; DB 7; Length 81;
Best Local Similarity 100.0%; Pred. No. 0.013;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RESLNLRGY 10
| | | | | | | | | |
Db 66 RESLNLRGY 75

RESULT 7
O19535 PRELIMINARY; PRT; 81 AA.
ID O19535
AC O19535;

DT 01-JAN-1998 (TREMBLrel. 05, Created)
DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
DT 01-NOV-1998 (TREMBLrel. 08, Last annotation update)
DE MHC CLASS I ANTIGEN HLA-B (FRAGMENT).
GN HLA-B.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Primates; Catarrhini; Hominidae; Homo.
RN [1]

RP SEQUENCE FROM N.A.
RA CHANDANAYINGYONG D., SIRIKONG M., LUANGTRAKOOL K., SRINAK D.,
RA RUNGROUNG E., BEJCHANDRA S.;
RL Submitted (JUL-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF014781; AAB67819.1; -
DR PFAM; PF00129; MHC_I; 1.
KW MHC.
FT NON_TER 1 1
FT NON_TER 81 81
SQ SEQUENCE 81 AA; 9405 MW; 073087CE CRC32;

Query Match 100.0%; Score 51; DB 7; Length 81;
Best Local Similarity 100.0%; Pred. No. 0.013;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RESLNLRGY 10
| | | | | | | | | |
Db 66 RESLNLRGY 75

RESULT 8
O19537 PRELIMINARY; PRT; 81 AA.
ID O19537
AC O19537;

DT 01-JAN-1998 (TREMBLrel. 05, Created)
DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
DT 01-NOV-1998 (TREMBLrel. 08, Last annotation update)
DE MHC CLASS I ANTIGEN HLA-B (FRAGMENT).
GN HLA-B.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Primates; Catarrhini; Hominidae; Homo.
RN [1]

RP SEQUENCE FROM N.A.
RA CHANDANAYINGYONG D., SIRIKONG M., LUANGTRAKOOL K., SRINAK D.,
RA RUNGROUNG E., BEJCHANDRA S.;
RL Submitted (JUL-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF014783; AAB67821.1; -
DR PFAM; PF00129; MHC_I; 1.
KW MHC.
FT NON_TER 1 1
FT NON_TER 81 81
SQ SEQUENCE 81 AA; 9405 MW; 073087CE CRC32;

Query Match 100.0%; Score 51; DB 7; Length 81;
Best Local Similarity 100.0%; Pred. No. 0.013;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RESLNLRGY 10
| | | | | | | | | |
Db 66 RESLNLRGY 75

RESULT 9
O19539 PRELIMINARY; PRT; 83 AA.
ID O19539
AC O19539;

DT 01-JAN-1998 (TREMBLrel. 05, Created)
DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
DT 01-NOV-1998 (TREMBLrel. 08, Last annotation update)
DE MHC CLASS I ANTIGEN HLA-B (FRAGMENT).
GN HLA-B.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Primates; Catarrhini; Hominidae; Homo.
RN [1]

RP SEQUENCE FROM N.A.
RA CHANDANAYINGYONG D., SIRIKONG M., LUANGTRAKOOL K., SRINAK D.,
RA RUNGROUNG E., BEJCHANDRA S.;
RL Submitted (JUL-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF014785; AAB67823.1; -
DR PFAM; PF00129; MHC_I; 1.
KW MHC.
FT NON_TER 1 1
FT NON_TER 83 83
SQ SEQUENCE 83 AA; 9731 MW; 24B8D666 CRC32;

Query Match 100.0%; Score 51; DB 7; Length 83;
Best Local Similarity 100.0%; Pred. No. 0.013;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RESLNLRGY 10
| | | | | | | | | |
Db 68 RESLNLRGY 77

RESULT 10
O19541 PRELIMINARY; PRT; 83 AA.
ID O19541
AC O19541;

DT 01-JAN-1998 (TREMBLrel. 05, Created)
DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
DT 01-NOV-1998 (TREMBLrel. 08, Last annotation update)
DE MHC CLASS I ANTIGEN HLA-B (FRAGMENT).
GN HLA-B.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Primates; Catarrhini; Hominidae; Homo.
RN [1]

RP SEQUENCE FROM N.A.
RA CHANDANAYINGYONG D., SIRIKONG M., LUANGTRAKOOL K., SRINAK D.,
RA RUNGROUNG E., BEJCHANDRA S.;
RL Submitted (JUL-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF014787; AAB67825.1; -
DR PFAM; PF00129; MHC_I; 1.
KW MHC.
FT NON_TER 1 1
FT NON_TER 83 83
SQ SEQUENCE 83 AA; 9731 MW; 24B8D666 CRC32;

Query Match 100.0%; Score 51; DB 7; Length 83;
Best Local Similarity 100.0%; Pred. No. 0.013;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 RESLNLCY 10
DB 68 RESLNLCY 77

RESULT 11
O19543
ID O19543 PRELIMINARY; PRT; 83 AA.
AC O19543;
DT 01-JAN-1998 (TREMBlrel. 05, Created)
DT 01-JAN-1998 (TREMBlrel. 05, Last sequence update)
DT 01-NOV-1998 (TREMBlrel. 08, Last annotation update)
DE MHC CLASS I ANTIGEN HLA-B (FRAGMENT).
GN HLA-B.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Primates; Catarrhini; Hominidae; Homo.
RN [1]
RP SEQUENCE FROM N.A.
RA CHANDANAYONG D., SIRIKONG M., LUANGTRAKOOL K., SRINAK D.,
RA RUNGROUNG E., BEJCHANDRA S.;
RL Submitted (JUL-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF04789; AAB7827.1; -.
DR PFAM; PF00129; MHC_I; 1.
KW MHC.
FT NON_TER 1 1
FT NON_TER 83 83
SQ SEQUENCE 83 AA; 9731 MW; 24B8D666 CRC32;

Query Match 100.0%; Score 51; DB 7; Length 83;
Best Local Similarity 100.0%; Pred. No. 0.013;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RESLNLCY 10
DB 68 RESLNLCY 77

RESULT 12
Q9Y452
ID Q9Y452 PRELIMINARY; PRT; 89 AA.
AC Q9Y452;
DT 01-NOV-1999 (TREMBlrel. 12, Created)
DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)
DT 01-NOV-1999 (TREMBlrel. 12, Last annotation update)
DE HUMAN LEUCOCYTE ANTIGEN B (FRAGMENT).
GN HLA-B.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Primates; Catarrhini; Hominidae; Homo.
RN [1]
RP SEQUENCE FROM N.A.
RA CARTER V., DUNN P.P.;
RT "Identification of a novel HLA-B*07 allele.";
RL Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ237594; CAB40714.1; -.
FT NON_TER 1 1
FT NON_TER 89 89
SQ SEQUENCE 89 AA; 10609 MW; 659B735B CRC32;

Query Match 100.0%; Score 51; DB 4; Length 89;
Best Local Similarity 100.0%; Pred. No. 0.014;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RESLNLCY 10
DB 74 RESLNLCY 83

RESULT 13
P79615
ID P79615 PRELIMINARY; PRT; 89 AA.
AC P79615;
DT 01-MAY-1997 (TREMBlrel. 03, Created)
DT 01-MAY-1997 (TREMBlrel. 03, Last sequence update)
DT 01-NOV-1998 (TREMBlrel. 08, Last annotation update)
DE MHC CLASS I HLA-B (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Primates; Catarrhini; Hominidae; Homo.
RN [1]
RP SEQUENCE FROM N.A.
RA CHOPEK M., CAO K., ZHANG G.H.;
RL Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; U88249; AAB48493.1; -.
DR PFAM; PF00129; MHC_I; 1.
KW MHC.
FT NON_TER 1 1
FT NON_TER 89 89
SQ SEQUENCE 89 AA; 10489 MW; A7D3DF93 CRC32;

Query Match 100.0%; Score 51; DB 7; Length 89;
Best Local Similarity 100.0%; Pred. No. 0.014;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RESLNLCY 10
DB 74 RESLNLCY 83

RESULT 14
P79620
ID P79620 PRELIMINARY; PRT; 89 AA.
AC P79620;
DT 01-MAY-1997 (TREMBlrel. 03, Created)
DT 01-MAY-1997 (TREMBlrel. 03, Last sequence update)
DT 01-NOV-1998 (TREMBlrel. 08, Last annotation update)
DE MHC CLASS I HLA-B (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Primates; Catarrhini; Hominidae; Homo.
RN [1]
RP SEQUENCE FROM N.A.
RA CHOPEK M., CAO K., ZHANG G.H.;
RL Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; U88254; AAB48498.1; -.
DR PFAM; PF00129; MHC_I; 1.
KW MHC.
FT NON_TER 1 1
FT NON_TER 89 89
SQ SEQUENCE 89 AA; 10501 MW; FA3EFDCD CRC32;

Query Match 100.0%; Score 51; DB 7; Length 89;
Best Local Similarity 100.0%; Pred. No. 0.014;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RESLNLCY 10
DB 74 RESLNLCY 83

RESULT 15
O19548
ID O19548 PRELIMINARY; PRT; 89 AA.
AC O19548;
DT 01-JAN-1998 (TREMBlrel. 05, Created)
DT 01-JAN-1998 (TREMBlrel. 05, Last sequence update)
DT 01-NOV-1998 (TREMBlrel. 08, Last annotation update)
DE MHC CLASS I ANTIGEN (FRAGMENT).
GN HLA-B.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;

```


OC Eutheria; Primates; Catarrhini; Hominidae; Homo.
RN [1]
RP SEQUENCE FROM N.A.
RA CAO K., BURDETT L., ZHANG H., FERNANDEZ-VINA M.;
RL Submitted (JUL-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF016299; AAB69444.1; -
DR PFAM; PF00129; MHC_I; 1.
KW MHC.

FT NON_TER 1
FT NON_TER 89
SQ SEQUENCE 89 AA; 10550 MW; 11452E40 CRC32;

Query Match 100.0%; Score 51; DB 7; Length 89;
Best Local Similarity 100.0%; Pred. NO. 0.014;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RESLRNLGY 10
Db 74 RESLRNLGY 83

Search completed: February 8, 2000, 19:16:13
Job time: 21500 sec

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OM of: US-08-653-294-24 to: GenEmbl.* out_format : pfs
Date: Feb 8, 2000 10:22 PM
About: Results were produced by the GenCore software, version 4.5,
Copyright (c) 1993-2000 CompuGen Ltd.

Command line parameters:
-MODEL=frame+p2n.model -DEV=xlp
-O=/cgn1.1/USPTO_spool/US08653294/runat_04022000_160701_15779/app_query.fasta.2
-DB=GenEmbl -QPMI=fastcap -SUFFIX=rge -GAPOP=12.000 -GAPEXT=4.500
-MINMATCH=0.100 -LOOPCL=0.000 -XGAPEXT=0.500 -XGAPOP=6.000
-XGAPEXT=0.050 -XGAPOP=10.000 -XGAPEXT=0.500 -DELOP=6.000
-XGAPEXT=7.000 -XGAPOP=10.000 -XGAPEXT=0.500 -DELOP=6.000
-DELEX=7.000 -START=1 -MATRIX=blossum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE=pct -ALIGN=15 -MODE=LOCAL
-OUTFMT=pfs -NORM=ext -MINLEN=0 -MAXLEN=100000 -USER=US08653294
-NCPU=6 -ICPU=3 -NO_XLPXY -WAIT -THREADS=1

Search information block:

Query: US-08-653-294-24

Query length: 10

Database: GenEmbl.*

Database sequences: 821193

Database length: -1518192014

Search time (sec): 10176.920000

score_list:

Sequence	Strd Orig	zScore	EScore	Len	Documentation
gb_pr2: HSHLABK1	+	51.00	179.68	243	U91332 Human cell line THAI DCH
gb_pr2: HSHLABM1	+	51.00	179.68	243	U91334 Human cell line THAI DCH
gb_pr2: HSHLABO1	+	51.00	179.68	243	U91335 Human cell line THAI DCH
gb_pr2: AF014769	+	51.00	179.58	246	AF014769 Homo sapiens MHC class
gb_pr2: AF014771	+	51.00	179.58	246	AF014771 Homo sapiens MHC class
gb_pr2: AF014773	+	51.00	179.58	246	AF014773 Homo sapiens MHC class
gb_pr2: AF014775	+	51.00	179.58	246	AF014775 Homo sapiens MHC class
gb_pr2: AF014777	+	51.00	179.58	246	AF014777 Homo sapiens MHC class
gb_pr2: AF014779	+	51.00	179.58	246	AF014779 Homo sapiens MHC class
gb_pr2: AF014781	+	51.00	179.58	246	AF014781 Homo sapiens MHC class
gb_pr2: AF014783	+	51.00	179.58	246	AF014783 Homo sapiens MHC class
gb_pr2: AF014785	+	51.00	179.45	250	AF014785 Homo sapiens MHC class
gb_pr2: AF014787	+	51.00	179.45	250	AF014787 Homo sapiens MHC class
gb_pr2: AF014789	+	51.00	179.45	250	AF014789 Homo sapiens MHC class
gb_pr2: HSB1501N1	+	51.00	179.33	254	US9965 Human MHC class I protei
gb_pr1: D89333	+	51.00	178.85	270	D89333 Homo sapiens DNA for MHC
gb_pr1: HSA131852	+	51.00	178.85	270	AJ131852 Homo sapiens HLA-B gen
gb_pr1: HSA7603	+	51.00	178.85	270	AJ007603 Homo sapiens HLA-B*151
gb_pr1: HSA7605	+	51.00	178.85	270	AJ007605 Homo sapiens HLA-B*151
gb_pr1: UMMHB35052	+	51.00	178.85	270	M28110 Human MHC class I cell s
gb_pr2: AF002275	+	51.00	178.85	270	AF002275 Homo sapiens MHC class
gb_pr2: AF016299	+	51.00	178.85	270	AF016299 Homo sapiens MHC class
gb_pr2: AF01300S1	+	51.00	178.85	270	U93913 Homo sapiens MHC class I
gb_pr2: HS5602V1	+	51.00	178.85	270	AJ132713 Homo sapiens HLA-B gen
gb_pr2: HSA132713	+	51.00	178.85	270	AJ132713 Homo sapiens HLA-B gen
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gb_pr2: HSA243433	+	51.00	178.85	270	AJ243433 Homo sapiens HLA-B gen
gb_pr2: HSA243737	+	51.00	178.85	270	AJ243737 Homo sapiens HLA-B gen
gb_pr2: HSA249317	+	51.00	178.85	270	AJ249317 Homo sapiens HLA-B gen
gb_pr2: HSB0801S1	+	51.00	178.85	270	U67330 Human MHC class I antige
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gb_pr2: HSB3511H1	+	51.00	178.85	270	U76394 Human HLA-B gene, allele
gb_pr2: HSB3901V1	+	51.00	178.85	270	U76396 Human HLA-B gene, allele
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gb_pr2: HSB40N1	+	51.00	178.85	270	AF008926 Homo sapiens MHC class
gb_pr2: HSB5001V1	+	51.00	178.85	270	U80670 Human class I MHC antige
gb_pr2: HSB5602S1	+	51.00	178.85	270	U90244 Human MHC class I antige
gb_pr2: HSHLAB60N1	+	51.00	178.85	270	U90244 Human MHC class I antige
gb_pr2: HSHLABM1	+	51.00	178.85	270	U90244 Human MHC class I antige
gb_pr2: HSHLABV01	+	51.00	178.85	270	U91330 Homo sapiens MHC class I
gb_pr2: HSHLABT1	+	51.00	178.85	270	U91330 Homo sapiens MHC class I

gb_pr2: HSHYUNAL + 51.00 178.85 0.0613 270 ! U52177 Human MHC class I ant
gb_pr2: HSU88249 + 51.00 178.85 0.0613 270 ! U88249 Human MHC class I HLA
gb_pr4: HUM31HLA1 + 51.00 178.85 0.0613 270 ! AF181842 Homo sapiens MHC cl

seq_name: gb_pr2: HSHLABK1

seq_documentation_block:
LOCUS HSHLABK1 243 bp DNA 26-MAR-1997
DEFINITION Human cell line THAI DCH022 MHC class I HLA-B gene (allele
HLA-B*1521), exon 2.

ACCESSION U91332
VERSION U91332.1 GI:1906671

KEYWORDS

SEGMENT

1 of 2

SOURCE

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;

Eutheria; Primates; Catarrhini; Homnidae; Homo.

1 (bases 1 to 243)

AUTHORS Chandanayingyong,D., Sirikong,M., Srinak,D., Longta,K.,

Rungroung,E. and Bejchandra,S.

B15 alleles (B*1521)

Unpublished

2 (bases 1 to 243)

AUTHORS Chandanayingyong,D., Sirikong,M., Srinak,D., Longta,K.,

Rungroung,E. and Bejchandra,S.

Direct Submission

TITLE Submitted (26-FEB-1997) Transfusion Medicine, Faculty of Medicine,

JOURNAL Siriraj Hospital, Mahidol University, Prannok Road, Bangkok 10700,

Thailand

FEATURES

source

1. 243

/organism="Homo sapiens"

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/map="6p21"

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BASE COUNT 53 a 79 c 83 g 28 t

ORIGIN

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Quality: 51.00 Length: 10
Ratio: 5.100 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

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US-08-653-294-24 x HSHLABK1 ..

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195 CGAGAGAGCTGCGGACCTGCGGCGCTAC 224

seq_name: gb_pr2: HSHLABM1

seq_documentation_block:
LOCUS HSHLABM1 243 bp DNA 26-MAR-1997
DEFINITION Human cell line THAI DCH023 MHC class I HLA-B gene (allele
HLA-B*1525), exon 2.

ACCESSION U91334

VERSION U91334.1 GI:1906675

KEYWORDS

1 of 2

SOURCE

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;

Eutheria; Primates; Catarrhini; Homnidae; Homo.

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alignment_block:
US-08-653-294-24 x HSHLAB01 ..

Align seg 1/1 to: HSHLAB01 from: 1 to: 243

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195 CGAGAGGCGCTGGGACCTGCGGCGCTAC 224

seq_name: gb_pr2:AF014769

seq_documentation_block:
LOCUS      AF014769      246 bp      DNA      PRI      27-AUG-1997
DEFINITION Homo sapiens MHC class I antigen HLA-B gene (HLA-B*1502 allele),
            exon 2 and partial cds.
ACCESSION      AF014769
VERSION      Submitted (18-JUL-1997) Transfusion Medicine, Faculty of Medicine,
            Siriraj Hospital, Mahidol University, Prannok Road, Bangkok 10700,
            Thailand
KEYWORDS
SOURCE      human.
ORGANISM      Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS      Chandanayingyong,D., Sirikong,M., Luangtrakool,K., Srinak,D.,
            Rungroung,E. and Bejchandra,S.
            B15 alleles (B*1502)
            Unpublished
TITLE      2 (bases 1 to 246)
REFERENCE
AUTHORS      Chandanayingyong,D., Sirikong,M., Luangtrakool,K., Srinak,D.,
            Rungroung,E. and Bejchandra,S.
            Direct Submission
TITLE      Submitted (18-JUL-1997) Transfusion Medicine, Faculty of Medicine,
            Siriraj Hospital, Mahidol University, Prannok Road, Bangkok 10700,
            Thailand
FEATURES
            Location/Qualifiers
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 BASE COUNT 55 a 81 c 82 g 28 t
 ORIGIN

alignment_scores:
 Quality: 51.00 Length: 10
 Ratio: 5.100 Gaps: 0
 Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
 US-08-653-294-24 x AF014769 ..
 Align seg 1/1 to: AF014769 from: 1 to: 246

1 ArgGluSerLeuArgAsnLeuArgGlyTyr 10
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 198 CGAGAGAGCCTGCGAACCTGCGGCGTAC 227

seq_name: gb_pr2:AF014771

seq_documentation_block:
 LOCUS AF014771 246 bp DNA PRI 27-AUG-1997
 DEFINITION Homo sapiens MHC class I antigen HLA-B gene (HLA-B*1502 allele),
 exon 2 and partial cds.

ACCESSION AF014771
 VERSION AF014771.1 GI:2345107

KEYWORDS
 SOURCE human.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 246)

AUTHORS Chandanayingyong,D., Sirikong,M., Luangtrakool,K., Srinak,D.,
 Rungroung,E. and Bejchandra,S.

TITLE B15 alleles (B*1502)
 JOURNAL Unpublished

REFERENCE 2 (bases 1 to 246)

AUTHORS Chandanayingyong,D., Sirikong,M., Luangtrakool,K., Srinak,D.,
 Rungroung,E. and Bejchandra,S.

TITLE Direct Submission
 JOURNAL Submitted (18-JUL-1997) Transfusion Medicine, Faculty of Medicine,
 Siriraj Hospital, Mahidol University, Prannok Road, Bangkok 10700,
 Thailand

FEATURES
 source Location/Qualifiers

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gene

exon

CDS

BASE COUNT 55 a 81 c 82 g 28 t
 ORIGIN

alignment_scores:
 Quality: 51.00 Length: 10
 Ratio: 5.100 Gaps: 0
 Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
 US-08-653-294-24 x AF014771 ..
 Align seg 1/1 to: AF014771 from: 1 to: 246

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 198 CGAGAGAGCCTGCGAACCTGCGGCGTAC 227

seq_name: gb_pr2:AF014773

seq_documentation_block:
 LOCUS AF014773 246 bp DNA PRI 27-AUG-1997
 DEFINITION Homo sapiens MHC class I antigen HLA-B gene (HLA-B*1502 allele),
 exon 2 and partial cds.

ACCESSION AF014773
 VERSION AF014773.1 GI:2345111

KEYWORDS

SOURCE human.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 246)

AUTHORS Chandanayingyong,D., Sirikong,M., Luangtrakool,K., Srinak,D.,
 Rungroung,E. and Bejchandra,S.

TITLE B15 alleles (B*1502)
 JOURNAL Unpublished

REFERENCE 2 (bases 1 to 246)

AUTHORS Chandanayingyong,D., Sirikong,M., Luangtrakool,K., Srinak,D.,
 Rungroung,E. and Bejchandra,S.

TITLE Direct Submission
 JOURNAL Submitted (18-JUL-1997) Transfusion Medicine, Faculty of Medicine,
 Siriraj Hospital, Mahidol University, Prannok Road, Bangkok 10700,
 Thailand

FEATURES
 source Location/Qualifiers

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gene

exon

CDS

BASE COUNT 55 a 81 c 82 g 28 t
 ORIGIN

alignment_scores:
 Quality: 51.00 Length: 10
 Ratio: 5.100 Gaps: 0
 Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:

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US-08-653-294-24 x AF014773
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198 CGAGAGACCTGCGGAACCTGCGGCGCTAC 227

seq_name: gb_pr2:AF014775
seq_documentation_block:
LOCUS AF014775 246 bp DNA 27-AUG-1997
DEFINITION Homo sapiens MHC class I antigen HLA-B gene (HLA-B*1502 allele),
exon 2 and partial cds.
ACCESSION AF014775
VERSION AF014775.1 GI:2345115
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 246)
AUTHORS Chandanayingyong,D., Sirikong,M., Luangtrakool,K., Srinak,D.,
Rungroung,E. and Bejchandra,S.
TITLE B15 alleles (B*1502)
JOURNAL Unpublished
REFERENCE
2 (bases 1 to 246)
AUTHORS Chandanayingyong,D., Sirikong,M., Luangtrakool,K., Srinak,D.,
Rungroung,E. and Bejchandra,S.
DIRECT SUBMISSION
TITLE Direct Submission
JOURNAL Submitted (18-JUL-1997) Transfusion Medicine, Faculty of Medicine,
Siriraj Hospital, Mahidol University, Prannok Road, Bangkok 10700,
Thailand

FEATURES
source
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BASE COUNT 55 a 81 c 82 g 28 t
ORIGIN

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Ratio: 5.100 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
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Align seg 1/1 to: AF014775 from: 1 to: 246

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198 CGAGAGACCTGCGGAACCTGCGGCGCTAC 227

seq_name: gb_pr2:AF014777
seq_documentation_block:
LOCUS AF014777 246 bp DNA 27-AUG-1997
DEFINITION Homo sapiens MHC class I antigen HLA-B gene (HLA-B*1502 allele),
exon 2 and partial cds.
ACCESSION AF014777
VERSION AF014777.1 GI:2345119
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 246)
AUTHORS Chandanayingyong,D., Sirikong,M., Luangtrakool,K., Srinak,D.,
Rungroung,E. and Bejchandra,S.
TITLE B15 alleles (B*1502)
JOURNAL Unpublished
REFERENCE
2 (bases 1 to 246)
AUTHORS Chandanayingyong,D., Sirikong,M., Luangtrakool,K., Srinak,D.,
Rungroung,E. and Bejchandra,S.
DIRECT SUBMISSION
TITLE Direct Submission
JOURNAL Submitted (18-JUL-1997) Transfusion Medicine, Faculty of Medicine,
Siriraj Hospital, Mahidol University, Prannok Road, Bangkok 10700,
Thailand

FEATURES
source
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ORIGIN

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Ratio: 5.100 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

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seq_name: gb_pr2:AF014779
seq_documentation_block:
LOCUS AF014779 246 bp DNA 27-AUG-1997
DEFINITION Homo sapiens MHC class I antigen HLA-B gene (HLA-B*1502 allele),
exon 2 and partial cds.

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VERSION        AF014779.1  GI:2345123
KEYWORDS
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ORGANISM       Homo sapiens
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               Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE      1 (bases 1 to 246)
AUTHORS       Chandanayingyong,D., Sirikong,M., Luangtrakool,K., Srinak,D.,
               Rungroung,E. and Bejchandra,S.
TITLE         B15 alleles (B*1502)
JOURNAL        Unpublished
REFERENCE      2 (bases 1 to 246)
AUTHORS       Chandanayingyong,D., Sirikong,M., Luangtrakool,K., Srinak,D.,
               Rungroung,E. and Bejchandra,S.
TITLE         Direct Submission
JOURNAL        Submitted (18-JUL-1997) Transfusion Medicine, Faculty of Medicine,
               Siriraj Hospital, Mahidol University, Prannok Road, Bangkok 10700,
               Thailand
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  Ratio: 5.100       Gaps: 0
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alignment_block:
US-08-653-294-24 x AF014779 ..
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seq_name: gb_pr2:AF014781
seq_documentation_block:
LOCUS      AF014781      246 bp      DNA      PRI      27-AUG-1997
DEFINITION Homo sapiens MHC class I antigen HLA-B gene (HLA-B*1502 allele),
            exon 2 and partial cds.
ACCESSION  AF014781
VERSION    AF014781.1  GI:2345131
KEYWORDS
SOURCE     human.
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1 (bases 1 to 246)
AUTHORS    Chandanayingyong,D., Sirikong,M., Luangtrakool,K., Srinak,D.,
            Rungroung,E. and Bejchandra,S.
TITLE      B15 alleles (B*1502)
JOURNAL     Unpublished
REFERENCE   2 (bases 1 to 246)
AUTHORS     Chandanayingyong,D., Sirikong,M., Luangtrakool,K., Srinak,D.,
            Rungroung,E. and Bejchandra,S.

```

TITLE
JOURNAL
Rungroung, E. and Bejchandra, S.
Direct Submission
Submitted (18-JUL-1997) Transfusion Medicine, Faculty of Medicine,
Siriraj Hospital, Mahidol University, Prannok Road, Bangkok 10700,
Thailand

FEATURES

source

Location/Qualifiers
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BASE COUNT 55 a 81 c 82 g 28 t
ORIGIN

alignment_scores:
Quality: 51.00 Length: 10
Ratio: 5.100 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:

US-08-653-294-24 x AF014783

Align seg 1/1 to: AF014783 from: 1 to: 246

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|||||
198 CGAGAGAGCTGCGGAACCTGCGGGCTAC 227

seq_name: gb_pr2:AF014785

seq_documentation_block:
LOCUS AF014785 250 bp DNA PRI 27-AUG-1997
DEFINITION Homo sapiens MHC class I antigen HLA-B gene (HLA-B*1525 allele),
exon 2 and partial cds.

ACCESSION AF014785

VERSION AF014785.1 GI:2345135

KEYWORDS

SOURCE human.

ORGANISM

Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 250)

AUTHORS Chananayong, D., Sirikong, M., Luangtrakool, K., Srinak, D.,

TITLE B15 alleles (B*1525)

JOURNAL Unpublished

REFERENCE 2 (bases 1 to 250)

AUTHORS Chananayong, D., Sirikong, M., Luangtrakool, K., Srinak, D.,

TITLE Rungroung, E. and Bejchandra, S.

JOURNAL Direct Submission

TITLE Submitted (18-JUL-1997) Transfusion Medicine, Faculty of Medicine,

JOURNAL Siriraj Hospital, Mahidol University, Prannok Road, Bangkok 10700,

Thailand

FEATURES

source

Location/Qualifiers
1. .250

gene
1. .250
/organism="Homo sapiens"
/db_xref="taxon:9606"
/cell_line="Thai DCH1109"
/chromosome="6"
/map="6p21"
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1. .250
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/allele="HLA-B*1525"
1. .250
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/protein_id="AAB67823.1"
/db_xref="GI:2345136"
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BASE COUNT 54 a 81 c 84 g 31 t
ORIGIN

alignment_scores:
Quality: 51.00 Length: 10
Ratio: 5.100 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:

US-08-653-294-24 x AF014785

Align seg 1/1 to: AF014785 from: 1 to: 250

1 ArgGlusSerLeuArgAsnLeuArgGlyTyr 10
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202 CGAGAGAGCTGCGGAACCTGCGGGCTAC 231

seq_name: gb_pr2:AF014787

seq_documentation_block:
LOCUS AF014787 250 bp DNA PRI 27-AUG-1997
DEFINITION Homo sapiens MHC class I antigen HLA-B gene (HLA-B*1525 allele),
exon 2 and partial cds.

ACCESSION AF014787

VERSION AF014787.1 GI:2345139

KEYWORDS

SOURCE human.

ORGANISM

Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 250)

AUTHORS Chananayong, D., Sirikong, M., Luangtrakool, K., Srinak, D.,

TITLE Rungroung, E. and Bejchandra, S.

JOURNAL Unpublished

REFERENCE 2 (bases 1 to 250)

AUTHORS Chananayong, D., Sirikong, M., Luangtrakool, K., Srinak, D.,

TITLE Direct Submission

JOURNAL Submitted (18-JUL-1997) Transfusion Medicine, Faculty of Medicine,

JOURNAL Siriraj Hospital, Mahidol University, Prannok Road, Bangkok 10700,

Thailand

FEATURES

source

Location/Qualifiers
1. .250

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/cell_line="Thai DCH3258"

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exon

CDS

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IEQEGPYWDRETOISKNTQTYRESLRLRGYNNQSEA"
BASE COUNT 54 a 81 c 84 g 31 t
ORIGIN

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Quality: 51.00 Length: 10
Ratio: 5.100 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
US-08-653-294-24 x AF014787 ..

Align seg 1/1 to: AF014787 from: 1 to: 250

1 ArgGluSerLeuArgAsnLeuArgGlyTyr 10
|||||
202 CGAGAGAGCTCGGAACTCGCGGCTAC 231

seq_name: gb_pr2:AF014789

seq_documentation_block:
LOCUS AF014789 250 bp DNA PRI 27-AUG-1997
DEFINITION Homo sapiens MHC class I antigen HLA-B gene (HLA-B*1525 allele),
exon 2 and partial cds.

ACCESSION AF014789
VERSION AF014789.1 GI:2345143
KEYWORDS
SOURCE human.

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 250)
AUTHORS Chandanayingyong,D., Sirikong,M., Luangtrakool,K., Srinak,D.,
Rungrong,E. and Bejchandra,S.

TITLE B15 alleles (B*1525)

JOURNAL Unpublished

REFERENCE 2 (bases 1 to 250)

AUTHORS Chandanayingyong,D., Sirikong,M., Luangtrakool,K., Srinak,D.,
Rungrong,E. and Bejchandra,S.

TITLE Direct Submission

JOURNAL Submitted (18-JUL-1997) Transfusion Medicine, Faculty of Medicine,
Siriraj Hospital, Mahidol University, Prannok Road, Bangkok 10700,
Thailand

FEATURES Location/Qualifiers

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/organism="Homo sapiens"
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/chromosome="6"
/map="6p21"
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1. .250

exon

/gene="HLA-B"
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/number=2
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CDS

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BASE COUNT 54 a 81 c 84 g 31 t
ORIGIN

alignment_scores:
Quality: 51.00 Length: 10
Ratio: 5.100 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
US-08-653-294-24 x AF014789 ..

Align seg 1/1 to: AF014789 from: 1 to: 250

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|||||
202 CGAGAGAGCTCGGAACTCGCGGCTAC 231

seq_name: gb_pr2:HSB1501N1

seq_documentation_block:
LOCUS HSB1501N1 254 bp DNA PRI 10-JUL-1996
DEFINITION Human MHC class I protein HLA-B heavy chain (B*1501new allele),
gene, partial exon 2.

ACCESSION U59965
VERSION U59965.1 GI:1399896
KEYWORDS HLA B antigen; major histocompatibility complex.
SEGMENT 1 of 2
SOURCE human.

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 254)
AUTHORS Mitsuishi,Y.

TITLE Direct Submission

JOURNAL Submitted (04-JUN-1996) Tissue Typing Laboratory, UCLA School of
Medicine, 950 Veteran Ave., Los Angeles, CA 90095, USA

FEATURES Location/Qualifiers

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1. .254
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/chromosome="6"
/map="6p21.3"
<1. .254
/gene="HLA-B"
/number=2
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BASE COUNT
ORIGIN

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Quality: 51.00 Length: 10
Ratio: 5.100 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
US-08-653-294-24 x HSB1501N1 ..

Align seg 1/1 to: HSB1501N1 from: 1 to: 254

1 ArgGluSerLeuArgAsnLeuArgGlyTyr 10
|||||
206 CGAGAGAGCTCGGAACTCGCGGCTAC 235

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OM of: US-08-653-294-24 to: N_Geneseq_36:* out_format : pfs
Date: Feb 8, 2000 7:31 PM
About: Results were produced by the GenCore software, version 4.5.
Copyright (c) 1993-2000 Compugen Ltd.

Command line parameters:

-MODEL=frame.p2n.model -DEV=xlp
-Q=/cgnl1/USFTO_spool/US08653294/runat_04022000_160701_15807/app_query.fasta.2
-DB=N_Geneseq_36 -OFRM=fastap -SURFIX=ring -GAPOP=12.000
-GAPEXT=4.000 -MINMATCH=0.100 -LOOPCL=0.000 -LOOPEXT=0.000
-GAPOP=4.500 -GAPEXT=0.050 -XGAPOP=10.000 -XGAPEXT=0.500
-GAPOP=6.000 -GAPEXT=7.000 -XGAPOP=10.000 -XGAPEXT=0.500
-DELOP=6.000 -DELEXT=7.000 -START=1 -MATRIX=blotsum62
-TRANS=human40.cdi -LISN=45 -DOCALIGN=200 -THR_SCORE=pct
-ALIGN=15 -MODE=LOCAL -OUTFMT=pfs -NORM=ext -MINLEN=0
-MAXLEN=1000000 -USER=US08653294 -NCPU=6 -ICPU=3 -NO_XLPXY -WAIT
-THREADS=1

Search information block:

Query: US-08-653-294-24
Query length: 10
Database: N_Geneseq_36:*
Database sequences: 311585
Database length: 125096042
Search time (sec): 873.190000

score_list:

Sequence	Strid	Orig	zScore	Escore	Len	Documentation
N_Geneseq_36:Q12115	+	51.00	169.52	0.0767	1089	HLA-B35 exon ...
N_Geneseq_36:Q75974	+	51.00	157.69	0.3497	4059	HLA-B7 expression vector. New
N_Geneseq_36:Q75973	+	51.00	155.88	0.4411	4965	HLA-B7/beta-2 microglobulin e
N_Geneseq_36:Q12116	+	44.00	143.58	2.14	1101	HLA-C exon Cb-1. HLA-C gene, D
N_Geneseq_36:Q12117	+	44.00	143.58	2.14	1101	HLA-C exon Cb-2. HLA-C gene, D
N_Geneseq_36:X22446	+	39.00	123.46	28.18	1323	Human CPM2 DNA. New chemprot
N_Geneseq_36:X22450	+	39.00	123.46	28.21	1324	Human CPM2 mutant DNA. New ch
N_Geneseq_36:T32217	+	38.00	118.70	51.91	1490	Acyl-ACP-thioesterase coding s
N_Geneseq_36:T32447	+	38.00	117.74	58.75	1859	Rat truncated rSK3 coding sequ
N_Geneseq_36:T35458	+	38.00	117.65	59.37	1874	Truncated human hSK3 coding se
N_Geneseq_36:T35472	+	38.00	115.10	82.38	2224	Rat rSK3 coding sequence. DNA
N_Geneseq_36:T35473	+	38.00	114.19	92.63	2462	Human hSK3 coding sequence. DN
N_Geneseq_36:X08414	+	38.00	113.97	95.20	2521	Human small conductance calciu
N_Geneseq_36:X41493	+	37.00	126.48	19.13	416	Human secreted protein 5' EST
N_Geneseq_36:T30458	+	37.00	76.32	1.2e+04	110000	Rhizobium species plasmid p
N_Geneseq_36:T30459	+	37.00	76.32	1.2e+04	110000	Rhizobium species symbiotic
N_Geneseq_36:Q11953	+	35.00	120.86	39.35	342	Anti-human Rhd BRAD-3 MAB (VH
N_Geneseq_36:N91381	+	35.00	120.76	39.88	346	Intron 2 from human follistatin
N_Geneseq_36:Q56202	+	35.00	105.64	277.17	1858	Partial coding sequence of sal
N_Geneseq_36:Q30126	+	35.00	105.64	277.17	1858	Plasmid pCK1 SABP cDNA insert.
N_Geneseq_36:T38418	+	35.00	105.64	277.17	1858	pCK1 cDNA insert encoding sal
N_Geneseq_36:Q94624	+	35.00	99.84	583.35	3342	Brush-1 cDNA probe. New cDNA s
N_Geneseq_36:T15158	+	35.00	98.12	726.84	4286	CDK41 cyclin-dependent kinase-
N_Geneseq_36:Q34625	+	35.00	97.97	741.13	4359	Brush-1 cDNA. New cDNA sequen
N_Geneseq_36:X33449	+	35.00	97.44	793.74	4626	Oryza sativa L. pistil specifi
N_Geneseq_36:T59528	+	34.00	113.84	96.79	4955	Human secreted protein gene 18
N_Geneseq_36:N91608	+	34.00	107.13	228.91	1044	Insert of pCCA10 encoding carb
N_Geneseq_36:Q52673	+	34.00	105.57	279.97	1242	HTLE receptor DNA. Stably co-t
N_Geneseq_36:Q47076	+	34.00	104.68	313.43	1371	B. canis 21B4/rhoxyr antigen
N_Geneseq_36:V01731	+	34.00	100.81	514.80	2108	Mouse liver cancer-originated
N_Geneseq_36:Q43711	+	34.00	99.41	616.03	2463	Sequence of the human gene 5-H
N_Geneseq_36:X13139	+	34.00	85.96	3.5e+03	10996	Enterococcus faecalis genome
N_Geneseq_36:X13401	+	34.00	85.93	3.5e+03	10936	Enterococcus faecalis genome
N_Geneseq_36:T12120	+	34.00	70.94	2.3e+04	58407	Methanococcus jannaschii larg
N_Geneseq_36:X20248	+	34.00	65.25	4.7e+04	110000	Continuation (8 of 10) of
N_Geneseq_36:T54815	+	33.00	139.96	3.40	18	Human leukocyte antigen class I
N_Geneseq_36:T42475	+	33.00	123.93	26.56	107	Hunt1 coding sequence. Hunt1 an
N_Geneseq_36:Q72980	+	33.00	120.03	43.77	165	Huntingtin gene antisense produ
N_Geneseq_36:X23425	+	33.00	107.02	232.16	701	Mouse TRNL3 DNA. New Tumor Necr
N_Geneseq_36:T69757	+	33.00	106.47	249.05	745	Isopentenyl transferase ipt gen
N_Geneseq_36:V18599	+	33.00	102.43	418.34	1168	Mus musculus tumour necrosis f

N_Geneseq_36:V43032 + 33.00 101.43 475.43 1305 ! Streptococcus pneumoniae po
N_Geneseq_36:V32620 - 33.00 101.11 495.66 1353 ! Genomic DNA sequence of Str
N_Geneseq_36:Q80003 - 33.00 98.73 672.62 1763 ! ADP-glucose-prophosphoryla
N_Geneseq_36:V29686 + 33.00 95.40 1.0e+03 2553 ! A. thermophilum thermostabi

seq_name: N_Geneseq_36:Q12115

seq_documentation_block:

ID Q12115 standard; DNA; 1089 BP.
AC Q12115;
DT 29-AUG-1991 (first entry)
DE HLA-B35 exon.
KW Human leukocyte antigen; probe; major histocompatibility complex;
KW MHC; class I; ss.
OS Homo sapiens.
FH Key Location/Qualifiers
FT cds 1..1089
FT /tag= a
PN J03112486-A.
PD 14-MAY-1991.
PF 22-SEP-1989; 247697.
PR 22-SEP-1989; JP-247697.
PA (OLYU) OLYMPUS OPTICAL KK.
DR WPI; 91-182991/25.
DR P-PSDB; R12464.
PT HLA-B35 gene - used in DNA probe and transformant cells for
PT immunising animals, for developing monoclonal antibody.
PS Claim 1; Page 1; lipp; Japanese.
CC Probes comprising part of the sequence can be used to identify
CC class I genes. The DNA can be expressed for immunisation of
CC animals and prodn. of monoclonal antibodies specific for the
CC HLA-B35 antigen. See also J03112485 and J03112487.
SQ Sequence 1089 BP; 221 A; 336 C; 359 G; 173 T;

alignment_scores:

Quality: 51.00 Length: 10
Ratio: 5.100 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:

US-08-653-294-24 x Q12115 ..
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1 ArgGluSerLeuArgAsnLeuArgGlyTyr 10
295 CGAGAGAGCCTCGGAACCTCGCGGCTAC 324

seq_name: N_Geneseq_36:Q75974

seq_documentation_block:

ID Q75974 standard; cDNA; 4059 BP.
AC Q75974;
DT 23-AUG-1995 (first entry)
DE PHLA-B7 expression vector.
KW expression vector; PHLA-B7; heavy human HLA-B7; bicistronic mRNA;
KW light beta-2 microglobulin; class I major histocompatibility complex;
KW MHC; human leukocyte antigen; HLA; covalently closed circular DNA; ds.
OS Synthetic.
FH Key Location/Qualifiers
FT misc_feature 1..354
FT /tag= a
FT /note= "pBR322 backbone contg. bacterial origin of
FT replication"
FT 355..1170
FT /tag= b
FT /note= "kanamycin resistance gene open reading frame;
FT the gene is taken from the transposable element
FT Tn903"
FT polyA_signal complement (1410..1177)
FT /tag= c
FT /note= "SV40 polyA signal sequence"

FT intron complement (1412..1560)
 FT /tag= d
 FT /note= "SV40 small t intron"
 FT 3'utr complement (1561..1794)
 FT /tag= e
 FT /note= "3' untranslated region of HLA-B7
 FT heavy chain mRNA"
 FT cds complement (1795..2880)
 FT /tag= f
 FT /note= "HLA-B7 open reading frame"
 FT ltr complement (2886..3415)
 FT /tag= g
 FT /note= "Rous sarcoma virus 3' LTR promoter region"
 FT misc_feature 3416..4059
 FT /tag= h
 FT /note= "pBR322 backbone"
 FT W09429469-A.
 PD 22-DEC-1994.
 PF 27-MAY-1994; U06069.
 PR 07-JUN-1993; US-074344.
 PA (UNMI) UNIV MICHIGAN.
 PA (VICA-) VICAL INC.
 PI Lew D, Marquet M, Nabel EG, Nabel GJ;
 DR WPI; 95-036494/05.
 PT New vectors for gene therapy, partic for tumours - comprising
 PT genetic material encoding one or more cistron(s) which express
 PT immunogenic or therapeutic peptide(s)
 PS Claim 9; Page 42-43; 50pp; English.
 CC This HLA-B7 antigen encoding plasmid was developed to incorporate many
 CC advantageous features, eg. the kanamycin resistance gene. The
 CC eradication of two open reading frames encoding portions of SV40 viral
 CC proteins lowers the risk of tumorigenicity. The vector may also operate
 CC as a cassette into which cistrons may be inserted and removed at will
 CC for the transcription and subsequent translation of peptides of interest.
 CC The vector is used partic. for the treatment of neoplastic disease,
 CC eg. melanoma, and provides enhanced gene delivery and expression
 CC in vivo.
 SQ Sequence 4059 BP; 975 A; 1051 C; 1033 G; 1000 T;

alignment_scores:
 Quality: 51.00 Length: 10
 Ratio: 5.100 Gaps: 0
 Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
 US-08-653-294-24 x Q75974/rev ..
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 2589 CGAGAGACCTGCGGAACTGCGGGCTAC 2560

seq_name: N_Geneseq_36:Q75973
 seq_documentation_block:
 ID Q75973 standard; cDNA; 4965 BP.
 AC Q75973;
 DT 23-AUG-1995 (first entry)
 DE pHLA-B7/beta-2 microglobulin expression vector.
 KW expression vector; pHLA-B7/beta-2 microglobulin; heavy human HLA-B7;
 KW light beta-2 microglobulin; class I major histocompatibility complex;
 KW MHC; bicistronic mRNA; human leukocyte antigen; HLA;
 KW covalently closed circular DNA; ds.
 OS Synthetic.
 FH Key Location/Qualifiers
 FT 1..529
 FT ltr /tag= a
 FT /note= "Rous sarcoma virus LTR promoter domain, derived
 FT for the Schmidt-Rupin strain nucleotides
 FT 8673-9146. This region also includes a 56 bp
 FT region of a synthetic oligonucleotide which

FT modifies this regulatory sequence to effect a
 FT higher level of expression of downstream
 FT sequences. The oligonucleotide removes a
 FT polyadenylation signal sequence originally found
 FT in the RSV DNA sequence."
 FT misc_signal 531..534
 FT /tag= b
 FT /label= consensus_kozak_signal_sequence
 FT cds 535..1620
 FT /tag= c
 FT /note= "HLA-B7 heavy chain open reading frame"
 FT signal_peptide 535..606
 FT /tag= d
 FT /note= "encodes putative signal peptide of the
 FT HLA-B7 heavy chain"
 FT mat_peptide 607..1620
 FT /tag= e
 FT /note= "encodes putative HLA-B7 heavy chain mature
 FT peptide"
 FT 3'utr 1621..1853
 FT /tag= f
 FT /note= "3' untranslated sequence of HLA-B7 heavy
 FT chain mRNA"
 FT misc_feature 1854..1888
 FT /tag= g
 FT /note= "Multiple cloning site, forms a junction
 FT between the HLA-B7 sequence and the EMCV-CITE
 FT sequence, and is used to facilitate subcloning"
 FT rbs 1889..2479
 FT /tag= h
 FT /note= "murine encephalomyocarditis CAP-independent
 FT translational enhancer (EMCV-CITE); taken from
 FT nucleotides 255-843 of cloned EMCV genomic DNA.
 FT It is a non-coding regulatory sequence functioning
 FT as an internal entry point for the eukaryotic
 FT ribosomal subunits when located within a mRNA
 FT mol. . It enables the translational start codon of
 FT the beta-2 microglobulin, downstream of the HLA-B7
 FT stop codon on this bicistronic mRNA to be
 FT recognised by the ribosome"
 FT cds 2480..2839
 FT /tag= i
 FT /note= "encodes beta-2 microglobulin; this cDNA is
 FT deriv. from chimpanzee (differs to the human
 FT cDNA by only 4 bases)"
 FT 3'utr 2840..2846
 FT /tag= j
 FT /note= "3' untranslated region of the beta-2
 FT microglobulin mRNA"
 FT misc_feature 2847..2870
 FT /tag= k
 FT /note= "synthetic linker"
 FT 3'utr .3111
 FT /tag= l
 FT /note= "Bovine growth hormone 3'UTR and transcriptional
 FT terminator; it starts at a blunt-ended BglI site
 FT within the 3'UTR of the mRNA coding sequence"
 FT polya_signal 2979..2984
 FT /tag= m
 FT misc_feature 3112..3151
 FT /tag= n
 FT /note= "Synthetic linker to facilitate cloning"
 FT complement (3151..3967)
 FT cds /tag= o
 FT /note= "Kanamycin resistance gene open reading frame;
 FT the gene is taken from the transposable element
 FT Tn903"
 FT misc_feature 4014..4965
 FT /tag= p
 FT /note= "pBR322 backbone contg. bacterial origin of
 FT replication, it represents nucleotides 2244-3193"
 FT W09429469-A.
 PD 22-DEC-1994.


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FT FT WO9859055-A2. /*tag- a
PN /product= "CPRM2"
PD
PF 30-DEC-1998.
PR 24-JUN-1998; D01796.
PA (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.
PI Praml C, Schwab M;
DR WPI: 99-081282/07.
DR P-PSDB: W93087.
PT New chemoprotector regulated modifier proteins - useful in the
PT detoxification of metabolites, particularly aflatoxins
PS Claim 2; Fig 8; 31pp; German.
CC This sequence encodes a novel protein designated CPRM2 (chemoprotector
CC regulated modifier) that inhibits the effects of genotoxic and/or
CC cytotoxic substances. The invention describes the isolation of CPRM1,
CC CPRM2, CPRM3, mCPRM1, allele s, and mCPRM1, allele r. Transformants
CC containing such proteins are used to produce recombinant proteins and
CC nucleic acids for use in gene therapy and to raise antibodies which are
CC used to (i) detoxify geno- and/or cyto-toxic metabolites and (ii) detect
CC presence of CPRM proteins (or nucleic acid encoding them, including
CC detection of mutations indicative of increased risk of cancer, e.g.
CC prenatal). The proteins can be used to eliminate carcinogenic
CC aflatoxins and to treat neurodegeneration, e.g. Alzheimer's disease,
CC associated with production of malondialdehyde, a toxic product or the
CC cyclo-oxygenase reaction and prostaglandin metabolism.
SQ Sequence 1323 BP; 331 A; 368 C; 338 G; 286 T;

alignment_scores:
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Ratio: 4.333 Gaps: 0
Percent Similarity: 90.000 Percent Identity: 70.000

alignment_block:
US-08-653-294-24 x X22446/rev ..
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1058 AAGAAGAGTGTGAGAAACAAAGAGGTTAC 1029

seq_name: N_Geneseq_36:X22450

seq_documentation_block:
ID X22450 standard; DNA; 1324 BP.
AC X22450;
DT 20-MAY-1999 (first entry)
DE Human CPRM2 mutant DNA.
KW CPRM1; mouse: chemoprotector regulated modifier; genotoxin; cytotoxin;
KW CPRM2; CPRM3; mCPRM1; allele s; allele r; gene therapy; antibody;
KW detoxification; detection; mutant; cancer; carcinogenic; aflatoxin;
KW treatment; neurodegeneration; Alzheimer's disease; malondialdehyde;
KW cyclo-oxygenase reaction; prostaglandin metabolism; ss.
OS Homo sapiens.
FH Key Location/Qualifiers
FT CDS
FT 74..223
FT /*tag- a
FT /product= "CPRM2 mutant"

PN FT WO9859055-A2.
PD 30-DEC-1998.
PF 24-JUN-1998; D01796.
PR 24-JUN-1997; DE-026823.
PA (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.
PI Praml C, Schwab M;
DR WPI: 99-081282/07.
DR P-PSDB: W93091.
PT New chemoprotector regulated modifier proteins - useful in the
PT detoxification of metabolites, particularly aflatoxins
PS Disclosure; Fig 12; 31pp; German.
CC This sequence encodes a novel protein designated CPRM2 which is a mutant

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CC chemoprotector regulated modifier that inhibits the effects of
CC genotoxic and/or cytotoxic substances. The invention describes the
CC isolation of CPRM1, CPRM2, CPRM3, mCPRM1, allele s, and mCPRM1,
CC allele r. Transformants containing such proteins are used to produce
CC recombinant proteins and nucleic acids for use in gene therapy and to
CC raise antibodies which are used to (i) detoxify geno- and/or cyto-toxic
CC metabolites and (ii) detect presence of CPRM proteins (or nucleic acid
CC encoding them, including detection of mutations indicative of increased
CC risk of cancer, e.g. prenatal). The proteins can be used to eliminate
CC carcinogenic aflatoxins and to treat neurodegeneration, e.g. Alzheimer's
CC disease, associated with production of malondialdehyde, a toxic product
CC or the cyclo-oxygenase reaction and prostaglandin metabolism.
SQ Sequence 1324 BP; 332 A; 368 C; 338 G; 286 T;

alignment_scores:
Quality: 39.00 Length: 10
Ratio: 4.333 Gaps: 0
Percent Similarity: 90.000 Percent Identity: 70.000

alignment_block:
US-08-653-294-24 x X22450/rev ..
Align seg 1/1 to reverse of: X22450 from: 1 to: 1324

1 ArgGluSerLeuArgAsnLeuArgGlyTyr 10
:::|||||:|||||: |||||
1059 AAGAAGAGTGTGAGAAACAAAGAGGTTAC 1030

seq_name: N_Geneseq_36:T32217

seq_documentation_block:
ID T32217 standard; cDNA to mRNA; 1490 BP.
AC T32217;
DT 07-FEB-1997 (first entry)
DE Acyl-ACP-thioesterase coding sequence.
KW Acyl-ACP-thioesterase; AAT; cuphea leptopoda; aliphatic acid synthesis;
KW middle chain aliphatic acid; ss.
OS Cuphea leptopoda hemsl.
FH Key Location/Qualifiers
FT CDS
FT 30..1289
FT /*tag- a
FT /product= Acyl-ACP-thioesterase

PN J08173165-A.
PD 09-JUL-1996.
PF 22-DEC-1994; 320547.
PR 22-DEC-1994; JP-320547.
PA (NORO ) NORINSUISANSHO CHUGOKU NOGYO SHIKENBACH.
DR WPI: 96-365584/37.
DR P-PSDB: W02020.
PT DNA encoding Cuphea leptopoda hemsl. acyl-ACP-thio:esterase - for
PT synthesis of middle chain aliphatic acids, useful in pharmaceutical
PT preps. and foods
PS Claim 2; Page 6; 7pp; Japanese.
CC This sequence represents the coding sequence for the Cuphea leptopoda
CC acyl-ACP-thioesterase (AAT). This sequence was isolated by synthesizing
CC a AAT cDNA, and using that sequence to probe for a fragment of the AAT
CC gene (see T32217). The isolated fragment was then used to isolate the
CC AAT gene, which was then amplified. AAT is a key enzyme in the synthesis
CC of middle chain aliphatic acids, and as such is useful in pharmaceutical
CC preparations, and foods.
SQ Sequence 1490 BP; 351 A; 332 C; 402 G; 405 T;

alignment_scores:
Quality: 38.00 Length: 9
Ratio: 4.222 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 66.667

alignment_block:
US-08-653-294-24 x T32217/rev ..
Align seg 1/1 to reverse of: T32217 from: 1 to: 1490

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2 GluSerLeuArgAsnLeuArgGlyTyr 10
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1472 AATCAATCCGGAACATGCGAGGATAC 1446

seq_name: N_Geneseq_36:V35447

seq_documentation_block:
ID V35447 standard; CDNA; 1659 BP.
AC V35447;
DT 01-OCT-1998 (first entry)
DE Rat truncated rSK3 coding sequence.
KW Small conductance calcium-activated potassium channel protein 1;
KW rSK3; rat; potassium ion flux; ss.
OS Rattus sp.
PN WO9811139-A1.
PD 19-MAR-1998.
PF 10-SEP-1997; U16033.
PR 17-APR-1997; US-045233.
PR 11-SEP-1996; US-026451.
PR 07-MAR-1997; US-040052.
PA (ICAG-) ICAGEN INC.
PA (UYOR-) UNIV OREGON HEALTH SCI.
PI Adelman JP, Bond CT, Maylie J, Silvia CP;
DR WPI: 98-207332/18.
DR P-PSDB; W63703.
PT DNA encoding calcium-activated potassium channel - useful in assays
PT to identify compounds which increase or decrease potassium ion flux
PS Claim 3; Page 105; 151pp; English.
CC This sequence encodes the rat small conductance calcium-activated
CC potassium channel protein 3 (rSK3) of the invention. The proteins of the
CC invention are monomers of a calcium-activated potassium channel, where
CC the monomer: (i) has a calculated molecular weight of between 40 and
CC 80 kDa; and (ii) has a unit conductance of between 2 and 60 pS when the
CC monomer is in the functional polymeric form of a potassium chain and is
CC expressed in a Xenopus oocyte. Antibodies specific for the protein, and
CC probes specific for the DNA can be used to detect the presence of the
CC protein or DNA sequences in a sample. Host cells expression of the
CC protein can be used in assays to identify compounds which increase or
CC decrease the potassium ion flux through the protein. The transfected host
CC cell can also be used for the recombinant production of the protein. The
CC DNA sequences can also be used for determine mutations in the SK and IK
CC genes in a computer system. The proteins encoded by the SK and IK genes
CC can be used in a computer system for determining their three dimensional
CC structure, which is useful for determining ligands that bind to the
CC proteins.
SQ Sequence 1659 BP; 404 A; 499 C; 398 G; 358 T;

alignment_scores:
Quality: 38.00 Length: 10
Ratio: 3.800 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 70.000

alignment_block:
US-08-653-294-24 x V35447/rev ..
Align seg 1/1 to reverse of: V35447 from: 1 to: 1659

1 ArgGluSerLeuArgAsnLeuArgGlyTyr 10
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62 CGAGAGCGCTGAGCGGCTGAGGGGCTTC 33

seq_name: N_Geneseq_36:V35458

seq_documentation_block:
ID V35458 standard; CDNA; 1674 BP.
AC V35458;
DT 01-OCT-1998 (first entry)
DE Truncated human hSK3 coding sequence.
KW Small conductance calcium-activated potassium channel protein 3;
KW hSK3; human; potassium ion flux; ss.
OS Homo sapiens.

alignment_scores:
Quality: 38.00 Length: 10
Ratio: 3.800 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 70.000

alignment_block:
US-08-653-294-24 x V35447/rev ..
Align seg 1/1 to reverse of: V35447 from: 1 to: 1659

1 ArgGluSerLeuArgAsnLeuArgGlyTyr 10
|||||:|||||:|||||:|||||:
62 CGAGAGCGCTGAGCGGCTGAGGGGCTTC 33

seq_name: N_Geneseq_36:V35458

seq_documentation_block:
ID V35458 standard; CDNA; 1674 BP.
AC V35458;
DT 01-OCT-1998 (first entry)
DE Truncated human hSK3 coding sequence.
KW Small conductance calcium-activated potassium channel protein 3;
KW hSK3; human; potassium ion flux; ss.
OS Homo sapiens.

alignment_scores:
Quality: 38.00 Length: 10
Ratio: 3.800 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 70.000

alignment_block:
US-08-653-294-24 x V35458/rev ..
Align seg 1/1 to reverse of: V35458 from: 1 to: 1674

1 ArgGluSerLeuArgAsnLeuArgGlyTyr 10
|||||:|||||:|||||:|||||:
62 CGGAGGCGCTGAGCGGCTGAGGGGCTTC 33

seq_name: N_Geneseq_36:V35472

seq_documentation_block:
ID V35472 standard; CDNA; 2224 BP.
AC V35472;
DT 01-OCT-1998 (first entry)
DE Rat rSK3 coding sequence.
KW Small conductance calcium-activated potassium channel protein 3;
KW rSK3; rat; potassium ion flux; ss.
OS Rattus sp.
FH Key Location/Qualifiers
FT CDS 2..2200
FT /tag= a
PN WO9811139-A1.
PD 19-MAR-1998.
PF 10-SEP-1997; U16033.
PR 17-APR-1997; US-045233.
PR 11-SEP-1996; US-026451.
PR 07-MAR-1997; US-040052.
PA (ICAG-) ICAGEN INC.
PA (UYOR-) UNIV OREGON HEALTH SCI.
PI Adelman JP, Bond CT, Maylie J, Silvia CP;
DR WPI: 98-207332/18.
DR P-PSDB; W63715.
PT DNA encoding calcium-activated potassium channel - useful in assays

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PT to identify compounds which increase or decrease potassium ion flux
PS Claim 3; Page 123-124; 151pp; English.
CC This sequence encodes the rat small conductance calcium-activated
CC potassium channel protein 3 (rSK3) of the invention. The proteins of the
CC invention are monomers of a calcium-activated potassium channel, where
CC the monomer: (i) has a calculated molecular weight of between 40 and
CC 80 kDa; and (ii) has a unit conductance of between 2 and 60 pS when the
CC monomer is in the functional polymeric form of a potassium chain and is
CC expressed in a Xenopus oocyte. Antibodies specific for the protein, and
CC probes specific for the DNA can be used to detect the presence of the
CC protein or DNA sequences in a sample. Host cells expression of the
CC protein can be used in assays to identify compounds which increase or
CC decrease the potassium ion flux through the protein. The transfected host
CC cell can also be used for the recombinant production of the protein. The
CC DNA sequences can also be used for determine mutations in the SK and IK
CC genes in a computer system. The proteins encoded by the SK and IK genes
CC can be used in a computer system for determining their three dimensional
CC structure, which is useful for determining ligands that bind to the
CC proteins.
SQ Sequence 2224 BP; 531 A; 711 C; 537 G; 445 T;

alignment_scores:
Quality: 38.00 Length: 10
Ratio: 3.800 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 70.000

alignment_block:
US-08-653-294-24 x V35472/rev ..
Align seg 1/1 to reverse of: V35472 from: 1 to: 2224

1 ArgGluSerLeuArgAsnLeuArgGlyTyr 10
|||||:|||||:|||||:|||||:|||||:|
588 CGAGAGGCGCTGAGCGGCTGAGGGGCTTC 559

seq_name: N_Geneseq_36:V35473

seq_documentation_block:
ID V35473 standard; cDNA; 2462 BP.
AC V35473;
DT 01-OCT-1998 (first entry)
DE Human hsk3 coding sequence.
KW Small conductance calcium-activated potassium channel protein 3;
KW hSK3; human; potassium ion flux; ss.
OS Homo sapiens.
FH Key Location/Qualifiers
FT CDS 252..2462
FT /*tag= a
FT WO9811139-A1.
PD 19-MAR-1998.
PF 10-SEP-1997; U16033.
PR 17-APR-1997; US-045233.
PR 11-SEP-1996; US-026451.
PR 07-MAR-1997; US-040052.
PA (ICAG-) ICAGEN INC.
PA (UYOR-) UNIV OREGON HEALTH SCI.
PI Adelman JP, Bond CT, Maylie J, Silvia CP;
DR WPI: 98-207332/18.
DR P-PSDB: W63717.
PT DNA encoding calcium-activated potassium channel - useful in assays
PT to identify compounds which increase or decrease potassium ion flux
PS Claim 3; Page 128-129; 151pp; English.
CC This sequence encodes the human small conductance calcium-activated
CC potassium channel protein 3 (hSK3) of the invention. The proteins of the
CC invention are monomers of a calcium-activated potassium channel, where
CC the monomer: (i) has a calculated molecular weight of between 40 and
CC 80 kDa; and (ii) has a unit conductance of between 2 and 60 pS when the
CC monomer is in the functional polymeric form of a potassium chain and is
CC expressed in a Xenopus oocyte. Antibodies specific for the protein, and
CC probes specific for the DNA can be used to detect the presence of the
CC protein or DNA sequences in a sample. Host cells expression of the
CC protein can be used in assays to identify compounds which increase or

CC decrease the potassium ion flux through the protein. The transfected host
CC cell can also be used for the recombinant production of the protein. The
CC DNA sequences can also be used for determine mutations in the SK and IK
CC genes in a computer system. The proteins encoded by the SK and IK genes
CC can be used in a computer system for determining their three dimensional
CC structure, which is useful for determining ligands that bind to the
CC proteins.
SQ Sequence 2462 BP; 552 A; 814 C; 617 G; 479 T;

alignment_scores:
Quality: 38.00 Length: 10
Ratio: 3.800 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 70.000

alignment_block:
US-08-653-294-24 x V35473/rev ..
Align seg 1/1 to reverse of: V35473 from: 1 to: 2462

1 ArgGluSerLeuArgAsnLeuArgGlyTyr 10
|||||:|||||:|||||:|||||:|||||:|
850 CGGAGGCGCTGAGCGGCTGAGGGGCTTC 821

seq_name: N_Geneseq_36:X08414

seq_documentation_block:
ID X08414 standard; cDNA; 2521 BP.
AC X08414;
DT 28-JUN-1999 (first entry)
DE Human small conductance calcium activated potassium channel gene.
KW Human small conductance calcium activated potassium channel;
KW hKCa3/KCNN3; bipolar disease; schizophrenia; treatment; diagnosis;
KW detection; transgenic animal; gene therapy;
KW neuropsychiatric disorder; neurological disorder;
KW neuromuscular disorder; immunological disorder; ss.
OS Homo sapiens.
FH Key Location/Qualifiers
FT CDS 287..2482
FT /*tag= a
FT /*product= "Small conductance calcium activated
FT potassium channel polypeptide"
FT polyA_signal 2482..2487
FT /*tag= b
FT /*label= Poly-A signal
FT polyA_site 2509..2521
FT /*tag= c
FT /*label= Poly-A region
FT WO9903889-A1.
PN 28-JAN-1999.
PD 14-JUL-1998; U14902.
PF 08-JAN-1998; US-070741.
PR 15-JUL-1997; US-052556.
PA (REGC) UNIV CALIFORNIA.
PA Chandy KG, Fantino E, Gargus JJ, Gutman G, Kalman K;
PI WPI: 99-132165/11.
DR P-PSDB: W96312.
DR New human small conductance calcium activated potassium channel-3 -
PT useful for diagnosis, treatment and prevention of particularly
PT schizophrenia and bipolar disorders
PS Claim 3; Figure 5; 95pp; English.
CC Disorders associated with a dysfunctional or altered small
CC conductance calcium-activated potassium channel-3 (hKCa3/KCNN3)
CC comprise neuropsychiatric, neurological, neuromuscular and
CC immunological disorders, specifically bipolar disease and
CC schizophrenia. Transgenic animals comprising the hKCa3/KCNN3 gene
CC as a transgene in their somatic and germ cell lines can be used
CC as models for studying these conditions and their treatments.
CC Antibodies (Ab) directed against the hKCa3/KCNN3 polypeptide
CC or conservative variants of the polypeptide can be used to detect
CC those at risk from these disorders and also in therapy against
CC such disorders. Use of the wild type gene in gene therapy to treat
CC these disorders is also contemplated.


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FT FT /tag= k
FT FT /standard_name= "ORF K11"
FT FT /product= "protein of unknown function"
FT FT /note= "homologous to the FixU gene"
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FT FT /standard_name= "ORF K12"
FT FT /product= "protein of unknown function"
FT CDS complement (434517..434711)
FT FT /tag= m
FT FT /standard_name= "ORF K13"
FT FT /product= "ferrodoxin/ferrodoxin-like protein"
FT FT /note= "homologous to the FdxN gene"
FT CDS complement (434753..436234)
FT FT /tag= n
FT FT /standard_name= "ORF K14"
FT FT /gene= "nifB"
FT FT /product= "protein involved in FeMo co-factor biosynthesis"
FT CDS complement (436460..438130)
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FT FT /standard_name= "ORF K15"
FT FT /gene= "nifA"
FT FT /product= "positive regulator of nif, fix and other genes"
FT CDS complement (438297..438590)
FT FT /tag= p
FT FT /standard_name= "ORF K16"
FT FT /gene= "fixX"
FT FT /product= "protein required for nitrogenase activity"
FT CDS complement (438605..439912)
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FT FT /standard_name= "ORF K17"
FT FT /gene= "fixC"
FT FT /product= "protein required for nitrogenase activity"
FT CDS complement (439923..441032)
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FT FT /standard_name= "ORF K18"
FT FT /gene= "fixB"
FT FT /product= "protein required for nitrogenase activity"
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FT FT /standard_name= "ORF K19"
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FT FT /note= "homologous to the DctAI gene"
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FT FT /note= "homologous to the CamC gene"
FT CDS complement (447844..448500)
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FT FT /product= "gamma-hexachlorocyclohexane-dechlorinase-like

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FT FT /product= "putative protein with degradative function"
FT CDS complement (450341..451396)
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FT FT /standard_name= "ORF L4"
FT FT /product= "luciferase alpha-subunit-like protein"
FT FT /note= "homologous to the LuxA gene"
FT CDS complement (452980..454494)
FT FT /tag= ab
FT FT /standard_name= "ORF L6"
FT FT /gene= "nifD"
FT FT /product= "alpha-subunit of FeMo protein of nitrogenase"
FT CDS complement (454590..456131)
FT FT /tag= ac
FT FT /standard_name= "ORF L7"
FT FT /gene= "nifK"
FT FT /product= "beta-subunit of FeMo protein of nitrogenase"
FT CDS complement (456187..457677)
FT FT /tag= ad
FT FT /standard_name= "ORF L8"
FT FT /product= "protein involved in FeMo co-factor biosynthesis"
FT CDS complement (457687..459096)
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FT FT /standard_name= "ORF L9"
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FT FT /product= "protein similar to part of the Fe protein of nitrogenase"
FT CDS complement (461228..461545)
FT FT /tag= ai
FT FT /standard_name= "ORF L13"
FT FT /product= "protein of unknown function"
FT CDS complement (463201..464739)
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FT FT /product= "peptidase-like protein"
FT CDS complement (464736..466079)
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FT FT /standard_name= "ORF L15"
FT FT /product= "processing protease-like protein"

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alignment_scores:
  Quality: 37.00      Length: 9
  Ratio: 4.625      Gaps: 0
Percent Similarity: 88.889      Percent Identity: 88.889

alignment_block:
  US-08-653-294-24 x V30458_0      ..
Align seg 1/1 to: V30458_0 from: 1 to: 110000

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1 ArgGluSerLeuArgAsnLeuArgGly 9

15658 CGCGAAAGTCTTAGGAATCTCTTGGGG 15684
|||||

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GenCore version 4.5
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OM protein - protein search, using sw model

Run On: February 8, 2000, 04:05:42 ; Search time 133.56 Seconds
(without alignments)
1.773 Million cell updates/sec

Title: US-08-653-294-25
Perfect score: 50
Sequence: 1 RNLRTALRY 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 188963 seqs, 23686106 residues

Total number of hits satisfying chosen parameters: 188963

Minimum DB seq length: 0

Maximum DB seq length: 1000000

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database : A_Geneseq_36.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	50	100.0	10	1 R83095	HLA-B2702 CTL modu
2	50	100.0	10	1 R95426	HLA-B2702.75-84(T)
3	50	100.0	10	1 W33788	Peptide B2702.75-8
4	50	100.0	20	1 R92909	HLA-B2702 CTL modu
5	50	100.0	20	1 R92910	HLA-B2702 CTL modu
6	50	100.0	20	1 W33792	Peptide B2702.84-7
7	50	100.0	20	1 W33793	Peptide B2702.84-7
8	44	88.0	10	1 R41208	Peptide fragment o
9	44	88.0	10	1 R83062	HLA-B2702 CTL modu
10	44	88.0	10	1 R95413	Alphal-helix of HL
11	44	88.0	10	1 W07512	T-cell modulating
12	44	88.0	10	1 W47265	Immunomodulatory p
13	44	88.0	10	1 W33784	Peptide B2702.75-8
14	44	88.0	15	1 R92912	HLA-B2702 CTL modu
15	44	88.0	15	1 W33795	Peptide B2702.70-8
16	44	88.0	20	1 R92907	HLA-B2702 CTL modu
17	44	88.0	20	1 R92908	HLA-B2702 CTL modu
18	44	88.0	20	1 R95428	HLA-B2702.84-75-84
19	44	88.0	20	1 W33778	Immunomodulating d
20	44	88.0	20	1 W33791	Peptide B2702.84-7
21	44	88.0	25	1 R41205	Peptide fragment o
22	44	88.0	25	1 R48286	Peptide fragment o
23	44	88.0	25	1 R83090	HLA-B2702 CTL modu
24	44	88.0	25	1 R83093	HLAB38 CTL modulat
25	44	88.0	25	1 R95416	HLA-B2702.60-84. C
26	44	88.0	25	1 R95422	HLAB38.6084. Comps
27	44	88.0	25	1 W33794	Peptide B2702.60-8
28	44	88.0	184	1 Y06801	Peptide Seq ID No:
29	44	88.0	362	1 R03142	Sequence of HLA-Bw
30	44	88.0	362	1 R03144	Sequence of HLA-B5
31	44	88.0	362	1 R12463	HLA-Bw53 exon. HLA
32	43	86.0	10	1 W07522	T-cell modulating
33	40	80.0	10	1 R41212	Peptide fragment o
34	40	80.0	10	1 R83075	HLA-B2702 CTL modu

35 40 80.0 10 1 R95423 HLA-B2705.75-84. C
36 40 80.0 10 1 W33785 Peptide B2705.75-8
37 40 80.0 17 1 R71442 Human HLA-B27-(62-
38 40 80.0 17 1 R71443 Human [Phe74]-HLA-
39 40 80.0 25 1 R41221 Peptide fragment o
40 40 80.0 25 1 R83091 HLA-B2702 CTL modu
41 40 80.0 25 1 R95417 HLA-B2705.60-84. C
42 40 80.0 337 1 P70590 Sequence of the hu
43 40 80.0 362 1 P70155 Sequence encoded b
44 39 78.0 10 1 R83094 HLA-B2702 CTL modu
45 39 78.0 10 1 R83096 HLA-B2702 CTL modu

ALIGNMENTS

RESULT 1
R83095 ID R83095 standard; peptide; 10 AA.
AC R83095;
DT 16-MAY-1996 (first entry)
DE HLA-B2702 CTL modulating peptide (B2702.75-84(T)).
KW Cytotoxic T lymphocyte; CTL; major histocompatibility complex; MHC;
KW immunosuppressant; graft versus host disorder; transplantation; therapy;
KW class I MHC; HLA-B2702.
OS Synthetic.
PN W09526979-A1.
PD 12-OCT-1995.
PF 05-APR-1995; U04349.
PR 05-APR-1994; US-222851.
PA (STRD) UNIV LELAND STANFORD JUNIOR.
PI Clayberger C, Krensky AM, Parham P;
DR WPI: 95-358582/46.
PT Extension of acceptance period of transplants from MHC unmatched
PT donor hosts - using Class I B7-5-84 MHC antigen of the recipient
PT host
PS Example 14; Page 34; 80pp; English.
CC R83061-R83085, R83090-R83096 and R92907-R92913 represent fragments of
CC class I major histocompatibility complex (MHC) antigens. This sequence
CC corresponds to residues 75-84 of the alpha-1 domain of the class I MHC
CC HLA-B2702. This sequence showed no inhibitory effect upon cytotoxic T
CC lymphocytes (CTLs). These sequences can be used to extend the period of
CC acceptance by a recipient of a transplant from an MHC unmatched donor.
CC The peptides are administered to a patient in conjunction with
CC a subtherapeutic amount of an immunosuppressant. This is administered to
CC the patient for a limited period of time (compared to the lifetime
CC administration for current treatments). The peptides particularly
CC modulate (or inhibit) the activity of the CTLs of the patient.
SQ Sequence 10 AA;

Query Match 100.0%; Score 50; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.00033;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RNLRTALRY 10
| | | | | | | | | |
DB 1 RNLRTALRY 10

RESULT 2
R95426 ID R95426 standard; peptide; 10 AA.
AC R95426;
DT 12-NOV-1996 (first entry)
DE HLA-B2702.75-84(T).
KW HLA; p74; alpha1-helix; human-leucocyte-associated antigen; inhibitor;
KW T-cell lysate; membrane protein; mammal; heat shock protein; Hsc70; APC;
KW B cell; calcium influx; cytotoxic T lymphocyte; CTL; differentiation;
KW cytolysis; antigen presenting cell.
OS Synthetic.
PN Key
FT misc_difference 6

/note= "I6T mutation"

FT W09513288-A1.
 PN 18-MAY-1995.
 PF 10-NOV-1994; U12985.
 PR 10-NOV-1993; US-150493.
 PA (STRD) UNIV LELAND STANFORD JUNIOR.
 PI Clayberger C, Krensky AM;
 DR WPI; 95-194027/25.
 PT Compens. comprising lymphoid surface membrane proteins - which may
 PT inhibit cytolytic activity and differentiation of CTLs.
 PS Example; Page 11; 29pp; English.
 CC R95413, and R95415-R95431 represent palindromes and fragments of
 CC human-leucocyte-associated antigens. This sequence represents the
 CC HLA-B2702.75-84(T). These sequences can be used to isolate the protein
 CC p74 from a T-cell lysate. p74 is a T-cell surface membrane protein
 CC associated with T-cell activation in mammalian T-cells, and is also
 CC immunologically cross reactive with the heat shock protein Hsc70. p74 is
 CC found in a limited number of cell types, but is particularly expressed on
 CC B and T cells. p74 can be isolated by lysis of a suitable cell with an
 CC amphoteric detergent, and then passed through an affinity column
 CC containing a covalently bound HLA-B2702 palindromic peptide.
 CC Compositions comprising the extracellular fragment of p74 combined with
 CC HLA-B2702.60-84 (see R95416), induces calcium influx, and inhibits
 CC cytotoxic T lymphocyte (CTL) differentiation or cytotoxicity. Candidate
 CC compounds can be screened for their effect on the cytolytic activity of
 CC T-cells, by combining them with the extracellular portion of p74 and
 CC determining the amount of binding between the candidate compound and p74.
 CC Modulation of CTL activity can be inhibited in a cellular composition
 CC containing T-cells and antigen presenting cells (APCs), by adding to the
 CC mix the extracellular portion of p74, in an amount sufficient to compete
 CC with p74 for the binding of the p74 ligand.
 SQ Sequence 10 AA;

Query Match 100.0%; Score 50; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.00033;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RENLRTALRY 10
 |||||
 Db 1 RENLRTALRY 10

RESULT 3
 W33788
 ID W33788 standard; peptide; 10 AA.
 AC W33788:
 DT 19-JUN-1998 (first entry)
 DE Peptide B2702.75-84T80 tested for immunomodulating activity.
 KW Immunomodulating dimer; immunosuppressant drug; CTL activation;
 KW transplantation; autoimmune disease; Class I HLA-B alpha-1 domain;
 KW rejection.
 OS Synthetic.
 OS Homo sapiens.
 PN W09744351-A1.
 PD 27-NOV-1997.
 PF 22-MAY-1997; U08689.
 PR 24-MAY-1996; US-653294.
 PA (STRD) UNIV LELAND STANFORD JUNIOR.
 PI Beulow R, Clayberger C, Krensky AM;
 DR WPI; 98-086530/08.
 PT New immunomodulating dimer peptide(s) - based on a Class I HLA-B
 PT alpha-1 domain, used for preventing rejection of transplants or
 PT treating autoimmune diseases
 PS Example 1; Page 19; 41pp; English.
 CC Peptides W33784-98 and W33778-9 were assayed for their immunomodulating
 CC activity. A peptide-type compound or variant is claimed which has
 CC immunomodulating activity, including the N-terminal acylated and/or
 CC C-terminal amidated or esterified forms of up to 60 amino acids, where
 CC the peptide-type compound comprises the formula: A-B, where A, B =
 CC (R aa76-77L) (aa79-84) or (aa84-79) (Iaa77-76R); aa76 = E or V; aa77 =
 CC D, S or N; aa79 = R or G; aa80 = I or N; aa81, aa84 = a hydrophobic or
 CC small amino acid; aa82 = R or L; aa83 = G or R; and aa represents amino

CC acid. The sequence in the brackets may optionally be absent or truncated
 CC at any peptide type bond within the brackets. The compounds comprise
 CC amino acid sequences related to a Class I HLA-B alpha domain (positions
 CC 79-84). They can be used to inhibit cytotoxic T-lymphocytes (CTL) from
 CC undesirably attacking cells in a host or in vitro. They can also be
 CC used in combination with antigenic peptides or proteins of interest to
 CC activate CTLs. They can also inhibit the proliferation of T cells in
 CC response to anti-CD3. The peptide can be used for preventing rejection
 CC of transplants or for treating autoimmune diseases, e.g. diabetes,
 CC rheumatoid arthritis and lupus erythematosus. The products can also be
 CC used for detection and diagnosis.
 SQ Sequence 10 AA;

Query Match 100.0%; Score 50; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.00033;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RENLRTALRY 10
 |||||
 Db 1 RENLRTALRY 10

RESULT 4
 R92909
 ID R92909 standard; peptide; 20 AA.
 AC R92909;
 DT 16-MAY-1996 (first entry)
 DE HLA-B2702 CTL modulating peptide (B2702.84-75/75-84(T)).
 KW Cytotoxic T lymphocyte; CTL; major histocompatibility complex; MHC;
 KW immunosuppressant; graft versus host disorder; transplantation; therapy;
 KW class I MHC; HLA-B2702.
 OS Synthetic.
 PN W09526979-A1.
 PD 12-OCT-1995.
 PF 05-APR-1995; U04349.
 PR 05-APR-1994; US-222851.
 PA (STRD) UNIV LELAND STANFORD JUNIOR.
 PI Clayberger C, Krensky AM, Parham P;
 DR WPI; 95-358582/46.
 PT Extension of acceptance period of transplants from MHC unmatched
 PT donor hosts - using Class I B75-84 MHC antigen of the recipient
 PT host
 PS Example 15; Page 36; 80pp; English.
 CC R83061-R83085, R83090-R83096 and R92907-R92913 represent fragments of
 CC class I major histocompatibility complex (MHC) antigens. This sequence
 CC is an inverted dimer of residues 75-84 of the alpha-1 domain of the class
 CC I MHC HLA-B2702. These sequences can be used to extend the period of
 CC acceptance by a recipient of a transplant from an MHC unmatched donor.
 CC The peptides are administered to a patient in conjunction with a
 CC subtherapeutic amount of an immunosuppressant. This is administered to
 CC the patient for a limited period of time (compared to the lifetime
 CC administration for current treatments). The peptides particularly
 CC modulate (or inhibit) the activity of the cytotoxic T lymphocytes (CTLs)
 CC of the patient.
 SQ Sequence 20 AA;

Query Match 100.0%; Score 50; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 0.0007;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RENLRTALRY 10
 |||||
 Db 11 RENLRTALRY 20

RESULT 5
 R92910
 ID R92910 standard; peptide; 20 AA.
 AC R92910;
 DT 16-MAY-1996 (first entry)
 DE HLA-B2702 CTL modulating peptide (B2702.84-75(T)/75-84(T)).

KW Cytotoxic T lymphocyte; CTL; major histocompatibility complex; MHC;
 KW immunosuppressant; graft versus host disorder; transplantation; therapy;
 KW class I MHC; HLA-B*2702.
 OS Synthetic.
 PN W03528979-A1.
 PD 12-OCT-1995. PD
 PF 05-APR-1995; U04349.
 PR 05-APR-1994; US-222851.
 PA (STRD) UNIV LELAND STANFORD JUNIOR.
 PI Clayberger C, Krensky AM, Parham P;
 DR WPI; 95-358562/46.
 PT Extension of acceptance period of transplants from MHC unmatched
 PT donor hosts - using Class I B*5-84 MHC antigen of the recipient
 PT host
 PS Example 15; Page 36; 80pp; English.
 CC R83061-R83085, R83090-R83096 and R92907-R92913 represent fragments of
 CC class I major histocompatibility complex (MHC) antigens. This sequence
 CC is an inverted dimer of residues 75-84 of the alpha-1 domain of the class
 CC I MHC HLA-B*2702. These sequences can be used to extend the period of
 CC acceptance by a recipient of a transplant from an MHC unmatched donor.
 CC The peptides are administered to a patient in conjunction with a
 CC subtherapeutic amount of an immunosuppressant. This is administered to
 CC the patient for a limited period of time (compared to the lifetime
 CC administration for current treatments). The peptides particularly
 CC modulate (or inhibit) the activity of the cytotoxic T lymphocytes (CTLs)
 CC of the patient.
 CC Sequence 20 AA;

Query Match 100.0%; Score 50; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 0.0007;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RENLRTALRY 10
 Db 11 RENLRTALRY 20

RESULT 6

W33792
 ID W33792 standard; peptide; 20 AA.
 AC W33792;
 DT 19-JUN-1998 (first entry)
 DE Peptide B2702.84-75/75-84 tested for immunomodulating activity.
 KW Immunomodulating dimer; immunosuppressant drug; CTL activation;
 KW transplantation; autoimmune disease; Class I HLA-B alpha-1 domain;
 KW rejection.
 OS Synthetic.
 OS Homo sapiens.
 PN W09744351-A1.
 PD 27-NOV-1997.
 PF 22-MAY-1997; U08689.
 PR 24-MAY-1996; US-653294.
 PA (STRD) UNIV LELAND STANFORD JUNIOR.
 PI Beulow R, Clayberger C, Krensky AM;
 DR WPI; 98-086530/08.
 PT New immunomodulating dimer peptide(s) - based on a Class I HLA-B
 PT alpha-1 domain, used for preventing rejection of transplants or
 PT treating autoimmune diseases
 PS Example 1; Page 19; 41pp; English.
 CC Peptides W33784-98 and W33778-9 were assayed for their immunomodulating
 CC activity. A peptide-type compound or variant is claimed which has
 CC immunomodulating activity, including the N-terminal acylated and/or
 CC C-terminal amidated or esterified forms of up to 60 amino acids, where
 CC the peptide-type compound comprises the formula: A-B, where A, B =
 CC (R aa76-77L) (aa79-84) or (aa84-79) (Laa77-76R); aa76 = E or V; aa77 =
 CC D, S or N; aa79 = R or G; aa80 = I or N; aa81, aa84 = a hydrophobic or
 CC small amino acid; aa82 = R or L; aa83 = G or R; and aa represents amino
 CC acid. The sequence in the brackets may optionally be absent or truncated
 CC at any peptide type bond within the brackets. The compounds comprise
 CC amino acid sequences related to a Class I HLA-B alpha domain (positions
 CC 79-84). They can be used to inhibit cytotoxic T-lymphocytes (CTL) from
 CC undesirably attacking cells in a host or in vitro. They can also be

CC used in combination with antigenic peptides or proteins of interest to
 CC activate CTLs. They can also inhibit the proliferation of T cells in
 CC response to anti-CD3. The peptide can be used for preventing rejection
 CC of transplants or for treating autoimmune diseases, e.g. diabetes,
 CC rheumatoid arthritis and lupus erythematosus. The products can also be
 CC used for detection and diagnosis.
 SQ Sequence 20 AA;

Query Match 100.0%; Score 50; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 0.0007;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RENLRTALRY 10
 Db 11 RENLRTALRY 20

RESULT 7

W33793
 ID W33793 standard; peptide; 20 AA.
 AC W33793;
 DT 19-JUN-1998 (first entry)
 DE Peptide B2702.84-75/75-84 tested for immunomodulating activity.
 KW Immunomodulating dimer; immunosuppressant drug; CTL activation;
 KW transplantation; autoimmune disease; Class I HLA-B alpha-1 domain;
 KW rejection.
 OS Synthetic.
 OS Homo sapiens.
 PN W09744351-A1.
 PD 27-NOV-1997.
 PF 22-MAY-1997; U08689.
 PR 24-MAY-1996; US-653294.
 PA (STRD) UNIV LELAND STANFORD JUNIOR.
 PI Beulow R, Clayberger C, Krensky AM;
 DR WPI; 98-086530/08.
 PT New immunomodulating dimer peptide(s) - based on a Class I HLA-B
 PT alpha-1 domain, used for preventing rejection of transplants or
 PT treating autoimmune diseases
 PS Example 1; Page 19; 41pp; English.
 CC Peptides W33784-98 and W33778-9 were assayed for their immunomodulating
 CC activity. A peptide-type compound or variant is claimed which has
 CC immunomodulating activity, including the N-terminal acylated and/or
 CC C-terminal amidated or esterified forms of up to 60 amino acids, where
 CC the peptide-type compound comprises the formula: A-B, where A, B =
 CC (R aa76-77L) (aa79-84) or (aa84-79) (Laa77-76R); aa76 = E or V; aa77 =
 CC D, S or N; aa79 = R or G; aa80 = I or N; aa81, aa84 = a hydrophobic or
 CC small amino acid; aa82 = R or L; aa83 = G or R; and aa represents amino
 CC acid. The sequence in the brackets may optionally be absent or truncated
 CC at any peptide type bond within the brackets. The compounds comprise
 CC amino acid sequences related to a Class I HLA-B alpha domain (positions
 CC 79-84). They can be used to inhibit cytotoxic T-lymphocytes (CTL) from
 CC undesirably attacking cells in a host or in vitro. They can also be

CC used in combination with antigenic peptides or proteins of interest to
 CC activate CTLs. They can also inhibit the proliferation of T cells in
 CC response to anti-CD3. The peptide can be used for preventing rejection
 CC of transplants or for treating autoimmune diseases, e.g. diabetes,
 CC rheumatoid arthritis and lupus erythematosus. The products can also be
 CC used for detection and diagnosis.
 SQ Sequence 20 AA;

Query Match 100.0%; Score 50; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 0.0007;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RENLRTALRY 10
 Db 11 RENLRTALRY 20

RESULT 8

R41208

ID R41208 standard; peptide; 10 AA.
AC R41208;
DT 15-MAR-1994 (first entry)
DE Peptide fragment of Class I HLA peptide.
KW Human leukocyte antigen; HLA; peptide; transplantation; neoplasia;
KW parasitic disease; cytotoxic T lymphocyte; modulation.
OS Synthetic.
PN W09317699-A.
PD 16-SEP-1993.
PF 25-FEB-1993; U01758.
PR 02-MAR-1992; US-844716.
PA (STRD) UNIV LELAND STANFORD JUNIOR.
PI Clayberger CA, Krensky AM;
PT WPI: 93-303134/38.
PT New peptide(s) based on Class I HLA antigen domains - used for
PT modulating cytotoxic T-lymphocyte activity towards targets
PS Claim 11; Page 54; 61pp; English.
CC The peptide is used to modulate cytotoxic T-lymphocyte (CTL)
CC activity, either by inhibition or stimulation. It can be used
CC for inhibiting CTL toxicity in transplantations, for inducing CTL
CC activity in parasitic diseases and neoplasia and in studies on viral
CC infection. The peptide can also be used for identifying CTLs which
CC bind to it and removing subsets of CTLs from a T-cell composition.
CC This peptide sequence is more commonly found within larger peptide
CC compounds of not more than 30 amino acids in length.
SQ Sequence 10 AA;

Query Match 88.0%; Score 44; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 0.0051;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RENLRLALRY 10
DB 1 RENLRLALRY 10
||||| |||||

RESULT 9
ID R83062 standard; peptide; 10 AA.
AC R83062;
DT 16-MAY-1996 (first entry)
DE HLA-B2702 CTL modulating peptide (B2702.75-84).
KW Cytotoxic T lymphocyte; CTL; major histocompatibility complex; MHC;
KW immunosuppressant; graft versus host disorder; transplantation; therapy;
KW Class I MHC; HLA-B2702.
OS Synthetic.
PN W09526979-A1.
PD 12-OCT-1995.
PF 05-APR-1995; U04349.
PR 05-APR-1994; US-222851.
PA (STRD) UNIV LELAND STANFORD JUNIOR.
PI Clayberger C, Krensky AM, Parham P;
DR WPI: 95-358582/46.
PT Extension of acceptance period of transplants from MHC unmatched
PT donor hosts - using Class I B*5-84 MHC antigen of the recipient
PT host
PS Claim 15; Page 9; 80pp; English.
CC R83061-R83085, R83090-R83096 and R92907-R92913 represent fragments of
CC Class I major histocompatibility complex (MHC) antigens. This sequence
CC corresponds to residues 75-84 of the alpha-1 domain of the class I MHC
CC HLA-B2702. These sequences can be used to extend the period of
CC acceptance by a recipient of a transplant from an MHC unmatched donor.
CC The peptides are administered to a patient in conjunction with a
CC subtherapeutic amount of an immunosuppressant. This is administered to
CC the patient for a limited period of time (compared to the lifetime
CC administration for current treatments). The peptides particularly
CC modulate (or inhibit) the activity of the cytotoxic T lymphocytes (CTLs)
CC of the patient.
SQ Sequence 10 AA;

Query Match 88.0%; Score 44; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 0.0051;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RENLRLALRY 10
DB 1 RENLRLALRY 10
||||| |||||

RESULT 10
ID R95413 standard; peptide; 10 AA.
AC R95413;
DT 12-NOV-1996 (first entry)
DE Alpha-helix of HLA-B2702.
KW HLA; p74; alpha-helix; human-leucocyte-associated antigen; inhibitor;
KW T-cell lysate; membrane protein; mammal; heat shock protein; Hsc70; APC;
KW B cell; calcium influx; cytotoxic T lymphocyte; CTL; differentiation;
KW cytolysis; antigen presenting cell.
OS Synthetic.
PN W09513288-A1.
PD 18-MAY-1995.
PF 10-NOV-1994; U12985.
PR 10-NOV-1993; US-150493.
PA (STRD) UNIV LELAND STANFORD JUNIOR.
PI Clayberger C, Krensky AM;
DR WPI: 95-194027/25.
PT Compsns. comprising lymphoid surface membrane proteins - which may
PT inhibit cytolytic activity and differentiation of CTLs.
PS Example; Page 11; 29pp; English.
CC This sequence represents the alpha-helix of the
CC human-leucocyte-associated antigen B2702 (HLA-B2702). This sequence,
CC epitopes, and palindromes of it (such as R95428) can be used to isolate
CC the protein p74 from a T-cell lysate. p74 is a T-cell surface membrane
CC protein associated with T-cell activation in mammalian T-cells, and is
CC also immunologically cross reactive with the heat shock protein Hsc70.
CC p74 is found in a limited number of cell types, but is particularly
CC expressed on B and T cells. p74 can be isolated through an affinity
CC cell with an amphoteric detergent, and then passed through an affinity
CC column containing a covalently bound HLA-B2702 palindromic peptide.
CC Compositions comprising the extracellular fragment of p74 combined with
CC HLA-B2702.60-84 (see R95416), induces calcium influx, and inhibits
CC cytotoxic T lymphocyte (CTL) differentiation or cytolysis. Candidate
CC compounds can be screened for their effect on the cytolytic activity of
CC T-cells, by combining them with the extracellular portion of p74 and
CC determining the amount of binding between the candidate compound and p74.
CC Modulation of CTL activity can be inhibited in a cellular composition
CC containing T-cells and antigen presenting cells (APCs), by adding to the
CC mix the extracellular portion of p74, in an amount sufficient to compete
CC with p74 for the binding of the p74 ligand.
SQ Sequence 10 AA;

Query Match 88.0%; Score 44; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 0.0051;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RENLRLALRY 10
DB 1 RENLRLALRY 10
||||| |||||

RESULT 11
ID W07512 standard; peptide; 10 AA.
AC W07512;
DT 04-AUG-1997 (first entry)
DE T-cell modulating peptide #1.
KW mammal; major histocompatibility complex; MHC class I; antigen; perforin;
KW insulin-dependent diabetes mellitus; multiple sclerosis; inflammation;
KW rheumatoid arthritis; psoriasis; pemphigus vulgaris; Sjogren's disease;
KW thyroid disease; Hashimoto's thyroiditis; myasthenia gravis; granzyme;
KW autologous target cell; cytokine release; T cell activation; therapy.

OS Synthetic.
 PN WO9635443-A1.
 PD 14-NOV-1996.
 PF 05-APR-1996; U04710.
 PR 12-MAY-1995; US-440504.
 PA (SANG-) SANGSTAT MEDICAL CORP.
 PI Buelow R;
 DR WPI: 96-518410/51.
 PT Treatment of auto-immune disease by admin. of peptide(s) corresp. to
 PT major histocompatibility complex antigens - esp. for delaying onset
 PT of clinical symptoms of insulin dependent diabetes by modulating T
 PT cell mediated attack on target cells
 PS Claim 7; Page 20; 24pp; English.
 CC WO7512-W07518 represent T-cell modulating peptides that can be used in
 CC the method of the invention. These sequences are based on a portion of
 CC the generic peptide corresponding to residues 70-91 of the alpha-domain
 CC of the major histocompatibility complex (MHC) class I antigen (see
 CC WO7510). The method is for affecting the course of an autoimmune disease
 CC involving T-cell mediated destruction of tissue in mammals. These
 CC peptides are used especially to treat insulin-dependent diabetes
 CC mellitus, preferably being administered during the pre-clinical stage to
 CC delay onset of the disease. Other diseases that can be treated are
 CC multiple sclerosis, rheumatoid arthritis, psoriasis, pemphigus vulgaris,
 CC Sjogren's disease, thyroid disease, Hashimoto's thyroiditis, myasthenia
 CC gravis, etc. The peptides modulate T-cell mediated attack on autologous
 CC target cells, and may also reduce inflammation, swelling, and release of
 CC cytokines, perforins, granzymes etc. associated with T cell activation.
 CC Sequence 10 AA;
 SQ

Query Match 88.0%; Score 44; DB 1; Length 10;
 Best Local Similarity 90.0%; Pred. No. 0.0051;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RENLRLALRY 10
 Db 1 RENLRLALRY 10

RESULT 12
 W47265
 ID W47265 standard; peptide; 10 AA.
 AC W47265;
 DT 22-MAY-1998 (first entry)
 DE Immunomodulatory peptide.
 KW Immunomodulator; Class I HLA-B alpha-1 domain; inhibition;
 KW transplant rejection; treatment; autoimmune disease.
 OS Homo sapiens.
 OS Synthetic.
 FS Key
 FT Misc_difference 1..10
 FT Location/Qualifiers
 FT /note= "at least one of the amino acids is the
 FT D-isomer
 FT
 PN WO9744052-A1.
 PD 27-NOV-1997.
 PF 23-APR-1997; U06705.
 PR 22-MAY-1996; US-651650.
 PA (STRD) UNIV LELAND STANFORD JUNIOR.
 PI Clayberger C, Krensky AM;
 DR WPI: 98-018220/02.
 PT Novel immunomodulatory peptide-type compound - useful for inhibiting
 PT transplant rejection
 PS Claim 10; Page 36; 41pp; English.
 CC The present sequence is an immunomodulatory peptide, which
 CC comprises a Class I HLA-B alpha-1 domain sequence. It can be used
 CC in a pharmaceutical composition together with a subtherapeutic dose
 CC of an immunosuppressant, to extend the period of acceptance of a
 CC transplant from a major histocompatibility complex (MHC) unmatched
 CC donor, i.e. to inhibit transplant rejection. It can also be used in
 CC the treatment of autoimmune diseases.
 CC Peptides using the D-form amino acids are more effective
 CC immunomodulators than their diastereomers or enantiomers.
 CC Sequence 10 AA;
 SQ

Query Match 88.0%; Score 44; DB 1; Length 10;
 Best Local Similarity 90.0%; Pred. No. 0.0051;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RENLRLALRY 10
 Db 1 RENLRLALRY 10

RESULT 14
 R92912
 ID R92912 standard; peptide; 15 AA.
 AC R92912;
 DT 16-MAY-1996 (first entry)
 DE HLA-B*2702 CTL modulating peptide (B2702.70-84).
 KW Cytotoxic T lymphocyte; CTL; major histocompatibility complex; MHC;
 KW immunosuppressant; graft versus host disorder; transplantation; therapy;
 KW Class I MHC; HLA-B*2702.

Query Match 88.0%; Score 44; DB 1; Length 10;
 Best Local Similarity 90.0%; Pred. No. 0.0051;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RENLRLALRY 10
 Db 1 RENLRLALRY 10

RESULT 13
 W33784
 ID W33784 standard; peptide; 10 AA.
 AC W33784;
 DT 19-JUN-1998 (first entry)
 DE Peptide B2702.75-84 tested for immunomodulating activity.
 KW immunomodulating dimer; immunosuppressant drug; CTL activation;
 KW transplantation; autoimmune disease; Class I HLA-B alpha-1 domain;
 KW rejection.
 OS Synthetic.
 OS Homo sapiens.
 PN WO9744351-A1.
 PD 27-NOV-1997.
 PF 22-MAY-1997; U08689.
 PR 24-MAY-1996; US-653294.
 PA (STRD) UNIV LELAND STANFORD JUNIOR.
 PI Beulow R, Clayberger C, Krensky AM;
 DR WPI: 98-086530/08.
 PT New immunomodulating dimer peptide(s) - based on a Class I HLA-B
 PT alpha-1 domain, used for preventing rejection of transplants or
 PT treating autoimmune diseases
 PS Example 1; Page 19; 41pp; English.
 CC Peptides W33784-98 and W33778-9 were assayed for their immunomodulating
 CC activity. A peptide-type compound or variant is claimed which has
 CC immunomodulating activity, including the N-terminal acylated and/or
 CC C-terminal amidated or esterified forms of up to 60 amino acids, where
 CC the peptide-type compound comprises the formula: A-B, where A, B =
 CC (R aa76-77L) (aa79-84) or (aa84-79) (Laa77-76R); aa76 = E or V; aa77 =
 CC D, S or N; aa79 = R or G; aa80 = I or N; aa81, aa84 = a hydrophobic or
 CC small amino acid; aa82 = R or L; aa83 = G or R; and aa represents amino
 CC acid. The sequence in the brackets may optionally be absent or truncated
 CC at any peptide type bond within the brackets. The compounds comprise
 CC amino acid sequences related to a Class I HLA-B alpha-1 domain (positions
 CC 79-84). They can be used to inhibit cytotoxic T-lymphocytes (CTL) from
 CC undesirably attacking cells in a host or in vitro. They can also be
 CC used in combination with antigenic peptides or proteins of interest to
 CC activate CTLs. They can also inhibit the proliferation of T cells in
 CC response to anti-CD3. The peptide can be used for preventing rejection
 CC of transplants or for treating autoimmune diseases, e.g. diabetes,
 CC rheumatoid arthritis and lupus erythematosus. The products can also be
 CC used for detection and diagnosis.
 CC Sequence 10 AA;
 SQ

OS Synthetic.
PN W09526979-A1.
PD 12-OCT-1995.
PF 05-APR-1995; U04349.
PR 05-APR-1994; US-222851.
PA (STRD) UNIV LELAND STANFORD JUNIOR.
PI Clayberger C, Krensky AM, Parham P;
DR WPI: 95-358582/46.
PT Extension of acceptance period of transplants from MHC unmatched
PT donor hosts - using Class I B75-84 MHC antigen of the recipient
PT host
PS Example 15; Page 36; 80pp; English.
CC R83061-R83085, R83090-R83096 and R92907-R92913 represent fragments of
CC class I major histocompatibility complex (MHC) antigens. This sequence
CC corresponds to residues 70-84 of the alpha-1 domain of the class I MHC
CC HLA-B*2702. These sequences can be used to extend the period of
CC acceptance by a recipient of a transplant from an MHC unmatched donor.
CC The peptides are administered to a patient in conjunction with a
CC subtherapeutic amount of an immunosuppressant. This is administered to
CC the patient for a limited period of time (compared to the lifetime
CC administration for current treatments). The peptides particularly
CC modulate (or inhibit) the activity of the cytotoxic T lymphocytes (CTLs)
CC of the patient.
SQ Sequence 15 AA;

Query Match 88.0%; Score 44; DB 1; Length 15;
Best Local Similarity 90.0%; Pred. No. 0.008;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RENTLRLALRY 10
| | | | | | | |
DB 6 RENTLRLALRY 15

RESULT 15
W33795
ID W33795 standard; peptide; 15 AA.
AC W33795;
DT 19-JUN-1998 (first entry)
DE Peptide B2702.70-84 tested for immunomodulating activity.
KW Immunomodulating dimer; Immunosuppressant drug; CTL activation;
KW transplantation; autoimmune disease; Class I HLA-B alpha-1 domain;
KW rejection.
OS Synthetic.
OS Homo sapiens.
PN W09744351-A1.
PD 27-NOV-1997.
PF 22-MAY-1997; U08689.
PR 24-MAY-1996; US-653294.
PA (STRD) UNIV LELAND STANFORD JUNIOR.
PI Beulow R, Clayberger C, Krensky AM;
DR WPI: 98-086530/08.
PT New immunomodulating dimer peptide(s) - based on a Class I HLA-B
PT alpha-1 domain, used for preventing rejection of transplants or
PT treating autoimmune diseases
PS Example 1; Page 19; 41pp; English.
CC Peptides W33784-98 and W33778-9 were assayed for their immunomodulating
CC activity. A peptide-type compound or variant is claimed which has
CC immunomodulating activity, including the N-terminal acylated and/or
CC C-terminal amidated or esterified forms of up to 60 amino acids, where
CC the peptide-type compound comprises the formula: A-B, where A, B =
CC (R aa76-77L) (aa79-84) or (aa84-79) (Laa77-76R); aa76 = E or V; aa77 =
CC D, S or N; aa79 = R or G; aa80 = I or N; aa81, aa84 = a hydrophobic or
CC small amino acid; aa82 = R or L; aa83 = G or R; and aa represents amino
CC acid. The sequence in the brackets may optionally be absent or truncated
CC at any peptide type bond within the brackets. The compounds comprise
CC amino acid sequences related to a Class I HLA-B alpha1 domain (positions
CC 79-84). They can be used to inhibit cytotoxic T-lymphocytes (CTL) from
CC undesirably attacking cells in a host or in vitro. They can also be
CC used in combination with antigenic peptides or proteins of interest to
CC activate CTLs. They can also inhibit the proliferation of T cells in
CC response to anti-CD3. The peptide can be used for preventing rejection

CC of transplants or for treating autoimmune diseases, e.g. diabetes,
CC rheumatoid arthritis and lupus erythematosus. The products can also be
CC used for detection and diagnosis.
SQ Sequence 15 AA;

Query Match 88.0%; Score 44; DB 1; Length 15;
Best Local Similarity 90.0%; Pred. No. 0.008;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RENTLRLALRY 10
| | | | | | | |
DB 6 RENTLRLALRY 15

Search completed: February 8, 2000, 04:05:43
Job time: 9360 sec

OM of: US-08-653-294-24 to: EST.* out_format : pfs

Date: Feb 8, 2000 6:23 AM

About: Results were produced by the GenCore software, version 4.5,
Copyright (c) 1993-2000 CompuGen Ltd.

Command line parameters:

-MODEL=frame.p2n.model -DEV=xlp
-O/cnpl_1/USPTO.spool/US08653294/runat_04022000_160700_15770/app_query.fasta.2
-DB=EST -DB=FASTA -SUFFIX=rst -GAPOP=12.000 -GAPEXT=4.000
-MINMATCH=0.100 -LOOPCL=0.000 -LOOPEXT=0.000 -GAPOP=4.500
-GAPEXT=0.050 -XGAPOP=10.000 -XGAPEXT=0.500 -GAPOP=6.000
-XGAPEXT=7.000 -XGAPOP=10.000 -XGAPEXT=0.500 -DELOP=6.000
-DELEXT=7.000 -START=1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DCCALIGN=200 -THR_SCORE=pct -ALIGN=15 -MODE=LOCAL
-OUTFMT=pfs -NORM=ext -MINLEN=0 -MAXLEN=1000000 -USER=US08653294
-NCPU=6 -ICPU=3 -NO_XLPHY -WAIT -THREADS=1

Search information block:

Query: US-08-653-294-24

Query length: 10

Database: EST.*

Database sequences: 4538634

Database length: 1887831982

Search time (sec): 7600.090000

score_list:

Sequence	Strd	Orig	ZScore	Escore	Len	Documentation
gb_est12:AA319533	+	51.00	134.48	0.0457	103	AA319533 EST12772 Adrenal gland
gb_est13:AA361477	+	51.00	188.68	0.0961	189	AA361477 EST70761 T-cell lympho
gb_est13:AA352603	+	51.00	187.31	0.1145	218	AA352603 EST60051 Activated T-c
gb_est12:AA294911	+	51.00	185.65	0.1145	259	AA294911 EST100074 Pancreas tum
gb_est13:AA352960	+	51.00	185.26	0.1149	270	AA352960 EST61101 Activated T-c
gb_est8:AA058454	+	51.00	182.17	0.2213	373	AA058454 z167407.r1 Stratagene
gb_est11:AA224068	+	51.00	181.58	0.2389	397	AA224068 z111402.r1 Stratagene
gb_est10:AA160317	+	51.00	181.39	0.2448	405	AA160317 z056c07.r1 Stratagene
gb_est7:W40489	+	51.00	180.88	0.2613	427	W40489 zc84b01.r1 Pancreatic Is
gb_est12:AA310808	+	51.00	180.53	0.2733	443	AA310808 EST181593 Jurkat T-cell
gb_est9:Cl8310	+	51.00	179.86	0.2977	475	Cl8310 Cl8310 Human placenta cl
gb_est17:AA663896	+	51.00	179.78	0.3008	479	AA663896 ae74d01.s1 Stratagene
gb_est35:AL039796	+	51.00	179.31	0.3194	503	AL039796 DKF2p434B1912.r1 434
gb_est11:AA263135	+	51.00	176.02	0.4875	710	AA263135 PM0598 KGI-a Lambda Z
gb_est27:AA242623	-	44.00	161.23	3.25	209	AA242623 tf34g01.x1 NCI_CGAP_B
gb_est23:AA097437	-	44.00	160.03	3.79	237	AA097437 qb61e08.x1 NCI_CGAP_B
gb_est14:AA449607	+	44.00	156.00	6.33	360	AA449607 zx06h02.r1 Soares tota
gb_est1:TA5088	+	44.00	156.00	6.35	361	TA5088 yb45c09.r1 Stratagene fe
gb_est11:AA227277	+	44.00	155.64	6.65	375	AA227277 zr20h03.r1 Stratagene
gb_est31:AT706797	+	44.00	154.81	7.40	409	AT706797 UI-R-AA1-aab-h-09-0-UI
gb_est36:AA926862	+	44.00	154.67	7.53	415	AA926862 UI-R-AA1-aac-c-04-0-UI
gb_est23:AA089801	-	44.00	154.22	7.98	435	AA089801 qa11a09.x1 NCI_CGAP_B
gb_est11:AA242206	-	44.00	154.13	8.07	439	AA242206 zr26c11.r1 Stratagene
gb_est15:AA77506	-	44.00	153.69	8.55	460	AA77506 qy22d12.x1 NCI_CGAP_B
gb_est4:HA2327	+	44.00	153.30	8.75	469	HA2327 ym52e08.r1 Soares infant
gb_est26:AA949373	+	44.00	153.18	9.12	485	AA949373 EST192140 Normalized r
gb_est37:AA939506	-	44.00	152.85	9.51	502	AA939506 qy22d12.x5 NCI_CGAP_B
gb_est36:AA945159	+	44.00	152.30	10.22	532	AA945159 EST229271 Normalized r
gb_est36:AA945159	+	44.00	152.01	10.59	548	AA945159 EST200658 Normalized r
gb_est36:AA1232284	-	44.00	150.41	13.01	648	AA1232284 EST228972 Normalized r
gb_est10:AA0248102	-	42.00	144.36	28.27	553	AA0248102 HS.2015.A1.H09 MR CIT
gb_est27:AA10530	+	41.00	146.52	21.43	297	AA10530 EST238823 Normalized r
gb_est29:AA1602357	+	41.00	145.14	25.56	343	AA1602357 UI-R-AA0-wn-h-05-0-UI
gb_est38:AA060987	+	41.00	143.23	32.68	419	AA060987 UI-M-BH1-amm-c-01-0-UI
gb_est38:AA083156	+	40.00	141.70	39.76	331	AA083156 zn08a04.x1 Stratagene
gb_est9:AA121088	+	40.00	139.63	51.85	411	AA121088 zm22a05.r1 Stratagene
gb_gss11:AA0333000	-	40.00	138.21	62.24	477	AA0333000 HS-5003.A2.A08.r7 RPL1
gb_est10:AA158109	-	40.00	137.85	65.13	495	AA158109 zo57h10.s1 Stratagene
gb_est10:AA160714	+	40.00	137.22	70.66	529	AA160714 zo77e11.r1 Stratagene

gb_gss13:AA0468916 - 40.00 137.02 72.47 540 ! AA0468916 HS-5140.B2.H09.T7A
gb_est11:AA203261 - 40.00 132.13 135.60 900 ! AA203261 zx55d11.r1 Soares f
gb_est4:F14616 + 39.00 143.90 29.97 177 ! F14616 SSOAH02 Porcine small

seq_name: gb_est12:AA319533

seq_documentation_block:

LOCUS AA319533 103 bp mRNA EST 19-APR-1997

DEFINITION EST12772 Adrenal gland tumor Homo sapiens CDNA 5' end similar to
similar to major histocompatibility complex, class I, B
(GB:MI6102), mRNA sequence.

ACCESSION AA319533

VERSION AA319533

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;

Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 103)

AUTHORS

Adams,M.D., Kerlavage,A.R., Fleischmann,R.D., Fuldner,R.A.,
Bult,C.J., Lee,N.H., Kirkness,E.F., Weinstock,K.G., Gocayne,J.D.,
White,O., Sutton,G., Blake,J.A., Brandon,R.C., Man-Wai,C.,
Clayton,R.A., Cline,T.R., Cotton,M.D., Earle-Hughes,J., Fine,L.D.,
Fitzgerald,L.M., Fitzhugh,W.M., Fritchman,J.L., Geoghagen,N.S.,
Glodek,A., Gnehm,C.L., Hanna,M.C., Hedblom,E., Hinkle,P.S., Jr.,
Kelley,J.M., Kelley,J.C., Liu,L.-I., Marmaros,S.M., Merrick,J.M.,
Moreno-Palauques,R.F., McDonald,L.A., Nguyen,D.T., Pelligrino,S.M.,
Phillips,C.A., Ryder,S.E., Scott,J.L., Saudek,D.M., Shirley,R.,
Small,K.V., Spriggs,T.A., Utterback,T.R., Weidman,J.F., Li,Y.,
Bednarek,D.P., Cao,L., Cepeda,M.A., Coleman,T.A., Collins,E.J.,
Dimke,D., Feng,D.-F., Ferrie,A., Fischer,C., Hastings,G.A.,
He,W.W., Hu,J.S., Greene,J.M., Gruber,J., Hudson,P., Kim,A.K.,
Kozak,D.L., Kunsch,C., Hungjun,J., Li,H., Weissner,P.S., Olsen,H.,
Raymond,L., Wei,Y.F., Wing,J., Xu,C., Yu,G.L., Ruben,S.M.,
Dillon,P.J., Fannon,M.R., Rosen,C.A., Haseitine,W.A., Fields,C.,
Fraser,C.M. and Venter,J.C.

TITLE Initial assessment of human gene diversity and expression patterns

based upon 83 million nucleotides of cDNA sequence

Nature 377 (6547 Suppl), 3-174 (1995)

JOURNAL

MEDLINE

COMMENT On Sep 12, 1996 this sequence version replaced gi:1393672.

Other_ESTS: TH0169519

Contact: Kerlavage, AR

Bioinformatics

The Institute for Genomic Research

9712 Medical Center Drive, Rockville, MD 20850 USA

Tel: 3018699056

Fax: 3018699423

Email: arkerlavet@tigr.org

For clone availability, additional sequence and expression

information related to this EST, please check the TIGR Human Gene

Index (<http://www.tigr.org/cdb/hgi/hgi.html>)

Seq primer: M13 Reverse

Location/Qualifiers

source 1..103

/organism="Homo sapiens"

/db_xref="ATCC (inhost):120083"

/db_xref="taxon:9606"

/clone_lib="adrenal gland tumor"

/dev_stage="adult"

BASE COUNT 26 a 35 c 29 g 13 t

ORIGIN

alignment_scores:

Quality: 51.00 Length: 10

Ratio: 5.100 Gaps: 0

Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:

US-08-653-294-24 x AA319533

Align seg 1/1 to: AA319533 from: 1 to: 103

1 ArgGluSerLeuArgAsnLeuArgGlyTyr 10
|||||
27 CGAGAGACCTCGCGAACCTTCGGCGCTAC 56

seq_name: gb_est13:AA361477

seq_documentation_block: 189 bp mRNA EST 21-APR-1997
LOCUS AA361477 T-cell lymphoma Homo sapiens cDNA 5' end similar to
DEFINITION EST70761 T-cell lymphoma Homo sapiens cDNA 5' end similar to
similar to major histocompatibility complex, class I, Bw62.3, mRNA
sequence.

ACCESSION AA361477
VERSION AA361477.1 GI:2013795
KEYWORDS EST.
SOURCE human.

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 189)

AUTHORS Adams,M.D., Kerlavage,A.R., Fleischmann,R.D., Fuldner,R.A., Bult,C.J., Lee,N.H., Kirkness,E.F., Weinstock,K.G., Gocayne,J.D., White,O., Sutton,G., Blake,J.A., Brandon,R.C., Man,Wai,C., Clayton,R.A., Cline,T.R., Cotton,M.D., Earle-Hughes,J., Fine,L.D., Fitzgerald,L.M., Fitzhugh,W.M., Fritchman,J.L., Geoghagen,N.S., Glodek,A., Gnehm,C.L., Hanna,M.C., Hedblom,E., Hinkle,P.S.Jr., Kelley,J.M., Kelley,J.C., Liu,L.-I., Marmaros,S.M., Merrick,J.M., Moreno-Palancas,R.F., McDonald,L.A., Nguyen,D.T., Pelligrino,S.M., Phillips,C.A., Ryder,S.E., Scott,J.L., Sauder,D.M., Shirley,R., Small,K.V., Spriggs,T.A., Utterback,T.R., Weidman,J.F., Li,Y., Bednarek,D.P., Cao,L., Cepeda,M.A., Coleman,T.A., Collins,E.J., Dimke,D., Feng,D.-F., Ferrie,A., Fischer,C., Hastings,G.A., He,W.W., Hu,J.S., Greene,J.M., Gruber,J., Hudson,P., Kim,A.K., Kozak,D.L., Kunsch,C., Hungjun,J., Li,H., Weissner,P.S., Olsen,H., Raymond,L., Wei,Y.F., Wing,J., Xu,C., Yu,G.L., Ruben,S.M., Dillion,P.J., Fannon,M.R., Rosen,C.A., Haseltine,W.A., Fields,C., Fraser,C.M. and Venter,J.C.

TITLE Initial assessment of human gene diversity and expression patterns
based upon 83 million nucleotides of cDNA sequence

JOURNAL Nature 377 (6547 Suppl), 3-174 (1995)
MEDLINE 12140200

COMMENT On Sep 12, 1996 this sequence version replaced gi:1404737.

Other ESTs: THC169519
Contact: Kerlavage, AR
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9712 Medical Center Drive, Rockville, MD 20850 USA

Tel: 3018699056

Fax: 3018699423

Email: arkerlavetigr.org

For clone availability, additional sequence and expression

information related to this EST, please check the TIGR Human Gene

Index (<http://www.tigr.org/tdb/hgi/hgi.html>)

Seq primer: M13 Reverse.

FEATURES

Source

1..189

/organism="Homo sapiens"

/db_xref="ATCC (inhost):165623"

/db_xref="taxon:9606"

/clone_lib="T-cell lymphoma"

/cell_type="T-lymphocyte"

/note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2:

XhoI"

BASE COUNT 45 a 60 c 55 g 25 t 4 others

ORIGIN

alignment_scores:

Quality: 51.00

Ratio: 5.100

Percent similarity: 100.000

Length: 10

Gaps: 0

Percent identity: 100.000

alignment_block:

US-08-653-294-24 x AA361477

Align seg 1/1 to: AA361477 from: 1 to: 189

1 ArgGluSerLeuArgAsnLeuArgGlyTyr 10
|||||
37 CGAGAGACCTCGCGAACCTTCGGCGNTAC 66

seq_name: gb_est13:AA352603

seq_documentation_block: 218 bp mRNA EST 21-APR-1997
LOCUS AA352603
DEFINITION EST60621 Activated T-cells XX Homo sapiens cDNA 5' end similar to
similar to major histocompatibility complex, class I, Bw62.3, mRNA
sequence.

ACCESSION AA352603
VERSION AA352603.1 GI:2004923
KEYWORDS EST.
SOURCE human.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 218)

AUTHORS Adams,M.D., Kerlavage,A.R., Fleischmann,R.D., Fuldner,R.A., Bult,C.J., Lee,N.H., Kirkness,E.F., Weinstock,K.G., Gocayne,J.D., White,O., Sutton,G., Blake,J.A., Brandon,R.C., Man,Wai,C., Clayton,R.A., Cline,T.R., Cotton,M.D., Earle-Hughes,J., Fine,L.D., Fitzgerald,L.M., Fitzhugh,W.M., Fritchman,J.L., Geoghagen,N.S., Glodek,A., Gnehm,C.L., Hanna,M.C., Hedblom,E., Hinkle,P.S.Jr., Kelley,J.M., Kelley,J.C., Liu,L.-I., Marmaros,S.M., Merrick,J.M., Moreno-Palancas,R.F., McDonald,L.A., Nguyen,D.T., Pelligrino,S.M., Phillips,C.A., Ryder,S.E., Scott,J.L., Sauder,D.M., Shirley,R., Small,K.V., Spriggs,T.A., Utterback,T.R., Weidman,J.F., Li,Y., Bednarek,D.P., Cao,L., Cepeda,M.A., Coleman,T.A., Collins,E.J., Dimke,D., Feng,D.-F., Ferrie,A., Fischer,C., Hastings,G.A., He,W.W., Hu,J.S., Greene,J.M., Gruber,J., Hudson,P., Kim,A.K., Kozak,D.L., Kunsch,C., Hungjun,J., Li,H., Weissner,P.S., Olsen,H., Raymond,L., Wei,Y.F., Wing,J., Xu,C., Yu,G.L., Ruben,S.M., Dillion,P.J., Fannon,M.R., Rosen,C.A., Haseltine,W.A., Fields,C., Fraser,C.M. and Venter,J.C.

TITLE Initial assessment of human gene diversity and expression patterns
based upon 83 million nucleotides of cDNA sequence

JOURNAL Nature 377 (6547 Suppl), 3-174 (1995)
MEDLINE 12140200

COMMENT On May 8, 1995 this sequence version replaced gi:800964.

Other ESTs: THC172938

Contact: Kerlavage, AR

Bioinformatics

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Email: arkerlavetigr.org

For clone availability, additional sequence and expression

information related to this EST, please check the TIGR Human Gene

Index (<http://www.tigr.org/tdb/hgi/hgi.html>)

Seq primer: M13 Reverse.

FEATURES

Location/Qualifiers

1..218

/organism="Homo sapiens"

/db_xref="ATCC (inhost):152802"

/db_xref="taxon:9606"

/clone_lib="Activated T-cells XX"

/cell_type="T-lymphocyte"

/dev_stage="adult"

/note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2:

XhoI"

BASE COUNT

52 a 70 c 62 g 28 t 6 others

ORIGIN

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alignment_scores:
  Quality: 51.00      Length: 10
  Ratio: 5.100      Gaps: 0
  Percent Similarity: 100.000  Percent Identity: 100.000

alignment_block:
  US-08-653-294-24 x AA352603
  ..
  Align seg 1/1 to: AA352603 from: 1 to: 218

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  |||||||||||||||||||||||||||||||
  39 CGAGAGAGCCTGCGGAACTCGCGGCTAC 68

seq_name: gb_est12:AA294911

seq_documentation_block:
  LOCUS AA294911 259 bp mRNA EST 18-APR-1997
  DEFINITION EST100074 Pancreas tumor I Homo sapiens cDNA 5' end similar to
  similar to major histocompatibility complex, class I, BW62.3, mRNA
  sequence.
  ACCESSION AA294911
  VERSION AA294911.1 GI:1947266
  KEYWORDS EST.
  SOURCE human.
  ORGANISM Homo sapiens
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
  Eutheria; Primates; Catarrhini; Hominidae; Homo.
  REFERENCE 1 (bases 1 to 259)
  AUTHORS Adams,M.D., Kerlavage,A.R., Fleischmann,R.D., Fuldner,R.A.,
  Bult,C.J., Lee,N.H., Kirkness,E.F., Weinstock,K.G., Gocayne,J.D.,
  White,O., Sutton,G., Blake,J.A., Brandon,R.C., Man-Wai,C.,
  Clifton,R.A., Cline,T.R., Cotton,M.D., Earle-Hughes,J., Fine,L.D.,
  Fitzgerald,L.M., Fitzhugh,W.M., Fritchman,J.L., Geoghagen,N.S.,
  Glodek,A., Gnehm,C.L., Hanna,M.C., Hedblom,E., Hinkle,P.S., Jr.,
  Kelley,J.M., Kelley,J.C., Liu,L.-I., Marmaros,S.M., Merrick,J.M.,
  Moreno-Palauques,R.F., McDonald,L.A., Nguyen,D.T., Pelligrino,S.M.,
  Phillips,C.A., Ryder,S.E., Scott,J.L., Saudek,D.M., Shirley,R.,
  Small,K.V., Spriggs,T.A., Utterback,T.R., Weidman,J.F., Li,Y.,
  Bednarik,D.P., Cao,L., Cepeda,M.A., Coleman,T.A., Collins,E.J.,
  Dimke,D., Feng,D.-F., Ferrie,A., Fischer,C., Hastings,E.J.,
  He,W.W., Hu,J.S., Greene,J.M., Gruber,J., Hudson,P., Kim,A.K.,
  Kozak,D.L., Kunsch,C., Hungjun,J., Li,H., Weissner,P.S., Olsen,H.,
  Raymond,L., Wei,Y.F., Wing,J., Xu,C., Yu,G.L., Ruben,S.M.,
  Dillion,P.J., Fannon,M.R., Rosen,C.A., Haseltine,W.A., Fields,C.,
  Fraser,C.M. and Venter,J.C.
  TITLE Initial assessment of human gene diversity and expression patterns
  based upon 83 million nucleotides of cDNA sequence
  JOURNAL Nature 377 (6547 Suppl), 3-174 (1995)
  MEDLINE 12140200
  COMMENT On Nov 29, 1993 this sequence version replaced gi:430148.
  Other_ESTs: THC172938
  Contact: Kerlavage, AR
  Bioinformatics
  The Institute for Genomic Research
  9712 Medical Center Drive, Rockville, MD 20850 USA
  Tel: 3018699056
  Fax: 3018699423
  Email: arkerlavet@tigr.org
  For clone availability, additional sequence and expression
  information related to this EST, please check the TIGR Human Gene
  Index (http://www.tigr.org/tdb/hgi/hgi.html)
  Seq primer: M13 Reverse.
  Location/Qualifiers
  1..259
  /organism="Homo sapiens"
  /db_xref="ATCC (inhost):190413"
  /db_xref="taxon:9606"
  /clone_lib="Pancreas tumor I"
  /dev_stage="adult"
  /note="Organ: pancreas; Vector: pBluescript SK-; Site_1:
  EcoRI; Site_2: XhoI"
  BASE COUNT 60 a 87 c 30 t 7 others

```

```

ORIGIN
alignment_scores:
  Quality: 51.00      Length: 10
  Ratio: 5.100      Gaps: 0
  Percent Similarity: 100.000  Percent Identity: 100.000

alignment_block:
  US-08-653-294-24 x AA294911
  ..
  Align seg 1/1 to: AA294911 from: 1 to: 259

  1 ArgGluSerLeuArgAsnLeuArgGlyTyr 10
  |||||||||||||||||||||||||||||||
  42 CGAGAGAGCCTGCGGAACTCGCGGCTAC 71

seq_name: gb_est13:AA352960

seq_documentation_block:
  LOCUS AA352960 270 bp mRNA EST 21-APR-1997
  DEFINITION EST61101 Activated T-cells XX Homo sapiens cDNA 5' end similar to
  similar to major histocompatibility complex, class I, B61, mRNA
  sequence.
  ACCESSION AA352960
  VERSION AA352960.1 GI:2005353
  KEYWORDS EST.
  SOURCE human.
  ORGANISM Homo sapiens
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
  Eutheria; Primates; Catarrhini; Hominidae; Homo.
  REFERENCE 1 (bases 1 to 270)
  AUTHORS Adams,M.D., Kerlavage,A.R., Fleischmann,R.D., Fuldner,R.A.,
  Bult,C.J., Lee,N.H., Kirkness,E.F., Weinstock,K.G., Gocayne,J.D.,
  White,O., Sutton,G., Blake,J.A., Brandon,R.C., Man-Wai,C.,
  Clifton,R.A., Cline,T.R., Cotton,M.D., Earle-Hughes,J., Fine,L.D.,
  Fitzgerald,L.M., Fitzhugh,W.M., Fritchman,J.L., Geoghagen,N.S.,
  Glodek,A., Gnehm,C.L., Hanna,M.C., Hedblom,E., Hinkle,P.S., Jr.,
  Kelley,J.M., Kelley,J.C., Liu,L.-I., Marmaros,S.M., Merrick,J.M.,
  Moreno-Palauques,R.F., McDonald,L.A., Nguyen,D.T., Pelligrino,S.M.,
  Phillips,C.A., Ryder,S.E., Scott,J.L., Saudek,D.M., Shirley,R.,
  Small,K.V., Spriggs,T.A., Utterback,T.R., Weidman,J.F., Li,Y.,
  Bednarik,D.P., Cao,L., Cepeda,M.A., Coleman,T.A., Collins,E.J.,
  Dimke,D., Feng,D.-F., Ferrie,A., Fischer,C., Hastings,E.J.,
  He,W.W., Hu,J.S., Greene,J.M., Gruber,J., Hudson,P., Kim,A.K.,
  Kozak,D.L., Kunsch,C., Hungjun,J., Li,H., Weissner,P.S., Olsen,H.,
  Raymond,L., Wei,Y.F., Wing,J., Xu,C., Yu,G.L., Ruben,S.M.,
  Dillion,P.J., Fannon,M.R., Rosen,C.A., Haseltine,W.A., Fields,C.,
  Fraser,C.M. and Venter,J.C.
  TITLE Initial assessment of human gene diversity and expression patterns
  based upon 83 million nucleotides of cDNA sequence
  JOURNAL Nature 377 (6547 Suppl), 3-174 (1995)
  MEDLINE 12140200
  COMMENT On May 8, 1995 this sequence version replaced gi:801269.
  Other_ESTs: THC172938
  Contact: Kerlavage, AR
  Bioinformatics
  The Institute for Genomic Research
  9712 Medical Center Drive, Rockville, MD 20850 USA
  Tel: 3018699056
  Fax: 3018699423
  Email: arkerlavet@tigr.org
  For clone availability, additional sequence and expression
  information related to this EST, please check the TIGR Human Gene
  Index (http://www.tigr.org/tdb/hgi/hgi.html)
  Seq primer: M13 Reverse.
  Location/Qualifiers
  1..270
  /organism="Homo sapiens"
  /db_xref="ATCC (inhost):153240"
  /db_xref="taxon:9606"
  /clone_lib="Activated T-cells XX"
  /cell_type="T-lymphocyte"

```

/dev_stage="adult"
/note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2:
XhoI"

BASE COUNT 62 a 80 c 88 g 35 t 5 others
ORIGIN

alignment_scores:
Quality: 51.00 Length: 10
Ratio: 5.100 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:

US-08-653-294-24 x AA352960 ..

Align seg 1/1 to: AA352960 from: 1 to: 270

1 ArgGlusLeuArgAsnLeuArgGlyTyr 10

|||||
182 CGAGAGAGCTCGGAACCTCGCGGCTAC 211

seq_name: gb_est8:AA058454

seq_documentation_block:

LOCUS AA058454 373 bp mRNA EST 01-DEC-1996
DEFINITION z167d07.r1 Stratagene colon (#937204) Homo sapiens cDNA clone
IMAGE:509677 5' similar to gb:M24039_cds1 HLA CLASS I
HISTOCOMPATIBILITY ANTIGEN, B-18 B*1801 ALPHA (HUMAN);, mRNA
sequence.

ACCESSION AA058454

VERSION AA058454.1 GI:1551280

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 373)

AUTHORS Hillier, L., Lennon, G., Becker, M., Bonaldo, M.F., Chiapelli, B.,
Chissoe, S., Dietrich, N., Dubuque, T., Favello, A., Gish, W.,
Hawkins, M., Hultman, M., Kucaba, T., Lacy, M., Le, M., Le, N.,
Mardis, E., Moore, B., Morris, M., Parsons, J., Prange, C., Rifkin, L.,
Rohlfing, T., Schellenberg, K., Soares, M.B., Tan, F., Thierry-Mieg, J.,
Trevasakis, E., Underwood, K., Wohlmann, P., Waterston, R., Wilson, R.
and Marra, M.

TITLE Generation and analysis of 280,000 human expressed sequence tags

JOURNAL Genome Res. 6 (9), 807-828 (1996)

MEDLINE 97044478

COMMENT On Sep 12, 1996 this sequence version replaced gi:1393357.

Contact: Wilson RK

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800

Fax: 314 286 1810

Email: est@watson.wustl.edu

This clone is available royalty-free through LLNL; contact the

IMAGE Consortium (info@image.llnl.gov) for further information.

Insert Length: 1592 Std Error: 0.00

Seq primer: -28M13 rev2 from Amersham

High quality sequence stop: 268.

Location/Qualifiers

1..373

/organism="Homo sapiens"

/db_xref="GDB:3813009"

/db_xref="taxon:9606"

/clone="IMAGE:509677"

/clone_lib="Stratagene colon (#937204)"

/lab_host="SOLR cells (kanamycin resistant)"

/note="Organ: colon; Vector: pBluescript SK-; Site_1:

EcoRI; Site_2: XhoI; Cloned unidirectionally. Primer:

Oligo dT. 1-84 colonic epithelial cell line. Average

insert size: 1.0 kb; Uni-ZAP XR Vector; -5' adaptor

sequence: 5' GAATTCGCGCAG 3' -3' adaptor sequence: 5'

CTCGAGTTTTTTTTTTTTTTT 3'

BASE COUNT 73 a 119 c 116 g 57 t 8 others
ORIGIN

alignment_scores:

Quality: 51.00 Length: 10

Ratio: 5.100 Gaps: 0

Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:

US-08-653-294-24 x AA058454 ..

Align seg 1/1 to: AA058454 from: 1 to: 373

1 ArgGlusLeuArgAsnLeuArgGlyTyr 10

|||||

229 CGAGAGAGCTCGGAACCTCGCGGCTAC 258

seq_name: gb_est11:AA224068

seq_documentation_block:

LOCUS AA224068 397 bp mRNA EST 19-FEB-1997
DEFINITION zrlf02.r1 Stratagene hnt neuron (#937233) Homo sapiens cDNA clone
IMAGE:648507 5' similar to gb:L22649_cds1 HLA CLASS I
HISTOCOMPATIBILITY ANTIGEN, B-39 B*3901 ALPHA (HUMAN);, mRNA
sequence.

ACCESSION AA224068

VERSION AA224068.1 GI:1844610

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 397)

AUTHORS Hillier, L., Lennon, G., Becker, M., Bonaldo, M.F., Chiapelli, B.,
Chissoe, S., Dietrich, N., Dubuque, T., Favello, A., Gish, W.,
Hawkins, M., Hultman, M., Kucaba, T., Lacy, M., Le, M., Le, N.,
Mardis, E., Moore, B., Morris, M., Parsons, J., Prange, C., Rifkin, L.,
Rohlfing, T., Schellenberg, K., Soares, M.B., Tan, F., Thierry-Mieg, J.,
Trevasakis, E., Underwood, K., Wohlmann, P., Waterston, R., Wilson, R.
and Marra, M.

TITLE Generation and analysis of 280,000 human expressed sequence tags

JOURNAL Genome Res. 6 (9), 807-828 (1996)

MEDLINE 97044478

COMMENT On Nov 29, 1993 this sequence version replaced gi:430429.

Contact: Wilson RK

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800

Fax: 314 286 1810

Email: est@watson.wustl.edu

This clone is available royalty-free through LLNL; contact the

IMAGE Consortium (info@image.llnl.gov) for further information.

Seq primer: -28M13 rev1 ET from Amersham

High quality sequence stop: 295.

Location/Qualifiers

1..397

/organism="Homo sapiens"

/db_xref="GDB:558245"

/db_xref="taxon:9606"

/clone="IMAGE:648507"

/clone_lib="Stratagene hnt neuron (#937233)"

/lab_host="SOLR (kanamycin resistant)"

/note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2:

XhoI; Cloned unidirectionally. Primer: Oligo dT.

Differentiated, post mitotic hnt neurons. Average insert

size: 1.5 kb; Uni-ZAP XR Vector; -5' adaptor sequence: 5'

GAATTCGCGCAG 3' -3' adaptor sequence: 5'

CTCGAGTTTTTTTTTTTTTTT 3'

BASE COUNT 77 a 129 c 131 g 56 t 4 others

ORIGIN

alignment_scores:

Quality: 51.00 Length: 10
Ratio: 5.100 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:

US-08-653-294-24 x AA224068 ..

Align seg 1/1 to: AA224068 from: 1 to: 397

1 ArgGluSerLeuArgAsnLeuArgGlyTyr 10
|||||
297 CGAGAGCGCTCGNAACCTGCGCGCTAC 326

seq_name: gb_est10:AA160317

seq_documentation_block:

LOCUS AA160317 405 bp mRNA EST 09-MAR-1998
DEFINITION z056c07.r1 Stragatene pancreas (#937208) Homo sapiens cDNA clone IMAGE:590892 5' similar to gb:U11265 HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-35 B*3501 ALPHA (HUMAN);, mRNA sequence.

ACCESSION AA160317.1 GI:1734956
VERSION AA160317.1
KEYWORDS EST.
SOURCE human.

ORGANISM

Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE

1 (bases 1 to 405)
Hillier, L., Allen, M., Bowles, L., Dubuque, T., Geisel, G., Jost, S., Krizman, D., Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M., Martin, J., Moore, B., Schellenberg, K., Steptoe, M., Tan, F., Theising, B., White, Y., Wyllie, T., Waterston, R. and Wilson, R.
WashU-NCI human EST Project

TITLE

Unpublished (1997)

JOURNAL

COMMENT

On Sep 12, 1996 this sequence version replaced gi:1406818.
Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810

Email: est@wuston.wustl.edu

This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.

Insert Length: 1671 Std Error: 0.00

Seq primer: -28M13 rev2 from Amersham

High quality sequence stop: 332.

FEATURES

source

1..405
/organism="Homo sapiens"
/db_xref="GDB:4622278"
/db_xref="taxon:9606"
/clone="IMAGE:590892"
/clone_lib="Stragatene pancreas (#937208)"
/lab_host="SOLR cells (kanamycin resistant)"
/note="Organ: pancreas; Vector: pBluescript SK-; Site: 1: ECORI; Site: 2: XhoI; Cloned unidirectionally. Primer: Oligo dT. Pancreatic adenocarcinoma cell line. Average insert size: 1.0 kb; Uni-ZAP XR Vector; -5' adaptor sequence: 5' GAATTCGCGACGAG 3' -3' adaptor sequence: 5' CTCGAGTTTTTTTTTTT 3'"

BASE COUNT 80 a 132 c 132 g 58 t 3 others
ORIGIN

alignment_scores:

Quality: 51.00 Length: 10
Ratio: 5.100 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:

US-08-653-294-24 x AA160317 ..

Align seg 1/1 to: AA160317 from: 1 to: 405

1 ArgGluSerLeuArgAsnLeuArgGlyTyr 10
|||||
281 CGAGAGCGCTCGGAACCTGCGCGCTAC 310

seq_name: gb_est7:W40489

seq_documentation_block:

LOCUS W40489 427 bp mRNA EST 20-MAY-1996
DEFINITION z684b01.r1 Pancreatic Islet Homo sapiens cDNA clone IMAGE:328969 5' similar to gb:U11265 HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-35 B*3501 ALPHA (HUMAN);, mRNA sequence.

ACCESSION W40489.1 GI:1324496
VERSION W40489.1
KEYWORDS EST.
SOURCE human.

ORGANISM

Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE

1 (bases 1 to 427)
Hillier, L., Lennon, G., Becker, M., Bonaldo, M.F., Chiapelli, B., Chisoe, S., Dietrich, N., DuBuque, T., Favello, A., Gish, W., Hawkins, M., Hultman, M., Kucaba, T., Lacy, M., Le, N., Mardis, E., Moore, B., Morris, M., Parsons, J., Prange, C., Rifkin, L., Rohlfing, T., Schellenberg, K., Soares, M.B., Tan, F., Thierry-Mieg, J., Trevaskis, E., Underwood, K., Wohlmann, P., Waterston, R., Wilson, R. and Marra, M.

Generation and analysis of 280,000 human expressed sequence tags
Genome Res. 6 (9), 807-828 (1996)
97044478

COMMENT

On Jan 25, 1995 this sequence version replaced gi:637865.

Contact: Wilson RK

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800

Fax: 314 286 1810

Email: est@wuston.wustl.edu

This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.

Seq primer: mob.REGA+ET

High quality sequence stop: 397.

FEATURES

source

1..427
/organism="Homo sapiens"
/db_xref="GDB:1263173"
/db_xref="taxon:9606"
/clone="IMAGE:328969"
/clone_lib="Pancreatic Islet"
/tissue_type="pancreatic islet"
/lab_host="SOLR cells (kanamycin resistant)"
/note="Organ: pancreas; Vector: pBluescript SK-; Site: 1: ECORI; Site: 2: XhoI; Reference: Hum Mol Gen 2, 1795 (1993) Takeda et al. Cloned unidirectionally. Primer: Oligo dT. -5' adaptor sequence: 5' GAATTCGCGACGAG 3' -3' adaptor sequence: 5' CTCGAGTTTTTTTTTTT 3'"

BASE COUNT 87 a 141 c 134 g 62 t 3 others
ORIGIN

alignment_scores:

Quality: 51.00 Length: 10
Ratio: 5.100 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:

US-08-653-294-24 x W40489 ..

Align seg 1/1 to: W40489 from: 1 to: 427

1 ArgGluSerLeuArgAsnLeuArgGlyTyr 10
|||||

279 CGAGAGAGCTCGGAACCTCGCGGCTAC 308

seq_name: gb_est12:AA310808

seq_documentation_block: 443 bp mRNA EST 19-APR-1997
 LOCUS AA310808
 DEFINITION EST181593 Jurkat T-cells V Homo sapiens cDNA 5' end similar to similar to major histocompatibility complex, class I, B0704, mRNA sequence.
 ACCESSION AA310808
 VERSION AA310808.1 GI:1963136
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 443)
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 AUTHORS Adams,M.D., Kerlavage,A.R., Fleischmann,R.D., Fuldner,R.A., Bult,C.J., Lee,N.H., Kirkness,E.F., Weinstock,K.G., Gocayne,J.D., White,O., Sutton,G., Blake,J.A., Brandon,R.C., Man-Wai,C., Clayton,R.A., Cline,T.R., Cotton,M.D., Earle-Hughes,J., Fine,L.D., Fitzgerald,L.M., Fitzhugh,W.M., Fritchman,J.L., Geoghagen,N.S., Glodek,A., Gnehm,C.L., Hanna,M.C., Hedblom,E., Hinkle,P.S.Jr., Kelley,J.M., Kelley,J.C., Liu,L.-I., Marmaros,S.M., Merrick,J.M., Moreno-Palancas,R.F., McDonald,L.A., Nguyen,D.T., Pelligrino,S.M., Phillips,C.A., Ryder,S.E., Scott,J.L., Saudek,D.M., Shirley,R., Small,K.V., Spriggs,T.A., Utterback,T.R., Weidman,J.F., Li,Y., Bednarek,D.P., Cao,L., Cepeda,M.A., Coleman,T.A., Collins,E.J., Dimke,D., Feng,D.-F., Ferrie,A., Fischer,C., Hastings,G.A., He,W.W., Hu,J.S., Greene,J.M., Gruber,J., Hudson,P., Kim,A.K., Kozak,D.L., Kunsch,C., Hungjun,J., Li,H., Weissner,P.S., Olsen,H., Raymond,L., Wei,Y.F., Wing,J., Xu,C., Yu,G.L., Ruben,S.M., Dillion,P.J., Fannon,M.R., Rosen,C.A., Haseltine,W.A., Fields,C., Fraser,C.M. and Venter,J.C.
 TITLE Initial assessment of human gene diversity and expression patterns based upon 83 million nucleotides of cDNA sequence
 JOURNAL Nature 377 (6547 Suppl), 3-174 (1995)
 MEDLINE 12140200
 COMMENT On Sep 12, 1996 this sequence version replaced gi:1397854.
 Other_ESTs: THC180721
 Contact: Kerlavage, AR

FEATURES
 source
 1..443
 /organism="Homo sapiens"
 /db_xref="ATCC (inhost):156811"
 /db_xref="taxon:9606"
 /clone_lib="Jurkat T-cells V"
 /cell_type="T-lymphocyte"
 /note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2: XhoI"
 BASE COUNT 86 a 144 c 143 g 64 t 6 others
 ORIGIN
 alignment_scores:
 Quality: 51.00 Length: 10
 Ratio: 5.100 Gaps: 0
 Percent Similarity: 100.000 Percent Identity: 100.000
 alignment_block:
 US-08-653-294-24 x AA310808 from: 1 to: 443
 Seq primer: M13 Reverse

Location/Qualifiers
 1..443
 /organism="Homo sapiens"
 /db_xref="ATCC (inhost):156811"
 /db_xref="taxon:9606"
 /clone_lib="Jurkat T-cells V"
 /cell_type="T-lymphocyte"
 /note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2: XhoI"
 BASE COUNT 86 a 144 c 143 g 64 t 6 others
 ORIGIN

alignment_scores:
 Quality: 51.00 Length: 10
 Ratio: 5.100 Gaps: 0
 Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:

US-08-653-294-24 x AA310808

Align seg 1/1 to: AA310808 from: 1 to: 443

1 ArgGluSerLeuArgAsnLeuArgGlyTyr 10
 |||||
 292 CGAGAGAGCTTCGGAACTCGCGGCTAC 321

seq_name: gb_est9:C18310

seq_documentation_block: 475 bp mRNA EST 02-OCT-1996
 LOCUS C18310
 DEFINITION C18310 Human placenta cDNA (TFujiwara) Homo sapiens cDNA clone GEN-560D07 5', mRNA sequence.
 ACCESSION C18310
 VERSION C18310.1 GI:1579912
 KEYWORDS EST.
 SOURCE human.

ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 REFERENCE 1 (bases 1 to 475)
 AUTHORS Fujiwara,T., Hirano,H., Hishigaki,H., Horie,M., Kawai,A., Kuga,Y., Kyushiki,H., Nagata,M., Okuno,S., Ozaki,K., Shimizu,F., Shimada,Y., Shinomiya,H., Suzuki,M., Takaichi,A., Takeda,S., Watanabe,T., Maekawa,H., Nakamura,Y. and Takahashi,E.
 TITLE Otsuka cDNA project
 JOURNAL Unpublished (1996)
 COMMENT On Sep 12, 1996 this sequence version replaced gi:1393837.
 Contact: Tsutomu Fujiwara
 Otsuka GEN Research Institute
 Otsuka Pharmaceutical Co.,Ltd
 463-10 Kagasuno Kawauchi-cho, Tokushima, 771-01 Japan
 Tel: 0886-65-2888
 Fax: 0886-37-1035.

FEATURES
 source
 1..475
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="GEN-560D07"
 /clone_lib="Human placenta cDNA (TFujiwara)"
 /tissue_type="placenta"
 BASE COUNT 89 a 161 c 154 g 68 t 3 others
 ORIGIN

Location/Qualifiers
 1..475
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="GEN-560D07"
 /clone_lib="Human placenta cDNA (TFujiwara)"
 /tissue_type="placenta"
 BASE COUNT 89 a 161 c 154 g 68 t 3 others
 ORIGIN

alignment_scores:
 Quality: 51.00 Length: 10
 Ratio: 5.100 Gaps: 0
 Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:

US-08-653-294-24 x C18310

Align seg 1/1 to: C18310 from: 1 to: 475

1 ArgGluSerLeuArgAsnLeuArgGlyTyr 10
 |||||
 299 CGAGAGAGCTTCGGAACTCGCGGCTAC 328

seq_name: gb_est17:AA663896

seq_documentation_block: 479 bp mRNA EST 15-DEC-1997
 LOCUS AA663896
 DEFINITION ae74d01.s1 Stratagene schizo brain S11 Homo sapiens cDNA clone IMAGE:969889 3', similar to gb:M28203 HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-62 B*1504 ALPHA (HUMAN);, mRNA sequence.

ACCESSION AA663896
 VERSION AA663896.1 GI:2617887
 KEYWORDS EST.
 SOURCE human.

ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 REFERENCE 1 (bases 1 to 479)
 AUTHORS Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S.,

Krizman,D., Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M.,
Martin,J., Moore,B., Schellenberg,K., Steptoe,M., Tan,F.,
Theising,B., White,Y., Wylie,T., Waterston,R. and Wilson,R.
WashU-NCI human EST Project
Unpublished (1997)

On Sep 12, 1996 this sequence version replaced gi:1394858.

Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@wustl.wustl.edu

This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Possible reversed clone: polyT not found
Seq primer: -40m13 fwd. ET from Amersham
High quality sequence stop: 430.

FEATURES

Location/Qualifiers
1. .479
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:969889"
/tissue="Schizoprenic schizo brain S11"
/sex="male"
/tissue_type="schizoprenic brain S-11 frontal lobe"
/dev_stage="34 years old"
/lab_host="SOLR (kanamycin resistant)"
/note="Vector: Bluescript SK-; Site.1: EcoRI. Library
constructed from S-11 frontal lobe, male, 34 years old,
50% caucasian, 50% Aleutian. Schizophrenic suicide.
Random primed into EcoRI site of ZAP II Vector. Mass
excised. Custom library. Avg insert length 1.4kb.
Material obtained by Johnston N., Torrey, E.F., Yolken R.,
and the Stanley Neuropathology Consortium - Analysis of
RNAs from the Brains of Individuals with Psychiatric
Diseases (Unpublished) Stanley Neurovirology Laboratory,
Johns Hopkins School of Medicine, Baltimore MD."

BASE COUNT 91 a 165 c 158 g 64 t
ORIGIN
alignment_scores:
Quality: 51.00 Length: 10
Ratio: 5.100 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000
alignment_block:
US-08-653-294-24 x AA663896 ..
Align seg 1/1 to: AA663896 from: 1 to: 479
1 ArgGluserLeuArgAsnLeuArgGlyTyr 10
|||||
283 CGAGAGACCTCGGACCTCGCGGCTAC 312

seq_name: gb_est35:AL039796

seq_documentation_block:
LOCUS AL039796 503 bp mRNA EST 29-SEP-1999
DEFINITION DKFp434B1912-1 434 (synonym: htes3) Homo sapiens cDNA clone
DKFp434B1912 5', mRNA sequence.
ACCESSION AL039796
VERSION AL039796
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 503)
AUTHORS Duesterhoeft,A., Lauber,J., Mewes,H.W., Gassenhuber,J. and
Wiemann,S.
TITLE EST (Duesterhoeft, et al.)
JOURNAL Unpublished (1999)

COMMENT

On Jun 2, 1999 this sequence version replaced gi:4967270.
Contact: Duesterhoeft A
MIPS
Am Klopferpitz 18a D-82152 Martinsried, Germany
This is the 5' sequence of the clone insert
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
sequenced by Qiagen within the cDNA sequencing consortium of the
German Genome Project.
No sl sequence available.
This clone is available at the RZPD in Berlin.
Please contact the RZPD: Ressourcenzentrum, Reuberweg 6, 14059
Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.

FEATURES

Location/Qualifiers
1. .503
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="DKFp434B1912"
/clone_lib="434 (synonym: htes3)"
/tissue_type="testis"
/dev_stage="adult"
/lab_host="DH10B"
/note="Vector: pSPORT1; Site.1: NotI; Site.2: SalI"
BASE COUNT 96 a 172 c 165 g 68 t 2 others
ORIGIN

alignment_scores:
Quality: 51.00 Length: 10
Ratio: 5.100 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000
alignment_block:
US-08-653-294-24 x AL039796 ..
Align seg 1/1 to: AL039796 from: 1 to: 503

1 ArgGluserLeuArgAsnLeuArgGlyTyr 10
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300 CGAGAGACCTCGGACCTCGCGGCTAC 329

seq_name: gb_est11:AA263135

seq_documentation_block:
LOCUS AA263135 710 bp mRNA EST 02-JUL-1998
DEFINITION PMW0598 KG1-a Lambda Zap Express cDNA library Homo sapiens cDNA 5',
mRNA sequence.
ACCESSION AA263135
VERSION AA263135.1 GI:1898941
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 710)
AUTHORS Claudio,J.O., Liew,C.C., Dempsey,A.A., Cukerman,E., Stewart,A.K.,
Na,E., Atkins,H.I., Iscove,N.N. and Hawley,R.G.
Identification of sequence-tagged transcripts differentially
expressed within the human hematopoietic hierarchy
Genomics 50 (1), 44-52 (1998)
JOURNAL 98292493
MEDLINE
COMMENT On May 5, 1995 this sequence version replaced gi:797738.
Contact: Hawley RG
Oncology Research Laboratories
The Toronto Hospital
CRCS-424, 67 College St., Toronto, Ontario M5G 2M1, Canada
Tel: 416 3403834
Fax: 416 3403453
Email: r.hawley@utoronto.ca

Clone was randomly picked from KG1a primary library.
Seq primer: 5' GAATTAACCTCATTAAAGG 3'
High quality sequence stop: 710.
Location/Qualifiers

```

source
1. .710
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="KGI-a Lambda Zap Express cDNA library"
/cell_type="promyeloblast"
/clone_line="KGI-a"
/note="Vector: Lambda Zap Express (Stratagene); Site_1:
EcoRI; Site_2: XhoI; Unidirectional cloning sites:
EcoRI-XhoI. mRNA was purified from KGI-a cell line, cDNA
was synthesized using an XhoI-OligodT linker primer. EcoRI
adaptors were ligated, followed by digestion with XhoI for
directional cloning into predigested Lambda Zap Express"
BASE COUNT      150 a      224 c      227 g      109 t
ORIGIN

alignment_scores:
  Quality: 51.00      Length: 10
  Ratio: 5.100      Gaps: 0
  Percent Similarity: 100.000      Percent Identity: 100.000

alignment_block:
US-08-653-294-24 x AA263135 ..
Align seg 1/1 to: AA263135 from: 1 to: 710
1 ArgGlusSerLeuArgAsnLeuArgGlyTyr 10
|||||
300 CGAGAGAGCCTGGGACCTGCGCGGCTAC 329

seq_name: gb_est27:A1424623

seq_documentation_block:
LOCUS   A1424623      209 bp      mRNA      EST      30-MAR-1999
DEFINITION   tf34901.x1 NCI_CGAP_Brn23 Homo sapiens cDNA clone IMAGE:2098128 3',
mRNA sequence.
ACCESSION   A1424623
VERSION     A1424623.1 GI:4270554
KEYWORDS    EST.
SOURCE      human.
ORGANISM    Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 209)
AUTHORS    NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE      National Cancer Institute / National Institute of Neurological
Disorders and Stroke, Brain Tumor Genome Anatomy Project
(CGAP/BrGAP), Tumor Gene Index
JOURNAL    Unpublished (1998)
COMMENT    On Apr 21, 1998 this sequence version replaced gi:3072294.
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert.Strausberg@nih.gov
Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D.,
Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
Bonaldo, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html

Insert Length: 1183      Std Error: 0.00
Seq primer: 40UP from Gibco
High quality sequence stop: 208.
Location/Qualifiers
1. .209
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2098128"
/clone_lib="NCI_CGAP_Brn23"
/tissue_type="glioblastoma (pooled)"
FEATURES
Source

```

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/lab_host="DH10B"
/note="Organ: brain; Vector: pT7T3D-Pac (Pharmacia) with a
modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st
strand cDNA was primed with a Not I - oligo(dT) primer [5'
TGTACCAATCTGAAGTGGAGCGCCGATCTCTTTTCTTTTCTTTTCTTTT
T 3']; double-stranded cDNA was ligated to Eco RI
adaptors (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of the modified pT7T3 vector.
Library is normalized, and was constructed by Bento
Soares and M. Fatima Bonaldo."
BASE COUNT      63 a      55 c      33 g      57 t      1 others
ORIGIN

alignment_scores:
  Quality: 44.00      Length: 9
  Ratio: 4.889      Gaps: 0
  Percent Similarity: 100.000      Percent Identity: 100.000

alignment_block:
US-08-653-294-24 x A1424623/rev ..
Align seg 1/1 to reverse of: A1424623 from: 1 to: 209
1 ArgGlusSerLeuArgAsnLeuArgGly 9
|||||
157 AGAGAGTCCTTAGGAACCTTGAGAGG 131

```

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: February 7, 2000, 18:04:37 ; Search time 111.22 Seconds
(without alignments)
4.241 Million cell updates/sec

Title: US-08-653-294-25
Perfect score: 50
Sequence: 1 RENLRTALRY 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 142080 seqs, 47169319 residues

Total number of hits satisfying chosen parameters: 142080

Minimum DB seq length: 0
Maximum DB seq length: 1000000

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database : PIR_62:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	50	100.0	355	2 I37516	HLA-B alpha-chain
2	50	100.0	362	2 S25415	class I histocompa
3	50	100.0	362	2 A45850	MHC class I histoc
4	50	100.0	362	2 I61861	MHC HLA-B*44.2 chai
5	50	100.0	362	2 I54442	MHC class I histoc
6	45	90.0	137	2 I80174	class I histocompa
7	45	90.0	359	1 HLHUB4	MHC class I histoc
8	45	90.0	362	2 I54457	MHC class I lympho
9	44	88.0	273	2 I38509	MHC class I histoc
10	44	88.0	274	2 I54463	MHC HLA-B*38 chain
11	44	88.0	354	2 I59308	class I histocompa
12	44	88.0	354	2 I80168	class I histocompa
13	44	88.0	354	2 I80167	class I histocompa
14	44	88.0	355	2 I80169	class I histocompa
15	44	88.0	355	2 I80171	class I histocompa
16	44	88.0	359	1 HLHUB12	MHC class I histoc
17	44	88.0	362	1 HLHUB8	MHC class I histoc
18	44	88.0	362	2 B30345	MHC class I histoc
19	44	88.0	362	2 JH0541	class I histocompa
20	44	88.0	362	2 JH0539	class I histocompa
21	44	88.0	362	2 JH0540	class I histocompa
22	44	88.0	362	2 A45834	MHC class I histoc
23	44	88.0	362	2 I84486	transmembrane glyco
24	44	88.0	362	2 I62045	gene HLA B-1517 pr
25	44	88.0	362	2 I84490	lymphocyte antigen
26	44	88.0	362	2 I37521	HLA-B*57.2 antigen
27	44	88.0	362	2 A30345	MHC class I histoc
28	44	88.0	362	2 I59633	MHC HLA-B histocomp
29	44	88.0	362	2 S24434	class I histocompa
30	44	88.0	362	2 I37120	MHC class I histoc

31 44 88.0 363 2 S07113 class I histocompa
32 44 88.0 363 2 S03537 class I histocompa
33 44 88.0 364 2 D35997 MHC class I histoc
34 44 88.0 365 2 S77963 MHC class I histoc
35 44 88.0 365 2 I54416 HLA-AW24 protein -
36 44 88.0 365 2 I54493 MHC class I histoc
37 43 86.0 292 2 I57806 MHC H-2K-kml mRNA
38 43 86.0 362 2 B45876 class I histocompa
39 43 86.0 368 2 A60854 MHC class I histoc
40 43 86.0 368 2 I49712 H-2K-s - mouse
41 43 86.0 368 2 I49713 H-2K-sm1 - mouse
42 43 86.0 369 1 HLMSKK MHC class I histoc
43 40 80.0 338 2 I56116 MHC HLA-B*27-HS - h
44 40 80.0 362 1 HLHUB2 MHC class I histoc
45 40 80.0 362 2 C35997 MHC class I histoc

ALIGNMENTS

RESULT 1
I37516
HLA-B alpha-chain - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 04-Oct-1996 #sequence_revision 04-Oct-1996 #text_change 23-Jul-1999
C:Accession: I37516
R:Gauchat-Feliss, D.; Breur-Vriesendorp, B.S.; Rufer, N.; Jeannet, M.; Roosnek, E.; Ti
Tissue Antigens 44, 261-264, 1994
A:Title: Sequencing of a novel functional HLA-B*44 subtype differing in two residues 1
A:Reference number: I37516; MUID:95176328
A:Accession: I37516
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-355 <RES>
A:Cross-references: EMBL:X75953; NID:g791007; PIDN:CAA53566.1; PID:g791008
C:Superfamily: class I histocompatibility antigen; immunoglobulin homology

Query Match 100.0%; Score 50; DB 2; Length 355;
Best Local Similarity 100.0%; Pred. No. 0.014;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RENLRTALRY 10
|||||
DB 99 RENLRTALRY 108

RESULT 2
S25415
class I histocompatibility antigen HLA-B*4403 alpha chain - human
C:Species: Homo sapiens (man)
C>Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 23-Jul-1999
C:Accession: S25415
R:Feischauer, K.; Kernan, N.A.; Dupont, B.; Yang, S.Y.
Tissue Antigens 37, 133-137, 1991
A:Title: The two major subtypes of HLA-B*44 differ for a single amino acid in codon 15
A:Reference number: S25415; MUID:91335451
A:Accession: S25415
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-362 <FLE>
A:Cross-references: EMBL:X64366; NID:g32178; PIDN:CAA45718.1; PID:g32179
C:Genetics:
A:Gene: GBB:HLA-B
A:Cross-references: GDB:120048; OMIM:142830
A:Map position: 6p21.3-6p21.3
C:Superfamily: class I histocompatibility antigen; immunoglobulin homology
C:Keywords: transmembrane protein
P:220-285/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 50; DB 2; Length 362;
Best Local Similarity 100.0%; Pred. No. 0.014;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RENTLALRY 10
| | | | | | | | | |
DB 99 RENTLALRY 108

RESULT 3

A45850
MHC class I histocompatibility antigen HLA-B13.1 - human
C:Species: Homo sapiens (man)
C:Date: 03-Jun-1993 #sequence_revision 03-Jun-1993 #text_change 23-Jul-1999
C:Accession: A45850
R:Kato, K.; Dupont, B.; Yang, S.Y.
Immunogenetics 29, 117-120, 1989
A:Title: Localization of nucleotide sequence which determines mongoloid subtype of HLA-B
A:Reference number: A45850; MUID:89122134
A:Accession: A45850
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-362 <RAT>
A:Cross-references: GB:M24075; NID:g187703; PIDN:AAA59627.1; PID:g386884
C:Genetics:
A:Gene: GDB:HLA-B
A:Cross-references: GDB:120048; OMIM:142830
A:Map position: 6p21.3-6p21.3
C:Superfamily: class I histocompatibility antigen; immunoglobulin homology
F:220-285/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 50; DB 2; Length 362;
Best Local Similarity 100.0%; Pred. No. 0.014;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RENTLALRY 10
| | | | | | | | | |
DB 99 RENTLALRY 108

RESULT 4

I61861
MHC HLA-B44.2 chain - human
C:Species: Homo sapiens (man)
C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 23-Jul-1999
C:Accession: I61861
R:Parham, P.; Lawlor, D.A.; Lomen, C.E.; Ennis, P.D.
J. Immunol. 142, 3937-3950, 1989
A:Title: Diversity and diversification of HLA-A,B,C alleles.
A:Reference number: I36956; MUID:89235215
A:Accession: I61861
A:Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: DNA
A:Residues: 1-362 <RES>
A:Cross-references: GB:M24038; NID:g187811; PIDN:AAA59663.1; PID:g386900
C:Superfamily: class I histocompatibility antigen; immunoglobulin homology

Query Match 100.0%; Score 50; DB 2; Length 362;
Best Local Similarity 100.0%; Pred. No. 0.014;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RENTLALRY 10
| | | | | | | | | |
DB 99 RENTLALRY 108

RESULT 5

I54442
MHC class I histocompatibility antigen HLA-B13 precursor - human
C:Species: Homo sapiens (man)
C:Date: 07-Jun-1996 #sequence_revision 07-Jun-1996 #text_change 23-Jul-1999
C:Accession: I54442; I61858
R:Zemmour, J.; Ennis, P.D.; Parham, P.; Dupont, B.

Immunogenetics 27, 281-287, 1988
A:Title: Comparison of the structure of HLA-B*47 to HLA-B13 and its relationship to 2
A:Reference number: I54442; MUID:88152906
A:Accession: I54442
A:Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: DNA
A:Residues: 1-362 <ZEM>
A:Cross-references: GB:M19757; NID:g184161; PIDN:AAA52657.1; PID:g386774
R:Parham, P.; Lawlor, D.A.; Lomen, C.E.; Ennis, P.D.
J. Immunol. 142, 3937-3950, 1989
A:Title: Diversity and diversification of HLA-A,B,C alleles.
A:Reference number: I36956; MUID:89235215
A:Accession: I61858
A:Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: DNA
A:Residues: 1-362 <PAR>
A:Cross-references: GB:M24041; NID:g187805; PIDN:AAA59660.1; PID:g386897
C:Genetics:
A:Gene: GDB:HLA-B
A:Cross-references: GDB:120048; OMIM:142830
A:Map position: 6p21.3-6p21.3
C:Superfamily: class I histocompatibility antigen; immunoglobulin homology

Query Match 100.0%; Score 50; DB 2; Length 362;
Best Local Similarity 100.0%; Pred. No. 0.014;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RENTLALRY 10
| | | | | | | | | |
DB 99 RENTLALRY 108

RESULT 6

I80174
class I histocompatibility antigen - chimpanzee (fragment)
C:Species: Pan troglodytes (chimpanzee)
C:Date: 24-May-1996 #sequence_revision 24-May-1996 #text_change 23-Jul-1999
C:Accession: I80174
R:McAdam, S.N.; Boyson, J.E.; Liu, X.; Garber, T.L.; Hughes, A.L.; Bontrop, R.E.; Wat
Proc. Natl. Acad. Sci. U.S.A. 91, 5893-5897, 1994
A:Title: A uniquely high level of recombination at the HLA-B locus.
A:Reference number: I59308; MUID:94286344
A:Accession: I80174
A:Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: DNA
A:Residues: 1-137 <RES>
A:Cross-references: EMBL:U05585; NID:g454787; PIDN:AAA50188.1; PID:g454788
C:Superfamily: class I histocompatibility antigen; immunoglobulin homology

Query Match 90.0%; Score 45; DB 2; Length 137;
Best Local Similarity 90.0%; Pred. No. 0.052;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RENTLALRY 10
| | | | | | | | | |
DB 40 RENTLALRY 49

RESULT 7

HLHUB4
MHC class I histocompatibility antigen HLA-B44 alpha chain precursor - human (fragmen
C:Species: Homo sapiens (man)
C:Date: 31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change 22-Jun-1999
C:Accession: A25295
R:Kottmann, A.H.; Seemann, G.H.A.; Guesow, H.D.; Roos, M.H.
Immunogenetics 23, 396-400, 1986
A:Title: DNA sequence of the coding region of the HLA-B44 gene.
A:Reference number: A25295; MUID:86249389
A:Accession: A25295
A:Molecule type: mRNA
A:Residues: 1-359 <KOT>

A:Cross-references: GB:M15470; NID:g187680; PIDN:AAA59619.1; PID:g386883
C:Genetics:

A:Gene: GDB:HLA-B
A:Cross-references: GDB:120048; OMIM:142830
A:Map position: 6p21.3-6p21.3
C:Superfamily: class I histocompatibility antigen; immunoglobulin homology
C:Keywords: duplication; glycoprotein; heterodimer; transmembrane protein; transplantati
F:1-21/Domain: signal sequence (fragment) #status predicted <SIG>
F:22-359/Product: class I histocompatibility antigen HLA-B44 alpha chain #status predict
F:22-304/Domain: extracellular #status predicted <EXT>
F:22-111/Domain: alpha-1 <EX1>
F:112-203/Domain: alpha-2 <EX2>
F:217-282/Domain: immunoglobulin homology <IMM>
F:305-328/Domain: transmembrane #status predicted <TM>
F:329-359/Domain: intracellular #status predicted <INT>
F:107/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 90.0%; Score 45; DB 1; Length 359;
Best Local Similarity 90.0%; Pred. No. 0.14;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RENVLTALRY 10
||||| ||
DB 96 RENVLTAARY 105

RESULT 8
I54457
MHC class I lymphocyte antigen - human
C:Species: Homo sapiens (man)
C:Date: 07-Jun-1996 #sequence_revision 07-Jun-1996 #text_change 23-Jul-1999
C:Accession: I54457
R:Pohla, H.; Kuon, W.; Tabaczewski, P.; Doerner, C.; Weiss, E.H.
Immunogenetics 29, 297-307, 1989
A:Title: Allelic variation in HLA-B and HLA-C sequences and the evolution of the HLA-B a
A:Reference number: I54457; MUID:89233295
A:Accession: I54457
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-362 <RES>

A:Cross-references: GB:M28205; NID:g576470; PIDN:AAA57145.1; PID:g576471
C:Superfamily: class I histocompatibility antigen; immunoglobulin homology

Query Match 90.0%; Score 45; DB 2; Length 362;
Best Local Similarity 90.0%; Pred. No. 0.14;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RENVLTALRY 10
||||| ||
DB 99 RENVLTALRY 108

RESULT 9
I38509
MHC class I histocompatibility antigen - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 06-Sep-1996 #sequence_revision 06-Sep-1996 #text_change 23-Jul-1999
C:Accession: I38509
R:Cereb, N.; Choi, J.W.; Riu, K.Z.; Yang, S.Y.
Tissue Antigens 44, 271-273, 1994
A:Title: HLA-B*5105, a newly identified B51 IEF variant.
A:Reference number: I38509; MUID:95176331
A:Accession: I38509

A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-273 <RES>
A:Cross-references: EMBL:U06697; NID:g469544; PIDN:AAA92997.1; PID:g469545
C:Genetics:
A:Gene: GDB:HLA-B
A:Cross-references: GDB:120048; OMIM:142830
A:Map position: 6p21.3-6p21.3

C:Superfamily: class I histocompatibility antigen; immunoglobulin homology

Query Match 88.0%; Score 44; DB 2; Length 273;
Best Local Similarity 90.0%; Pred. No. 0.17;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RENVLTALRY 10
||||| ||
DB 74 RENVLTALRY 83

RESULT 10
I54463
MHC HLA-B38 chain - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 07-Jun-1996 #sequence_revision 07-Jun-1996 #text_change 23-Jul-1999
C:Accession: I54463
R:Mueller, C.A.; Engler-Blum, G.; Gekeler, V.; Steiert, I.; Weiss, E.; Schmidt, H.
Immunogenetics 30, 200-207, 1989
A:Title: Genetic and serological heterogeneity of the supertypic HLA-B locus specific
A:Reference number: I54463; MUID:89379286
A:Accession: I54463
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-274 <RES>
A:Cross-references: GB:M29864; NID:g187674; PIDN:AAA36222.1; PID:g187675
C:Superfamily: class I histocompatibility antigen; immunoglobulin homology

Query Match 88.0%; Score 44; DB 2; Length 274;
Best Local Similarity 90.0%; Pred. No. 0.17;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RENVLTALRY 10
||||| ||
DB 75 RENVLTALRY 84

RESULT 11
I59308
class I histocompatibility antigen - pygmy chimpanzee (fragment)
C:Species: Pan paniscus (pygmy chimpanzee, bonobo)
C:Date: 31-May-1996 #sequence_revision 31-May-1996 #text_change 23-Jul-1999
C:Accession: I59308
R:McAdam, S.N.; Boyson, J.E.; Liu, X.; Garber, T.L.; Hughes, A.L.; Bontrop, R.E.; Wat
Proc. Natl. Acad. Sci. U.S.A. 91, 5893-5897, 1994
A:Title: A uniquely high level of recombination at the HLA-B locus.
A:Reference number: I59308; MUID:94286544
A:Accession: I59308
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-354 <RES>

A:Cross-references: EMBL:U05575; NID:g454767; PIDN:AAA50178.1; PID:g454768
C:Superfamily: class I histocompatibility antigen; immunoglobulin homology

Query Match 88.0%; Score 44; DB 2; Length 354;
Best Local Similarity 90.0%; Pred. No. 0.22;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RENVLTALRY 10
||||| ||
DB 91 RENVLTALRY 100

RESULT 12
I80168
class I histocompatibility antigen - chimpanzee (fragment)
C:Species: Pan troglodytes (chimpanzee)
C:Date: 24-May-1996 #sequence_revision 24-May-1996 #text_change 23-Jul-1999
C:Accession: I80168
R:McAdam, S.N.; Boyson, J.E.; Liu, X.; Garber, T.L.; Hughes, A.L.; Bontrop, R.E.; Wat

Proc. Natl. Acad. Sci. U.S.A. 91, 5893-5897, 1994
A:Title: A uniquely high level of recombination at the HLA-B locus.
A:Reference number: I59308; MUID:94286544

A:Status: preliminary; translated from GB/EMBL/DBDJ

A:Molecule type: mRNA

A:Residues: 1-354 <RES>

A:Cross-references: EMBL:U05579; NID:q454775; PIDN:AAA50182.1; PID:q454776
C:Superfamily: class I histocompatibility antigen; immunoglobulin homology

Query Match 88.0%; Score 44; DB 2; Length 354;
Best Local Similarity 90.0%; Pred. No. 0.22;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RENLRLALRY 10
| | | | | | | | | |
Db 91 RENLRLALRY 100

RESULT 13

class I histocompatibility antigen - pygmy chimpanzee (fragment)
C:Species: Pan paniscus (pygmy chimpanzee, bonobo)

C:Date: 24-May-1996 #sequence_revision 24-May-1996 #text_change 23-Jul-1999
C:Accession: I80167

R:McAdam, S.N.; Boyson, J.E.; Liu, X.; Garber, T.L.; Hughes, A.L.; Bontrop, R.E.; Watkin

Proc. Natl. Acad. Sci. U.S.A. 91, 5893-5897, 1994

A:Title: A uniquely high level of recombination at the HLA-B locus.
A:Reference number: I59308; MUID:94286544

A:Accession: I80167

A:Status: preliminary; translated from GB/EMBL/DBDJ

A:Molecule type: mRNA

A:Residues: 1-354 <RES>

A:Cross-references: EMBL:U05578; NID:q454773; PIDN:AAA50181.1; PID:q454774
C:Superfamily: class I histocompatibility antigen; immunoglobulin homology

Query Match 88.0%; Score 44; DB 2; Length 354;
Best Local Similarity 90.0%; Pred. No. 0.22;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RENLRLALRY 10
| | | | | | | | | |
Db 91 RENLRLALRY 100

RESULT 14

class I histocompatibility antigen - chimpanzee (fragment)
C:Species: Pan troglodytes (chimpanzee)

C:Date: 24-May-1996 #sequence_revision 24-May-1996 #text_change 23-Jul-1999
C:Accession: I80169

R:McAdam, S.N.; Boyson, J.E.; Liu, X.; Garber, T.L.; Hughes, A.L.; Bontrop, R.E.; Watkin

Proc. Natl. Acad. Sci. U.S.A. 91, 5893-5897, 1994

A:Title: A uniquely high level of recombination at the HLA-B locus.
A:Reference number: I59308; MUID:94286544

A:Accession: I80169

A:Status: preliminary; translated from GB/EMBL/DBDJ

A:Molecule type: mRNA

A:Residues: 1-355 <RES>

A:Cross-references: EMBL:U05580; NID:q454777; PIDN:AAA50183.1; PID:q454778
C:Superfamily: class I histocompatibility antigen; immunoglobulin homology

Query Match 88.0%; Score 44; DB 2; Length 355;
Best Local Similarity 90.0%; Pred. No. 0.22;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RENLRLALRY 10
| | | | | | | | | |
Db 91 RENLRLALRY 100

RESULT 15

I80171

class I histocompatibility antigen - chimpanzee (fragment)

C:Species: Pan troglodytes (chimpanzee)

C:Date: 24-May-1996 #sequence_revision 24-May-1996 #text_change 23-Jul-1999

C:Accession: I80171

R:McAdam, S.N.; Boyson, J.E.; Liu, X.; Garber, T.L.; Hughes, A.L.; Bontrop, R.E.; Wat

Proc. Natl. Acad. Sci. U.S.A. 91, 5893-5897, 1994

A:Title: A uniquely high level of recombination at the HLA-B locus.
A:Reference number: I59308; MUID:94286544

A:Accession: I80171

A:Status: preliminary; translated from GB/EMBL/DBDJ

A:Molecule type: mRNA

A:Residues: 1-355 <RES>

A:Cross-references: EMBL:U05582; NID:q454781; PIDN:AAA50185.1; PID:q454782

C:Superfamily: class I histocompatibility antigen; immunoglobulin homology

Query Match 88.0%; Score 44; DB 2; Length 355;
Best Local Similarity 90.0%; Pred. No. 0.22;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RENLRLALRY 10
| | | | | | | | | |
Db 91 RENLRLALRY 100

Search completed: February 7, 2000, 18:04:37
Job time: 22203 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: February 8, 2000, 01:25:58 ; Search time 68.63 Seconds
(without alignments)
4.352 Million cell updates/sec

Title: US-08-653-294-25

Perfect score: 50

Sequence: 1 RENTRYALRY 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 82229 seqs, 29864866 residues

Total number of hits satisfying chosen parameters: 82229

Minimum DB seq length: 0

Maximum DB seq length: 1000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : SwissProt_38:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	50	100.0	362	1	1B05_HUMAN
2	50	100.0	362	1	1B41_HUMAN
3	50	100.0	362	1	1B42_HUMAN
4	45	90.0	359	1	1B40_HUMAN
5	44	88.0	359	1	1B01_PANTR
6	44	88.0	362	1	1B01_GORGO
7	44	88.0	362	1	1B02_GORGO
8	44	88.0	362	1	1B03_GORGO
9	44	88.0	362	1	1B15_HUMAN
10	44	88.0	362	1	1B47_HUMAN
11	44	88.0	362	1	1B49_HUMAN
12	44	88.0	362	1	1B52_HUMAN
13	44	88.0	362	1	1B53_HUMAN
14	44	88.0	362	1	1B54_HUMAN
15	44	88.0	362	1	1B60_HUMAN
16	44	88.0	362	1	1B61_HUMAN
17	44	88.0	362	1	1B62_HUMAN
18	44	88.0	362	1	HLAH_HUMAN
19	44	88.0	365	1	1A23_HUMAN
20	44	88.0	365	1	1A24_HUMAN
21	43	86.0	369	1	HA1K_MOUSE
22	40	80.0	338	1	1B20_HUMAN
23	40	80.0	361	1	1B14_HUMAN
24	40	80.0	362	1	1B16_HUMAN
25	40	80.0	362	1	1B18_HUMAN
26	40	80.0	362	1	1B19_HUMAN
27	40	80.0	362	1	1B29_HUMAN
28	40	80.0	362	1	1B45_HUMAN
29	39	78.0	365	1	1A25_HUMAN
30	39	78.0	365	1	1A32_HUMAN
31	38	76.0	298	1	HA1Y_MOUSE
32	38	76.0	361	1	HA1A_RABIT
33	38	76.0	361	1	HA1B_RABIT
34	38	76.0	365	1	HA12_MOUSE

RESULT 1

1B05_HUMAN
ID 1B05_HUMAN STANDARD; PRT; 362 AA.
AC P30461;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-13 B*1301 ALPHA CHAIN
DE PRECURSOR (B13.1).
GN HLA-B OR HLAB.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Primates; Catarrhini; Hominidae; Homo.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 89235215.
RA PARHAM P., LAWLER D.A., LOMEN C.E., ENNIS P.D.;
RT "Diversity and diversification of HLA-A,B,C alleles."
RL J. Immunol. 142:3937-3950(1989).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE; 88152906.
RA ZEMMOUR J., ENNIS P.D., PARHAM P., DUPONT B.;
RT "Comparison of the structure of HLA-B*47 to HLA-B13 and its
RT relationship to 21-hydroxylase deficiency."
RL Immunogenetics 27:281-287(1988).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE-BLOOD;
RX MEDLINE; 96053518.
RA LIN L., TOKUNAGA K., NAKAJIMA F., ISHIKAWA Y., KASHIWASE K.,
RA TANAKA H., KUNATA S., SIDELTSEVA E., AKAZA T., TADOKORO K.,
RA SHIBATA Y., CHANDANAYINGYONG D., JUJI T.;
RT "Both HLA-B*1301 and B*1302 exist in Asian populations and are
RT associated with different haplotypes."
RL Hum. Immunol. 43:51-56(1995).
CC -!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
CC THE IMMUNE SYSTEM.
CC -!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
CC MICROGLOBULIN).
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CC
CC EMBL; M24041; AAA59660.1; -;
CC EMBL; M19757; AAA52657.1; -;
CC EMBL; D50291; BAA08822.1; -;
CC HSSP; P30491; IALM.
CC MIM; 142830; -;
CC PROSITE; PS00290; IG_MHC; 1.
CC PFAM; PF00047; I9; 1.
CC PFAM; PF00129; MHC_I; 1.

35 35 70.0 555 1 POST_XENLA
36 34 68.0 361 1 HA1U_MOUSE
37 34 68.0 365 1 1A04_GORGO
38 34 68.0 384 1 HA1T_MOUSE
39 34 68.0 582 1 MNT_HUMAN
40 34 68.0 591 1 MNT_MOUSE
41 33 66.0 225 1 SODM_BACSU
42 33 66.0 267 1 YADB_SCHPO
43 33 66.0 328 1 HA1Q_MOUSE
44 33 66.0 362 1 HA13_MOUSE
45 33 66.0 368 1 HA1W_MOUSE
P27536 xenopus lae
P14433 mus musculus
P30378 gorilla gor
P14432 mus musculus
Q95883 homo sapien
Q08789 mus musculus
P54375 bacillus su
Q09836 schizosacch
P14428 mus musculus
P14426 mus musculus
P03991 mus musculus

ALIGNMENTS

KW MHC I; Transmembrane; Glycoprotein; Signal.
 FT SIGNAL 1 24
 FT CHAIN 25 362 HLA CLASS I HISTOCOMPATIBILITY ANTIGEN,
 FT B-13 B*1301 ALPHA CHAIN.
 FT DOMAIN 25 114
 FT DOMAIN 115 206 EXTRACELLULAR ALPHA-1.
 FT DOMAIN 207 298 EXTRACELLULAR ALPHA-2.
 FT DOMAIN 299 309 EXTRACELLULAR ALPHA-3.
 FT TRANSMEM 310 333 CONNECTING PEPTIDE.
 FT DOMAIN 334 362 CYTOPLASMIC TAIL.
 FT CARBOHYD 110 110 BY SIMILARITY.
 FT DISULFID 125 188 BY SIMILARITY.
 FT DISULFID 227 283 BY SIMILARITY.
 SQ SEQUENCE 362 AA; 40474 MW; 28B67875 CRC32;

Query Match 100.0%; Score 50; DB 1; Length 362;
 Best Local Similarity 100.0%; Pred. No. 0.0042;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RENLRTALRY 10
 (|||||)
 Db 99 RENLRTALRY 108

RESULT 2
 1B41_HUMAN
 ID 1B41_HUMAN STANDARD; PRT; 362 AA.
 AC P30481;
 DT 01-APR-1993 (Rel. 25, Created)
 DT 01-APR-1993 (Rel. 25, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, BW-44(B-12) B*4402 ALPHA CHAIN
 DE PRECURSOR (B44.2).
 GN HLA-B OR HLAB.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Eutheria; Primates; Catarrhini; Hominidae; Homo.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 89235215.
 RA PARHAM P.; LAWOR D.A.; LOMEN C.E.; ENNIS P.D.;
 RT "Diversity and diversification of HLA-A,B,C alleles."
 RL J. Immunol. 142:3937-3950(1989).
 CC -1- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
 THE IMMUNE SYSTEM.
 CC -1- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
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 CC EMBL; M24038; AAB59663.1; -
 CC HSSP; P30491; IALM.
 CC MIM; 142830; -
 CC DR PROSITE; PS00290; IG_MHC; 1.
 CC DR PFAM; PF00047; ig; 1.
 CC DR PFAM; PF00129; MHC.I; 1.
 KW MHC I; Transmembrane; Glycoprotein; Signal.
 FT SIGNAL 1 24
 FT CHAIN 25 362 HLA CLASS I HISTOCOMPATIBILITY ANTIGEN,
 FT BW-44(B-12) B*4402 ALPHA CHAIN.
 FT DOMAIN 25 114
 FT DOMAIN 115 206 EXTRACELLULAR ALPHA-1.
 FT DOMAIN 207 298 EXTRACELLULAR ALPHA-2.
 FT DOMAIN 299 309 EXTRACELLULAR ALPHA-3.
 FT TRANSMEM 310 333 CONNECTING PEPTIDE.
 FT DOMAIN 334 362 CYTOPLASMIC TAIL.

FT CARBOHYD 110 110 BY SIMILARITY.
 FT DISULFID 125 188 BY SIMILARITY.
 FT DISULFID 227 283 BY SIMILARITY.
 SQ SEQUENCE 362 AA; 40481 MW; D0AE6DD5 CRC32;

Query Match 100.0%; Score 50; DB 1; Length 362;
 Best Local Similarity 100.0%; Pred. No. 0.0042;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RENLRTALRY 10
 (|||||)
 Db 99 RENLRTALRY 108

RESULT 3
 1B42_HUMAN
 ID 1B42_HUMAN STANDARD; PRT; 362 AA.
 AC P30482;
 DT 01-APR-1993 (Rel. 25, Created)
 DT 01-APR-1993 (Rel. 25, Last sequence update)
 DT 15-JUL-1998 (Rel. 36, Last annotation update)
 DE HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, BW-44(B-12) B*4403 ALPHA CHAIN
 DE PRECURSOR.
 GN HLA-B OR HLAB.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Eutheria; Primates; Catarrhini; Hominidae; Homo.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 91335451.
 RA FLEISCHCHAUER K.; KERNAN N.A.; DUPONT B.; YANG S.Y.;
 RT "The two major subtypes of HLA-B44 differ for a single amino acid in
 RT codon 156."
 RL Tissue Antigens 37:133-137(1991).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 96435470.
 RA ADAMS E.J.; LITTLE A.M.; ARNETT K.L.; MCAULEY J.E.; WILLIAMS R.C.;
 RA PARHAM P.;
 RT "Three new HLA-B alleles found in Mexican-Americans."
 RL Tissue Antigens 46:414-416(1995).
 CC -1- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
 THE IMMUNE SYSTEM.
 CC -1- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
 MICROGLOBULIN).
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 CC EMBL; X64366; CAA45718.1; -
 CC EMBL; L42282; AAB51454.1; -
 CC EMBL; L42283; AAB51455.1; -
 CC FIR; S25415; S25415.
 CC HSSP; P30491; IALM.
 CC MIM; 142830; -
 CC DR PROSITE; PS00290; IG_MHC; 1.
 CC DR PFAM; PF00047; ig; 1.
 CC DR PFAM; PF00129; MHC.I; 1.
 KW MHC I; Transmembrane; Glycoprotein; Signal.
 FT SIGNAL 1 24
 FT CHAIN 25 362 HLA CLASS I HISTOCOMPATIBILITY ANTIGEN,
 FT BW-44(B-12) B*4403 ALPHA CHAIN.
 FT DOMAIN 25 114
 FT DOMAIN 115 206 EXTRACELLULAR ALPHA-1.
 FT DOMAIN 207 298 EXTRACELLULAR ALPHA-2.
 FT DOMAIN 299 309 EXTRACELLULAR ALPHA-3.
 FT TRANSMEM 310 333 CONNECTING PEPTIDE.


```

Best Local Similarity 90.0%; Pred. No. 0.047;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RNLRTALRY 10
DB 96 RNLRTAARY 105
      |||||
      |||||

RESULT 5
1B01_PANTR
ID 1B01_PANTR STANDARD; PRT; 359 AA.
AC P13750;
CT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 01-APR-1993 (Rel. 25, Last annotation update)
DE CHLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-1 ALPHA CHAIN PRECURSOR
DE (FRAGMENT).
OS Pan troglodytes (Chimpanzee).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutharia; Primates; Catarrhini; Hominidae; Pan.
[1]
RX SEQUENCE FROM N.A.
RX MEDLINE; 89030641.
RA MAYER W.E., JONKER M., KLEIN D., IVANYI P., VAN SEVENTER G.,
RA KLEIN J.;
RT "Nucleotide sequences of chimpanzee MHC class I alleles: evidence for
RT trans-species mode of evolution.";
RL EMBO J. 7:2765-2774(1988).
RN [2]
RP REVISIONS.
RA MAYER W.;
RL Submitted (FEB-1989) to the EMBL/GenBank/DDRJ databases.
CC -1- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
CC THE IMMUNE SYSTEM.
CC -1- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
CC MICROGLOBULIN).
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: X13115; CAA31507.1; -
CC PIR: S03537; S03537.
CC DR HSP: P03989; IHSA.
CC DR PROSITE; PS00290; IG_MHC; 1.
CC DR PFAM; PF00047; Ig; 1.
CC DR PFAM; PF00129; MHC I; 1.
CC KW MHC I; Transmembrane; Glycoprotein; Signal.
CC FT NON_TER 1
CC FT SIGNAL <1 20
CC FT CHAIN 21 359
CC -----
CC CHLA CLASS I HISTOCOMPATIBILITY ANTIGEN,
CC B-1 ALPHA CHAIN.
CC FT FT
CC FT DOMAIN 21 110
CC FT DOMAIN 111 202
CC FT DOMAIN 203 294
CC FT DOMAIN 295 305
CC FT TRANSMEM 306 329
CC FT DOMAIN 330 359
CC FT DISULFID 121 184
CC FT DISULFID 223 279
CC FT CARBOHYD 106 106
CC FT SEQUENCE 359 AA; 40173 MW; 5395FFC9 CRC32;
CC SQ

Query Match 88.0%; Score 44; DB 1; Length 359;
Best Local Similarity 90.0%; Pred. No. 0.075;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RNLRTALRY 10

```

Db 95 RENLIRALRY 104
||||| |||||

RESULT 6

1B01_GORGO STANDARD; PRT; 362 AA.
ID 1B01_GORGO
AC P30379;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 01-APR-1993 (Rel. 25, Last annotation update)
DE CLASS I HISTOCOMPATIBILITY ANTIGEN, GOGO-B0101 ALPHA CHAIN PRECURSOR.
OS Gorilla gorilla gorilla (Lowland gorilla).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Primates; Catarrhini; Hominidae; Gorilla.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 92078860.
RA LAWLOR D.A., WARREN E., TAYLOR P., PARHAM P.;
RT "Gorilla class I major histocompatibility complex alleles: comparison
to human and chimpanzee class I";
RL J. Exp. Med. 174:1491-1509(1991).
CC -!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
THE IMMUNE SYSTEM.
CC -!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
MICROGLOBULIN).
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CC EMBL; X60255; CAA42807.1; -.
DR PIR; JH0539; JH0539.
DR HSSP; P03989; ILSA.
DR PROSITE; PS00290; IG_MHC; 1.
DR PFAM; PF00047; Ig; 1.
DR PFAM; PF00129; MHC_I; 1.
KW MHC I; Transmembrane; Glycoprotein; Signal.
FT SIGNAL 1 24
FT CHAIN 25 362
FT DOMAIN 25 114
FT DOMAIN 115 206
FT DOMAIN 207 298
FT DOMAIN 299 308
FT TRANSMEM 309 332
FT DOMAIN 333 362
FT DISULFID 125 188
FT DISULFID 227 283
FT CARBOHYD 110 110
SQ SEQUENCE 362 AA; 40170 MW; 2E33E2B8 CRC32;
Query Match 88.0%; Score 44; DB 1; Length 362;
Best Local Similarity 90.0%; Pred. No. 0.076;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 RENLIRALRY 10
Db 99 RENLIRALRY 108
||||| |||||

RESULT 7

1B02_GORGO STANDARD; PRT; 362 AA.
ID 1B02_GORGO
AC P30380;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 01-APR-1993 (Rel. 25, Last annotation update)

DE OS

CLASS I HISTOCOMPATIBILITY ANTIGEN, GOGO-B0102 ALPHA CHAIN PRECURSOR.
Gorilla gorilla gorilla (Lowland gorilla).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Primates; Catarrhini; Hominidae; Gorilla.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 92078860.
RA LAWLOR D.A., WARREN E., TAYLOR P., PARHAM P.;
RT "Gorilla class I major histocompatibility complex alleles: comparison
to human and chimpanzee class I";
RL J. Exp. Med. 174:1491-1509(1991).
CC -!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
THE IMMUNE SYSTEM.
CC -!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
MICROGLOBULIN).
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or send an email to license@isb-sib.ch).
CC EMBL; X60693; CAA43101.1; -.
DR PIR; JH0540; JH0540.
DR HSSP; P03989; ILSA.
DR PROSITE; PS00290; IG_MHC; 1.
DR PFAM; PF00047; Ig; 1.
DR PFAM; PF00129; MHC_I; 1.
KW MHC I; Transmembrane; Glycoprotein; Signal.
FT SIGNAL 1 24
FT CHAIN 25 362
FT DOMAIN 25 114
FT DOMAIN 115 206
FT DOMAIN 207 298
FT DOMAIN 299 308
FT TRANSMEM 309 332
FT DOMAIN 333 362
FT DISULFID 125 188
FT DISULFID 227 283
FT CARBOHYD 110 110
SQ SEQUENCE 362 AA; 40204 MW; 3CF119AD CRC32;
Query Match 88.0%; Score 44; DB 1; Length 362;
Best Local Similarity 90.0%; Pred. No. 0.076;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 RENLIRALRY 10
Db 99 RENLIRALRY 108
||||| |||||

RESULT 8

1B03_GORGO STANDARD; PRT; 362 AA.
ID 1B03_GORGO
AC P30381;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 01-APR-1993 (Rel. 25, Last annotation update)
DE CLASS I HISTOCOMPATIBILITY ANTIGEN, GOGO-B0103 ALPHA CHAIN PRECURSOR.
OS Gorilla gorilla gorilla (Lowland gorilla).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Primates; Catarrhini; Hominidae; Gorilla.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 92078860.
RA LAWLOR D.A., WARREN E., TAYLOR P., PARHAM P.;
RT "Gorilla class I major histocompatibility complex alleles: comparison
to human and chimpanzee class I";
RL J. Exp. Med. 174:1491-1509(1991).

CC -1- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
 CC THE IMMUNE SYSTEM.
 CC -1- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
 CC MICROGLOBULIN).
 CC -----
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 CC -----

DR EMBL; X60254; CAA42806.1; -
 DR PIR; JH0541; JH0541.
 DR HSP; P03989; ILSA.
 DR PROSITE; PS00290; IG_MHC; 1.
 DR PFAM; PF00047; ig; 1.
 DR PFAM; PF00129; MHC_I; 1.
 KW MHC I; Transmembrane; Glycoprotein; Signal.
 FT SIGNAL 1 24
 FT CHAIN 25 362
 FT CLASS I HISTOCOMPATIBILITY ANTIGEN,
 FT GOGO-B0103 ALPHA CHAIN.
 FT DOMAIN 25 114
 FT DOMAIN 115 206
 FT DOMAIN 207 298
 FT DOMAIN 299 308
 FT DOMAIN 309 332
 FT TRANSMEM 309 332
 FT DOMAIN 333 362
 FT DISULFID 125 188
 FT DISULFID 227 283
 FT CARBOHYD 110 110
 SQ SEQUENCE 362 AA; 40248 MW; FEAGA941 CRC32;

Query Match 88.0%; Score 44; DB 1; Length 362;
 Best Local Similarity 90.0%; Pred. No. 0.076;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RENTRALRY 10
 ||||| |||||
 Db 99 RENTRALRY 108

RESULT 9
 ID 1B15_HUMAN STANDARD; PRT; 362 AA.
 AC P10317;
 DT 01-MAR-1989 (Rel. 10, Created)
 DT 01-MAR-1989 (Rel. 10, Last sequence update)
 DT 01-APR-1993 (Rel. 25, Last annotation update)
 DE HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-27 B*2702 ALPHA CHAIN
 DE PRECURSOR (B-27K) (B27.2).
 GN HLA-B OR HLAB.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Eutheria; Primates; Catarrhini; Hominidae; Homo.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 86220133.
 RA SEEMANN G.H.A., REIN R.S., BROWN C.S., PLOEGH H.L.;
 RT "Gene conversion-like mechanisms may generate polymorphism in human
 RT class I genes".
 RL EMBO J. 5:547-552(1986).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA PARHAM P., ARNETT K.L., ADAMS E.J.;
 RL Submitted (JUL-1995) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE OF 86-107 AND 171-181.
 RX MEDLINE; 86042671.
 RA VEGA M.A., EZQUERRA A., ROJO S., APARICIO P., BRAGADO R.,
 RA LOPEZ DE CASTRO J.A.;

RT *Structural analysis of an HLA-B27 functional variant: identification
 RT of residues that contribute to the specificity of recognition by
 RT cytolytic T lymphocytes*;
 RL Proc. Natl. Acad. Sci. U.S.A. 82:7394-7398(1985).
 CC -1- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
 CC THE IMMUNE SYSTEM.
 CC -1- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
 CC MICROGLOBULIN).
 CC -----
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 CC -----

DR EMBL; X03664; CAA27301.1; -
 DR EMBL; X03667; CAA27301.1; JOINED.
 DR EMBL; L38504; AAA69724.1; -
 DR PIR; B25092; HLHURK.
 DR HSP; P03989; ILSA.
 DR MIM; 142830; -
 DR PROSITE; PS00290; IG_MHC; 1.
 DR PFAM; PF00047; ig; 1.
 DR PFAM; PF00129; MHC_I; 1.
 KW MHC I; Transmembrane; Glycoprotein; Signal.
 FT SIGNAL 1 24
 FT CHAIN 25 362
 FT HLA CLASS I HISTOCOMPATIBILITY ANTIGEN,
 FT B-27 B*2702 ALPHA CHAIN.
 FT DOMAIN 25 114
 FT DOMAIN 115 206
 FT DOMAIN 207 298
 FT DOMAIN 299 308
 FT TRANSMEM 309 332
 FT DOMAIN 333 362
 FT CARBOHYD 110 110
 FT DISULFID 125 188
 FT DISULFID 227 283
 SQ SEQUENCE 362 AA; 40397 MW; 9798F0BB CRC32;

Query Match 88.0%; Score 44; DB 1; Length 362;
 Best Local Similarity 90.0%; Pred. No. 0.076;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RENTRALRY 10
 ||||| |||||
 Db 99 RENTRALRY 108

RESULT 10
 ID 1B47_HUMAN STANDARD; PRT; 362 AA.
 AC P30487;
 DT 01-APR-1993 (Rel. 25, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 01-FEB-1996 (Rel. 33, Last annotation update)
 DE HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-49(B-21) B*4901 ALPHA CHAIN
 DE PRECURSOR.
 GN HLA-B OR HLAB.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Eutheria; Primates; Catarrhini; Hominidae; Homo.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 89235215.
 RA PARHAM P., LAWOR D.A., LOMEN C.E., ENNIS P.D.;
 RT "Diversity and diversification of HLA-A,B,C alleles".
 RL J. Immunol. 142:3937-3950(1989).
 RN [2]
 RP REVISION TO 78.
 RX MEDLINE; 93056529.

RA HILDEBRAND W.H., MADRIGAL J.A., BELICH M.P., ZEMMOUR J., WARD F.E.,
 RA WILLIAMS R.C., PARHAM P.;
 RT "serologic cross-reactivities poorly reflect allelic relationships in
 RT the HLA-B12 and HLA-B21 groups. Dominant epitopes of the alpha 2
 RT helix.";
 RL J. Immunol. 149:3563-3568(1992).
 CC -!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
 CC THE IMMUNE SYSTEM.
 CC -!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
 CC MICROGLOBULIN).
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 CC
 DR EMBL; M24037; AAA02950.1; -;
 DR HSSP; P30491; 1A1M.
 DR MIM; 142830; -;
 DR PROSITE; PS00290; IG_MHC; 1.
 DR PFAM; PF00047; Ig; 1.
 DR PFAM; PF00129; MHC_I; 1.
 DR MHC I; Transmembrane; Glycoprotein; Signal.
 FT SIGNAL 1 24
 FT CHAIN 25 362 HLA CLASS I HISTOCOMPATIBILITY ANTIGEN,
 FT B-49(B-21) B*4901 ALPHA CHAIN.
 FT DOMAIN 25 114 EXTRACELLULAR ALPHA-1.
 FT DOMAIN 115 206 EXTRACELLULAR ALPHA-2.
 FT DOMAIN 207 298 EXTRACELLULAR ALPHA-3.
 FT DOMAIN 299 309 EXTRACELLULAR ALPHA-3.
 FT TRANSMEM 310 333 CONNECTING PEPTIDE.
 FT DOMAIN 334 362 CYTOPLASMIC TAIL.
 FT CARBOHYD 110 110 BY SIMILARITY.
 FT DISULFID 125 188 BY SIMILARITY.
 FT DISULFID 227 283 BY SIMILARITY.
 SQ SEQUENCE 362 AA; 40581 MW; E996F82F CRC32;

Query Match 88.0%; Score 44; DB 1; Length 362;
 Best Local Similarity 90.0%; Pred. No. 0.076;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RENLTRY 10
 Db 99 RENLTRY 108

RESULT 11
 ID 1B49 HUMAN STANDARD; PRT; 362 AA.
 AC P18464.
 DT 01-NOV-1990 (Rel. 16, Created)
 DT 01-NOV-1990 (Rel. 16, Last sequence update)
 DT 01-FEB-1996 (Rel. 33, Last annotation update)
 DE HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-51(B-5) B*5101 ALPHA CHAIN
 DE PRECURSOR.
 GN HLA-B OR HLAB.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Eutheria; Primates; Catarrhini; Hominidae; Homo.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 90207291.
 RA ENNIS P.D., ZEMMOUR J., SALTER R.D., PARHAM P.;
 RT "Rapid cloning of HLA-A,B cDNA by using the polymerase chain
 RT reaction: frequency and nature of errors produced in amplification.";
 RL Proc. Natl. Acad. Sci. U.S.A. 87:2833-2837(1990).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 85080265.

RA HAYASHI H., ENNIS P.D., ARIGA H., SALTER R.D., PARHAM P., KANO K.,
 RA TAKIGUCHI M.;
 RT "HLA-B51 and HLA-Bw52 differ by only two amino acids which are in the
 RT helical region of the alpha 1 domain.";
 RL J. Immunol. 142:306-311(1989).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 89233295.
 RA POHLA H., KUON W., TABACZEWSKI P., DOERNER C., WEISS E.H.;
 RT "Allelic variation in HLA-B and HLA-C sequences and the evolution of
 RT the HLA-B alleles.";
 RL Immunogenetics 29:297-307(1989).
 CC -!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
 CC THE IMMUNE SYSTEM.
 CC -!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
 CC MICROGLOBULIN).
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 CC
 DR EMBL; M32319; AAA36232.1; -;
 DR EMBL; M22792; AAA59620.1; ALT SEQ.
 DR EMBL; M22786; AAA59620.1; JOINED.
 DR EMBL; M22787; AAA59620.1; JOINED.
 DR EMBL; M22788; AAA59620.1; JOINED.
 DR EMBL; M22789; AAA59620.1; JOINED.
 DR EMBL; M22790; AAA59620.1; JOINED.
 DR EMBL; M22791; AAA59620.1; JOINED.
 DR EMBL; L41087; AAA64513.1; -;
 DR EMBL; L41086; AAA64513.1; JOINED.
 DR PIR; A30345; A30345.
 DR PIR; A30548; A30548.
 DR HSSP; P30491; 1A1M.
 DR MIM; 142830; -;
 DR PROSITE; PS00290; IG_MHC; 1.
 DR PFAM; PF00047; Ig; 1.
 DR PFAM; PF00129; MHC_I; 1.
 KW MHC I; Transmembrane; Glycoprotein; Signal.
 FT SIGNAL 1 24
 FT CHAIN 25 362 HLA CLASS I HISTOCOMPATIBILITY ANTIGEN,
 FT B-51(B-5) B*5101 ALPHA CHAIN.
 FT DOMAIN 25 114 EXTRACELLULAR ALPHA-1.
 FT DOMAIN 115 206 EXTRACELLULAR ALPHA-2.
 FT DOMAIN 207 298 EXTRACELLULAR ALPHA-3.
 FT DOMAIN 299 308 CONNECTING PEPTIDE.
 FT TRANSMEM 309 332 CYTOPLASMIC TAIL.
 FT DOMAIN 333 362 BY SIMILARITY.
 FT CARBOHYD 110 110 BY SIMILARITY.
 FT DISULFID 125 188 BY SIMILARITY.
 FT DISULFID 227 283 BY SIMILARITY.
 SQ SEQUENCE 362 AA; 40566 MW; 4D846F30 CRC32;

Query Match 88.0%; Score 44; DB 1; Length 362;
 Best Local Similarity 90.0%; Pred. No. 0.076;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RENLTRY 10
 Db 99 RENLTRY 108

RESULT 12
 ID 1B52 HUMAN STANDARD; PRT; 362 AA.
 AC P30489;
 DT 01-APR-1993 (Rel. 25, Created)
 DT 01-APR-1993 (Rel. 25, Last sequence update)

DT 01-APR-1993 (Rel. 25, Last annotation update)
 DE HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-51(B-5) B*5104 ALPHA CHAIN
 DE PRECURSOR.
 GN HLA-B OR HLAB.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Eutheria; Primates; Catarrhini; Hominidae; Homo.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 9226955.
 RA BELICH M.P., MADRIGAL J.A., HILDEBRAND W.H., ZEMMOUR J.,
 RA WILLIAMS R.C., LUZ R., PETZL-ERLER M.L., PARHAM P.;
 RL "Unusual HLA-B alleles in two tribes of Brazilian Indians."
 RT Nature 357:326-329(1992).
 CC -!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
 CC THE IMMUNE SYSTEM.
 CC -!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
 CC MICROGLOBULIN).
 CC
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 CC
 CC EMBL; M22799; AAA59645.1; ALT SEQ.
 CC EMBL; M22793; AAA59645.1; JOINED.
 CC EMBL; M22794; AAA59645.1; JOINED.
 CC EMBL; M22795; AAA59645.1; JOINED.
 CC EMBL; M22796; AAA59645.1; JOINED.
 CC EMBL; M22797; AAA59645.1; JOINED.
 CC EMBL; M22798; AAA59645.1; JOINED.
 CC PIR; B30345; B30345.
 CC PIR; B30548; B30548.
 CC HSP; P30491; IALM.
 CC MIN; 142830; -.
 CC PROSITE; PS00290; IG_MHC; 1.
 CC PFAM; PF00047; Ig; 1.
 CC PFAM; PF00129; MHC.I; 1.
 CC MHC I; Transmembrane: Glycoprotein; Signal.
 CC SIGNAL 1 24
 CC CHAIN 25 362 HLA CLASS I HISTOCOMPATIBILITY ANTIGEN,
 CC B-51(B-5) B*5104 ALPHA CHAIN.
 CC
 CC DOMAIN 25 114 EXTRACELLULAR ALPHA-1.
 CC DOMAIN 115 206 EXTRACELLULAR ALPHA-1.
 CC DOMAIN 207 298 EXTRACELLULAR ALPHA-2.
 CC DOMAIN 299 308 EXTRACELLULAR ALPHA-3.
 CC TRANSMEM 309 332 CONNECTING PEPTIDE.
 CC DOMAIN 333 362 CYTOPLASMIC TAIL.
 CC CARBOHYD 110 110 BY SIMILARITY.
 CC DISULFID 125 188 BY SIMILARITY.
 CC DISULFID 227 283 BY SIMILARITY.
 CC SEQUENCE 362 AA; 40560 MW; F22F08AB CRC32;
 SQ
 Query Match 88.0%; Score 44; DB 1; Length 362;
 Best Local Similarity 90.0%; Pred. No. 0.076;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 RENLRTALRY 10
 Db 99 RENLRTALRY 108
 RESULT 13
 ID 1B53_HUMAN STANDARD; PRT; 362 AA.
 AC P30490;
 DT 01-APR-1993 (Rel. 25, Created)
 DT 01-APR-1993 (Rel. 25, Last sequence update)
 DT 01-APR-1993 (Rel. 25, Last annotation update)
 DE HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, BW-52(B-5) B*5201 ALPHA CHAIN
 DE PRECURSOR.
 GN HLA-B OR HLAB.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Eutheria; Primates; Catarrhini; Hominidae; Homo.
 RN [1]
 RP SEQUENCE FROM N.A.

RX MEDLINE: 89080265.
 RA HAYASHI H., ENNIS P.D., ARIGA H., SALTER R.D., PARHAM P., KANO K.,
 RA TAKIGUCHI M.;
 RT "HLA-B51 and HLA-Bw52 differ by only two amino acids which are in the
 RT helical region of the alpha 1 domain."
 RL J. Immunol. 142:306-311(1989).
 CC -!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
 CC THE IMMUNE SYSTEM.
 CC -!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
 CC MICROGLOBULIN).
 CC
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 CC
 CC EMBL; M22799; AAA59645.1; ALT SEQ.
 CC EMBL; M22793; AAA59645.1; JOINED.
 CC EMBL; M22794; AAA59645.1; JOINED.
 CC EMBL; M22795; AAA59645.1; JOINED.
 CC EMBL; M22796; AAA59645.1; JOINED.
 CC EMBL; M22797; AAA59645.1; JOINED.
 CC EMBL; M22798; AAA59645.1; JOINED.
 CC PIR; B30345; B30345.
 CC PIR; B30548; B30548.
 CC HSP; P30491; IALM.
 CC MIN; 142830; -.
 CC PROSITE; PS00290; IG_MHC; 1.
 CC PFAM; PF00047; Ig; 1.
 CC PFAM; PF00129; MHC.I; 1.
 CC MHC I; Transmembrane: Glycoprotein; Signal.
 CC SIGNAL 1 24
 CC CHAIN 25 362 HLA CLASS I HISTOCOMPATIBILITY ANTIGEN,
 CC BW-52(B-5) B*5201 ALPHA CHAIN.
 CC
 CC DOMAIN 25 114 EXTRACELLULAR ALPHA-1.
 CC DOMAIN 115 206 EXTRACELLULAR ALPHA-1.
 CC DOMAIN 207 298 EXTRACELLULAR ALPHA-2.
 CC DOMAIN 299 308 EXTRACELLULAR ALPHA-3.
 CC TRANSMEM 309 332 CONNECTING PEPTIDE.
 CC DOMAIN 333 362 CYTOPLASMIC TAIL.
 CC CARBOHYD 110 110 BY SIMILARITY.
 CC DISULFID 125 188 BY SIMILARITY.
 CC DISULFID 227 283 BY SIMILARITY.
 CC SEQUENCE 362 AA; 40521 MW; 3B436FE8 CRC32;
 SQ
 Query Match 88.0%; Score 44; DB 1; Length 362;
 Best Local Similarity 90.0%; Pred. No. 0.076;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 RENLRTALRY 10
 Db 99 RENLRTALRY 108
 RESULT 14
 ID 1B54_HUMAN STANDARD; PRT; 362 AA.
 AC P30491;
 DT 01-APR-1993 (Rel. 25, Created)
 DT 01-APR-1993 (Rel. 25, Last sequence update)
 DT 15-JUL-1998 (Rel. 36, Last annotation update)
 DE HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, BW-53 B*5301 ALPHA CHAIN
 DE PRECURSOR.
 GN HLA-B OR HLAB.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Eutheria; Primates; Catarrhini; Hominidae; Homo.
 RN [1]
 RP SEQUENCE FROM N.A.

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RX MEDLINE: 91033941.
RA HAYASHI H., Ooba T., NAKAYAMA S., SEKIMATA M., KANO K.,
RA TAKIGUCHI M.;
RT "Allotopes between HLA-B*53 and HLA-B*35 are generated by
RT substitution of the residues associated with HLA-B*53 public
RT epitopes.";
RL Immunogenetics 32:195-199(1990).
RN [2]
RP X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF 25-302.
RX MEDLINE: 96209672.
RA SMITH K.J., REID S.W., HARLOS K., MCMICHAEL A.J., STUART D.I.,
RA BELL J.I., JONES E.Y.;
RT "Bound water structure and polymorphic amino acids act together to
RT allow the binding of different peptides to MHC class I HLA-B*53.";
RL Immunity 4:215-228(1996).
CC -!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
CC THE IMMUNE SYSTEM.
CC -!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
CC MICROGLOBULIN).
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CC -----
DR EMBL: M58636; AAA36228.1; -
DR PIR: A45834; A45834.
DR PDB: 1A10; 08-APR-98.
DR PDB: 1A10; 08-APR-98.
DR MIM: 142830; -
DR PROSITE: PS00290; IG_MHC; 1.
DR PFAM: PF00047; ig; 1.
DR PFAM: PF00129; MHC_I; 1.
KW MHC I; Transmembrane; Glycoprotein; Signal; 3D-structure.
FT SIGNAL 1 24
FT CHAIN 25 362
FT HLA CLASS I HISTOCOMPATIBILITY ANTIGEN,
FT BW-53 B*5301 ALPHA CHAIN.
FT DOMAIN 25 114
FT EXTRACELLULAR ALPHA-1.
FT DOMAIN 115 206
FT EXTRACELLULAR ALPHA-2.
FT DOMAIN 207 298
FT EXTRACELLULAR ALPHA-3.
FT DOMAIN 299 308
FT CONNECTING PEPTIDE.
FT TRANSMEM 309 332
FT DOMAIN 333 362
FT CYTOPLASMIC TAIL.
FT CARBOHYD 110 110
FT BY SIMILARITY.
FT DISULFID 125 188
FT DISULFID 227 283
SQ SEQUENCE 362 AA; 40495 MW; 2BDC746E CRC32;

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Query Match 88.0%; Score 44; DB 1; Length 362;
 Best Local Similarity 90.0%; Pred. No. 0.076;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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OY 1 RENLRLALRY 10
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DB 99 RENLRLALRY 108

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RESULT 15
1B60 HUMAN
ID 1B60 HUMAN STANDARD; PRT; 362 AA.
AC P18465.
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 01-APR-1993 (Rel. 25, Last annotation update)
DE HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-57(B-17) B*5701 ALPHA
DE CHAIN PRECURSOR (BW57.1).
GN HLA-B OR HLAB
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia;

```

```

OC Eutheria; Primates; Catarrhini; Hominidae; Homo.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE: 90207291.
RA ENNIS P.D., ZEMMOUR J., SALTER R.D., PARHAM P.;
RT "Rapid cloning of HLA-A,B CDNA by using the polymerase chain
RT reaction: frequency and nature of errors produced in amplification.";
RL Proc. Natl. Acad. Sci. U.S.A. 87:2833-2837(1990).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE: 91067476.
RA ISAMAT M., GRIDLESTONE J., MILSTEIN C.;
RT "Nucleotide sequence of an HLA-B*57 gene.";
RL Nucleic Acids Res. 18:6702-6702(1990).
CC -!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
CC THE IMMUNE SYSTEM.
CC -!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
CC MICROGLOBULIN).
CC -----
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CC -----
DR EMBL: M32318; AAA36231.1; -
DR EMBL: X55711; CAA39244.1; -
DR PIR: S12622; S12622.
DR PIR: D35997; D35997.
DR HSSP: P30491; 1A1M.
DR MIM: 142830; -
DR PROSITE: PS00290; IG_MHC; 1.
DR PFAM: PF00047; ig; 1.
DR PFAM: PF00129; MHC_I; 1.
KW MHC I; Transmembrane; Glycoprotein; Signal.
FT SIGNAL 1 24
FT CHAIN 25 362
FT HLA CLASS I HISTOCOMPATIBILITY ANTIGEN,
FT B-57(B-17) B*5701 ALPHA CHAIN.
FT EXTRACELLULAR ALPHA-1.
FT EXTRACELLULAR ALPHA-2.
FT EXTRACELLULAR ALPHA-3.
FT CONNECTING PEPTIDE.
FT CYTOPLASMIC TAIL.
FT BY SIMILARITY.
FT BY SIMILARITY.
FT BY SIMILARITY.
FT DISULFID 125 188
FT DISULFID 227 283
SQ SEQUENCE 362 AA; 40224 MW; D91DF8DD CRC32;

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Query Match 88.0%; Score 44; DB 1; Length 362;
 Best Local Similarity 90.0%; Pred. No. 0.076;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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OY 1 RENLRLALRY 10
    ||||| |||||
DB 99 RENLRLALRY 108

```

Search completed: February 8, 2000, 01:25:58
 Job time: 1558 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: February 8, 2000, 19:16:13 ; Search time 176.54 Seconds
(without alignments)
3.927 Million cell updates/sec

Title: US-08-653-294-25
Perfect score: 50
Sequence: 1 RENLRTALRY 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 225878 seqs, 59334122 residues

Total number of hits satisfying chosen parameters: 225878

Minimum DB seq length: 0
Maximum DB seq length: 1000000

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database : SPTREMBL_12.*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	50	100.0	89	7 019674	019674 homo sapien
2	50	100.0	89	7 019565	019565 homo sapien
3	50	100.0	131	7 097998	097998 homo sapien
4	50	100.0	131	7 097999	097999 homo sapien
5	50	100.0	181	7 019779	019779 homo sapien
6	50	100.0	181	7 030197	030197 homo sapien
7	50	100.0	181	7 019669	019669 homo sapien
8	50	100.0	181	7 078028	078028 homo sapien
9	50	100.0	355	7 029853	029853 homo sapien
10	50	100.0	361	7 09XR00	09XR00 pongo pygma
11	50	100.0	362	7 029637	029637 homo sapien
12	50	100.0	362	7 029935	029935 homo sapien
13	50	100.0	362	7 079524	079524 homo sapien
14	50	100.0	362	7 029850	029850 homo sapien
15	50	100.0	362	7 029661	029661 homo sapien
16	50	100.0	362	7 078180	078180 homo sapien
17	50	100.0	362	7 029933	029933 homo sapien
18	45	90.0	89	4 095956	095956 homo sapien
19	45	90.0	89	7 077959	077959 homo sapien
20	45	90.0	137	7 095533	095533 pan troglod

21	45	90.0	181	7 077934	077934 homo sapien
22	45	90.0	330	7 019356	019356 macaca mula
23	45	90.0	331	7 002944	002944 macaca mula
24	45	90.0	331	7 002945	002945 macaca mula
25	45	90.0	345	7 095459	095459 rattus norv
26	45	90.0	345	7 078088	078088 rattus norv
27	45	90.0	348	7 046875	046875 rattus norv
28	45	90.0	362	7 029938	029938 homo sapien
29	44	88.0	89	7 019569	019569 homo sapien
30	44	88.0	90	7 046693	046693 pan troglod
31	44	88.0	90	7 046694	046694 pan troglod
32	44	88.0	90	7 046695	046695 pan troglod
33	44	88.0	90	7 046696	046696 pan paniscu
34	44	88.0	90	7 046697	046697 gorilla gor
35	44	88.0	133	7 019189	019189 homo sapien
36	44	88.0	138	7 078209	078209 homo sapien
37	44	88.0	172	7 019770	019770 homo sapien
38	44	88.0	172	7 019774	019774 homo sapien
39	44	88.0	172	7 019775	019775 homo sapien
40	44	88.0	172	7 019780	019780 homo sapien
41	44	88.0	172	7 095364	095364 homo sapien
42	44	88.0	172	7 019771	019771 homo sapien
43	44	88.0	172	7 019772	019772 homo sapien
44	44	88.0	172	7 019773	019773 homo sapien
45	44	88.0	175	7 029694	029694 homo sapien

ALIGNMENTS

RESULT 1
019674 ID 019674 PRELIMINARY; PRT; 89 AA.
AC 019674;
DT 01-JAN-1998 (TREMBLrel. 05, Created)
DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
DE 01-NOV-1998 (TREMBLrel. 08, Last annotation update)
DE HLA-B*13 (FRAGMENT).
GN HLA-B*13.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Primates; Catarrhini; Hominidae; Homo.
RN [1]
RP SEQUENCE FROM N.A.
RA MAERTENS R., DE CANCK I.;
RL Submitted (APR-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; Y12378; CAA73021.1; -
DR PFAM; PF00129; MHC_I; 1.
KW MHC.
FT NON_TER 1 1
FT NON_TER 89 89
SQ SEQUENCE 89 AA; 10581 MW; 9AC7631C CRC32;

Query Match 100.0%; Score 50; DB 7; Length 89;
Best Local Similarity 100.0%; Pred. No. 0.009;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RENLRTALRY 10
Db 74 RENLRTALRY 83

RESULT 2
019565 ID 019565 PRELIMINARY; PRT; 89 AA.
AC 019565;
DT 01-JAN-1998 (TREMBLrel. 05, Created)
DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
DT 01-MAY-1999 (TREMBLrel. 10, Last annotation update)
DE MHC CLASS I ANTIGEN (FRAGMENT).
GN HLA-B.
OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Eutheria; Primates; Catarrhini; Hominidae; Homo.
 RN [1]
 RP SEQUENCE FROM N.A.
 RA CAO K., BURDETT L., ZHANG G., FERNANDEZ-VINA M.;
 RL Submitted (AUG-1997) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF017316; AAB70282.2; -.
 KW MHC.
 FT NON_TER 1 1
 FT NON_TER 89 89
 SQ SEQUENCE 89 AA; 10581 MW; 9AC7631C CRC32;

Query Match 100.0%; Score 50; DB 7; Length 89;
 Best Local Similarity 100.0%; Pred. No. 0.009;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RENLRTALRY 10
 Db 74 RENLRTALRY 83

RESULT 3

O97998
 ID O97998 PRELIMINARY; PRT; 131 AA.
 AC O97998;
 DT 01-MAY-1999 (T-EMBLrel. 10, Created)
 DT 01-MAY-1999 (T-EMBLrel. 10, Last sequence update)
 DT 01-MAY-1999 (T-EMBLrel. 10, Last annotation update)
 DE MHC CLASS I ANTIGEN (FRAGMENT).
 GN HLA-B.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Eutheria; Primates; Catarrhini; Hominidae; Homo.
 RN [1]
 RP SEQUENCE FROM N.A.
 RA HOLDSWORTH R.;
 RL Submitted (NOV-1997) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF035648; AAD02035.1; -.
 KW MHC.
 FT NON_TER 1 1
 FT NON_TER 131 131
 SQ SEQUENCE 131 AA; 15134 MW; 931C8D27 CRC32;

Query Match 100.0%; Score 50; DB 7; Length 131;
 Best Local Similarity 100.0%; Pred. No. 0.013;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RENLRTALRY 10
 Db 40 RENLRTALRY 49

RESULT 4

O97999
 ID O97999 PRELIMINARY; PRT; 131 AA.
 AC O97999;
 DT 01-MAY-1999 (T-EMBLrel. 10, Created)
 DT 01-MAY-1999 (T-EMBLrel. 10, Last sequence update)
 DT 01-MAY-1999 (T-EMBLrel. 10, Last annotation update)
 DE MHC CLASS I ANTIGEN (FRAGMENT).
 GN HLA-B.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Eutheria; Primates; Catarrhini; Hominidae; Homo.
 RN [1]
 RP SEQUENCE FROM N.A.
 RA HOLDSWORTH R.;
 RL Submitted (NOV-1997) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF035649; AAD02036.1; -.
 KW MHC.
 FT NON_TER 1 1

FT NON_TER 131 131
 SQ SEQUENCE 131 AA; 15057 MW; 32C865A3 CRC32;

Query Match 100.0%; Score 50; DB 7; Length 131;
 Best Local Similarity 100.0%; Pred. No. 0.013;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RENLRTALRY 10
 Db 40 RENLRTALRY 49

RESULT 5

O19779
 ID O19779 PRELIMINARY; PRT; 181 AA.
 AC O19779;
 DT 01-JAN-1998 (T-EMBLrel. 05, Created)
 DT 01-JAN-1998 (T-EMBLrel. 05, Last sequence update)
 DT 01-NOV-1999 (T-EMBLrel. 12, Last annotation update)
 DE MHC CLASS I ANTIGEN (FRAGMENT).
 GN HLA-B.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Eutheria; Primates; Catarrhini; Hominidae; Homo.
 RN [1]
 RP SEQUENCE FROM N.A.
 RA STEINER N.K., NG J., BUSH J., HARTZMAN R.J., JOHNSON-DOW L.,
 RA HURLEY C.K.;
 RL Hum. Immunol. 56:0-0(1997).
 DR EMBL; U90241; AAB82305.1; -.
 DR EMBL; U90240; AAB82305.1; JOINED.
 DR HSSP; P10318; 1ROG.
 DR PFAM; PF00129; MHC_I; 1.
 KW MHC.
 FT NON_TER 1 1
 FT NON_TER 181 181
 SQ SEQUENCE 181 AA; 21095 MW; 97EC2597 CRC32;

Query Match 100.0%; Score 50; DB 7; Length 181;
 Best Local Similarity 100.0%; Pred. No. 0.019;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RENLRTALRY 10
 Db 74 RENLRTALRY 83

RESULT 6

O30197
 ID O30197 PRELIMINARY; PRT; 181 AA.
 AC O30197;
 DT 01-NOV-1996 (T-EMBLrel. 01, Created)
 DT 01-NOV-1996 (T-EMBLrel. 01, Last sequence update)
 DT 01-NOV-1999 (T-EMBLrel. 12, Last annotation update)
 DE MHC CLASS I ANTIGEN (FRAGMENT).
 GN HLA-B.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Eutheria; Primates; Catarrhini; Hominidae; Homo.
 RN [1]
 RP SEQUENCE FROM N.A.
 RA HURLEY C.K., HOYER R.J.;
 RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
 DR EMBL; U63560; AAB05925.1; -.
 DR EMBL; U63559; AAB05925.1; JOINED.
 DR HSSP; P10318; 1ROG.
 DR PFAM; PF00129; MHC_I; 1.
 KW MHC.
 FT NON_TER 1 1
 FT NON_TER 181 181
 SQ SEQUENCE 181 AA; 20997 MW; 7DFABE37 CRC32;

Query Match 100.0%; Score 50; DB 7; Length 181;
 Best Local Similarity 100.0%; Pred. No. 0.019;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RENLRTALRY 10
 DB 74 RENLRTALRY 83
 |||||

RESULT 7
 ID Q19669 PRELIMINARY; PRT; 181 AA.
 AC Q19669;
 DT 01-JAN-1998 (TRENBLrel. 05, Created)
 DT 01-JAN-1998 (TRENBLrel. 05, Last sequence update)
 DT 01-NOV-1999 (TRENBLrel. 12, Last annotation update)
 DE MHC CLASS I ANTIGEN SHCHA (FRAGMENT).
 GN HLA-B.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Eutheria; Primates; Catarrhini; Hominidae; Homo.
 RN [1]
 RP SEQUENCE FROM N.A.
 RA HURLEY C.K., STEINER N.K.;
 RL Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.
 DR EMBL; U58470; AAB02607.1; -;
 DR EMBL; U58469; AAB02607.1; JOINED.
 DR HSSP; P10318; IROG.
 DR PFAM; PF00129; MHC_I; 1.
 KW MHC.
 FT NON_TER 1 181
 FT NON_TER 181
 SQ SEQUENCE 181 AA; 21028 MW; EC872642 CRC32;

Query Match 100.0%; Score 50; DB 7; Length 181;
 Best Local Similarity 100.0%; Pred. No. 0.019;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RENLRTALRY 10
 DB 74 RENLRTALRY 83
 |||||

RESULT 8
 ID O78028 PRELIMINARY; PRT; 181 AA.
 AC O78028;
 DT 01-NOV-1998 (TRENBLrel. 08, Created)
 DT 01-NOV-1998 (TRENBLrel. 08, Last sequence update)
 DT 01-NOV-1999 (TRENBLrel. 12, Last annotation update)
 DE HLA-B*15MD. (FRAGMENT).
 GN HLA-B*15MD.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Eutheria; Primates; Catarrhini; Hominidae; Homo.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=BLOOD;
 RA GAO X., MATHESON B.;
 RL Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.
 DR EMBL; U58316; AAB87723.1; -;
 DR EMBL; U58315; AAB87723.1; JOINED.
 DR HSSP; P10318; IROG.
 DR PFAM; PF00129; MHC_I; 1.
 KW MHC.
 FT NON_TER 1 181
 FT NON_TER 181
 SQ SEQUENCE 181 AA; 21029 MW; C35A18BE CRC32;

Query Match 100.0%; Score 50; DB 7; Length 181;
 Best Local Similarity 100.0%; Pred. No. 0.019;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RENLRTALRY 10
 DB 74 RENLRTALRY 83
 |||||

RESULT 9
 ID Q29853 PRELIMINARY; PRT; 355 AA.
 AC Q29853;
 DT 01-NOV-1996 (TRENBLrel. 01, Created)
 DT 01-NOV-1996 (TRENBLrel. 01, Last sequence update)
 DT 01-NOV-1999 (TRENBLrel. 12, Last annotation update)
 DE HLA-B ALPHA-CHAIN (FRAGMENT).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Eutheria; Primates; Catarrhini; Hominidae; Homo.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 95176328.
 RA GAUCHAT-FEISS D., BREUR-VRISENDORP B.S., RUFER N., JEANNET M.,
 RA ROOSNEK E., TIERCY J.M.;
 RT "Sequencing of a novel functional HLA-B*44 subtype differing in two
 RT residues in the alpha 2 domain.";
 RL Tissue Antigens 44:261-264(1994).
 DR EMBL; X75953; CAA53566.1; -;
 DR HSSP; P30491; IALM.
 DR PROSITE; PS00290; IG_MHC; 1.
 DR PFAM; PF00047; Ig; 1.
 DR PFAM; PF00129; MHC_I; 1.
 KW MHC.
 FT NON_TER 355 355
 FT NON_TER 355
 SQ SEQUENCE 355 AA; 39845 MW; EF81934E CRC32;

Query Match 100.0%; Score 50; DB 7; Length 355;
 Best Local Similarity 100.0%; Pred. No. 0.037;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RENLRTALRY 10
 DB 99 RENLRTALRY 108
 |||||

RESULT 10
 ID Q9XRY0 PRELIMINARY; PRT; 361 AA.
 AC Q9XRY0;
 DT 01-NOV-1999 (TRENBLrel. 12, Created)
 DT 01-NOV-1999 (TRENBLrel. 12, Last sequence update)
 DT 01-NOV-1999 (TRENBLrel. 12, Last annotation update)
 DE MHC CLASS I ANTIGEN (FRAGMENT).
 GN POPY B.
 OS Pongo pygmaeus (Orangutan).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Eutheria; Primates; Catarrhini; Hominidae; Pongo.
 RN [1]
 RP SEQUENCE FROM N.A.
 RA ADAMS E.J., THOMSON G., PARHAM P.;
 RT "Evidence for an HLA-C-like locus in the orangutan Pongo pygmaeus.";
 RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF118895; AAD28435.1; -;
 DR PROSITE; PS00290; IG_MHC; 1.
 DR NON_TER 1 361
 FT NON_TER 1
 SQ SEQUENCE 361 AA; 40466 MW; CB177B4F CRC32;

Query Match 100.0%; Score 50; DB 7; Length 361;
 Best Local Similarity 100.0%; Pred. No. 0.038;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RENLRTALRY 10
 DB 98 RENLRTALRY 107

RESULT 11

Q29637 PRELIMINARY; PRT; 362 AA.
 AC Q29637; 1996 (TREMBlrel. 01, Created)
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
 DT 01-NOV-1999 (TREMBlrel. 12, Last annotation update)
 DE MHC CLASS I ANTIGEN.
 GN HLA-B.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Eutheria; Primates; Catarrhini; Hominidae; Homo.
 RN [1]
 RP SEQUENCE FROM N.A.
 RA DOMENA J.D., PARHAM P.;
 RL Submitted (DEC-1993) to the EMBL/GenBank/DBJ databases.
 DR EMBL: U04244; AAA87397.1; -.
 DR HSSP: P30460; IAGE.
 DR PROSITE: PS00290; IG_MHC; 1.
 DR PFAM: PF00047; ig; 1.
 DR PFAM: PF00129; MHC_I; 1.
 KW MHC.
 SQ SEQUENCE 362 AA; 40359 MW; EA895D7 CRC32;

Query Match 100.0%; Score 50; DB 7; Length 362;
 Best Local Similarity 100.0%; Pred. No. 0.038;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RENLRTALRY 10
 DB 99 RENLRTALRY 108

RESULT 12

Q29935 PRELIMINARY; PRT; 362 AA.
 AC Q29935;
 DT 01-NOV-1996 (TREMBlrel. 01, Created)
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
 DT 01-NOV-1999 (TREMBlrel. 12, Last annotation update)
 DE MHC CLASS I HLA-B*3802.
 GN HLA-B.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Eutheria; Primates; Catarrhini; Hominidae; Homo.
 RN [1]
 RP SEQUENCE FROM N.A.
 RA LITTLE A.M., DOMENA J.D., HILDEBRAND W.H., PARHAM P.;
 RL Submitted (FEB-1994) to the EMBL/GenBank/DBJ databases.
 DR EMBL: L22028; AAA59618.1; -.
 DR HSSP: P30491; IALM.
 DR PROSITE: PS00290; IG_MHC; 1.
 DR PFAM: PF00047; ig; 1.
 DR PFAM: PF00129; MHC_I; 1.
 KW MHC.
 SQ SEQUENCE 362 AA; 40404 MW; 83A8399C CRC32;

Query Match 100.0%; Score 50; DB 7; Length 362;
 Best Local Similarity 100.0%; Pred. No. 0.038;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RENLRTALRY 10
 DB 99 RENLRTALRY 108

RESULT 13

P79524 PRELIMINARY; PRT; 362 AA.
 AC P79524;
 DT 01-MAY-1997 (TREMBlrel. 03, Created)
 DT 01-MAY-1997 (TREMBlrel. 03, Last sequence update)
 DT 01-NOV-1999 (TREMBlrel. 12, Last annotation update)
 DE MHC CLASS I HLA-B*44BO.
 GN HLA-B.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Eutheria; Primates; Catarrhini; Hominidae; Homo.
 RN [1]
 RP SEQUENCE FROM N.A.
 RA ARNETT K.L., DARKE C., PARHAM P.;
 RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
 DR EMBL: U64801; AAB40632.1; -.
 DR HSSP: P30491; IALM.
 DR PROSITE: PS00290; IG_MHC; 1.
 DR PFAM: PF00047; ig; 1.
 DR PFAM: PF00129; MHC_I; 1.
 KW MHC.
 SQ SEQUENCE 362 AA; 40396 MW; AC0FAF3C CRC32;

Query Match 100.0%; Score 50; DB 7; Length 362;
 Best Local Similarity 100.0%; Pred. No. 0.038;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RENLRTALRY 10
 DB 99 RENLRTALRY 108

RESULT 14

Q29850 PRELIMINARY; PRT; 362 AA.
 AC Q29850;
 DT 01-NOV-1996 (TREMBlrel. 01, Created)
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
 DT 01-NOV-1999 (TREMBlrel. 12, Last annotation update)
 DE HLA-B ALPHA CHAIN B*4407 PRECURSOR.
 GN HLA-B*4407.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Eutheria; Primates; Catarrhini; Hominidae; Homo.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 97004417.
 RA VILCHES C., SANZ L., DE PABLO R., MORENO M.E., PUENTE S., KREISLER M.;
 RT "Molecular characterization of the new alleles HLA-B*8101 and
 RT B*4407".
 RL Tissue Antigens 47:139-142(1996).
 DR EMBL: X90391; CAA62036.1; -.
 DR HSSP: P30491; IALM.
 DR PROSITE: PS00290; IG_MHC; 1.
 DR PFAM: PF00047; ig; 1.
 DR PFAM: PF00129; MHC_I; 1.
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OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Primates; Catarrhini; Homnidae; Homo.
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RP SEQUENCE FROM N.A.
RC TISSUE=BLOOD;
RX MEDLINE; 96232969.
RA BALAS A., GARCIA-SANCHEZ F., VICARIO J.L.;
RT "HLA-B*1303: a new example of poor correlation between serology and
RT structure.";
RL Hum. Immunol. 45:32-36(1996).
DR EMBL; U14943; AAB06829.1; -.
DR HSP; P30491; IALM.
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DR PFAM; PF00047; Ig; 1.
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About: Results were produced by the GenCore software, version 4.5, Copyright (c) 1993-2000 CompuGen Ltd.

Search time (sec): 10176.920000

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REFERENCE 2 (bases 1 to 187)
AUTHORS Yao, Z.
TITLE Direct Submission
JOURNAL Submitted (18-MAR-1994) Z. Yao, Immunogenetics Laboratory,
Kinderpoliklinik University of Munich, Pettenkaferstr 8a, 80336
Munich, FRG
REMARK revised by [3] MAT
REFERENCE 3 (bases 1 to 187)
AUTHORS Yao, Z.
TITLE Direct Submission
JOURNAL Submitted (15-APR-1994) Z. Yao, Immunogenetics Laboratory,
Kinderpoliklinik University of Munich, Pettenkaferstr 8a, 80336
Munich, FRG
COMMENT On Apr 17, 1994 this sequence version replaced gi:468539.
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VERSION Y18648.1 GI:4160522
KEYWORDS HLA-B gene; HLA-B*0802 allele; human leucocyte antigen B; major
histocompatibility complex; MHC class I antigen.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
Primates; Catarrhini; Hominidae; Homo.
Guttridge, M.G.
Direct Submission
Submitted (12-JAN-1999) M.G. Guttridge, Welsh Blood Service, Ely
Valley Road, Talbot Green, Pontyclun, CF72 9WB, UK
REFERENCE 1 (bases 1 to 270)
AUTHORS Guttridge, M.G.
TITLE Direct Submission
JOURNAL Submitted (12-JAN-1999) M.G. Guttridge, Welsh Blood Service, Ely
Valley Road, Talbot Green, Pontyclun, CF72 9WB, UK
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ACCESSION Y12378
VERSION Y12378.1 GI:1934896
KEYWORDS exon 2; HLA-B*13.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
Primates; Catarrhini; Hominoidea; Homo.
REFERENCE 1 (bases 1 to 270)
AUTHORS Maertens,R. and De Canck,I.
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 270)
AUTHORS De Canck,I.
TITLE Direct Submission
JOURNAL Submitted (07-APR-1997) I. De Canck, INNOGENETICS N.V.,
Industriepark Zwijnaarde 7 box 4, B-9052 Gent, BELGIUM

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variant, exon 2.
ACCESSION AJ249724
VERSION AJ249724.1 GI:5919229
KEYWORDS HLA-B gene; HLA-B*44 variant; human leucocyte antigen B; major
histocompatibility complex; MHC class I antigen.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominoidea; Homo.
REFERENCE 1 (bases 1 to 270)
AUTHORS Elsner,H.A., Schmitz,G. and Blasczyk,R.
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 270)
AUTHORS Blasczyk,R.
TITLE Direct Submission
JOURNAL Submitted (17-SEP-1999) Blasczyk R., Department of Transfusion
Medicine, Hannover Medical School, Carl-Neuberg-Str. 1, Hannover,
30625, GERMANY

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DEFINITION Human MHC class I antigen SHCHA (HLA-B*4403 variant) gene, exon 2.
ACCESSION U58469
VERSION U58469.1 GI:1378136
KEYWORDS
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ORGANISM
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Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE
1 (bases 1 to 270)
AUTHORS Hurley,C.K. and Steiner,N.K.
TITLE Novel HLA-B alleles
JOURNAL Unpublished
AUTHORS Hurley,C.K. and Steiner,N.K.
TITLE Direct Submission
JOURNAL Submitted (16-MAY-1996) C.K. Hurley, Microbiology & Immunology,
Georgetown University, 3970 Reservoir Rd.NW, Washington, DC 20007,
USA
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ACCESSION U90240
VERSION U90240.1 GI:1905853
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ORGANISM
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE
1 (bases 1 to 270)
AUTHORS Steiner,N.K., Ng,J., Bush,J., Hartzman,R.J., Johnson-Dow,L. and
Hurley,C.K.
TITLE HLA-B Alleles Associated with the B15 Serologically Defined
Antigens
JOURNAL Hum. Immunol. 56 (1997) In press
REFERENCE 2 (bases 1 to 270)
AUTHORS Steiner,N.K. and Hurley,C.K.
TITLE Direct Submission
JOURNAL Submitted (20-FEB-1997) Microbiology & Immunology, Georgetown
University, 3970 Reservoir Rd. NW, Washington, DC 20007, USA
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ORGANISM
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE
1 (bases 1 to 270)
AUTHORS Steiner,N.K., Ng,J., Bush,J., Hartzman,R.J., Johnson-Dow,L. and
Hurley,C.K.
TITLE HLA-B Alleles Associated with the B15 Serologically Defined
Antigens
JOURNAL Hum. Immunol. 56 (1997) In press
REFERENCE 2 (bases 1 to 270)
AUTHORS Steiner,N.K. and Hurley,C.K.
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JOURNAL Submitted (20-FEB-1997) Microbiology & Immunology, Georgetown
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ACCESSION U58315
VERSION U58315.1 GI:2654406
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE
1 (sites)
AUTHORS Gao,X. and Matheson,B.
TITLE A novel B15 variant found in oceanic populations

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JOURNAL Unpublished
REFERENCE 2 (bases 1 to 270)
AUTHORS Gao, X.
TITLE Direct Submission
JOURNAL Submitted (15-MAY-1996) Xiaojiang Gao, The Australian National
University, Human Genetics Group, Acton, Canberra, Act, Australia,
2601
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VERSION U90240.1 GI:1905853
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Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE
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AUTHORS Steiner,N.K., Ng,J., Bush,J., Hartzman,R.J., Johnson-Dow,L. and
Hurley,C.K.
TITLE HLA-B Alleles Associated with the B15 Serologically Defined
Antigens
JOURNAL Hum. Immunol. 56 (1997) In press
REFERENCE 2 (bases 1 to 270)
AUTHORS Steiner,N.K. and Hurley,C.K.
TITLE Direct Submission
JOURNAL Submitted (20-FEB-1997) Microbiology & Immunology, Georgetown
University, 3970 Reservoir Rd. NW, Washington, DC 20007, USA
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/isolate="GN00155"
/db_xref="taxon:9606"
1..270
/gene="HLA-B"
/number=2
BASE COUNT 60 a 88 c 85 g 37 t
ORIGIN

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exon

alignment_scores:
Quality: 50.00 Length: 10
Ratio: 5.000 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
US-08-653-294-25 x HSSHCHA01 ..
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1 ArgGluAsnLeuArgThrAlaLeuArgTyr 10
|||||
222 CGAGAGAACCTGCGCACCCTCCGCTAC 251

seq_name: gb_pr3:HSHLABSH1

seq_documentation_block:
LOCUS HSHLABSH1 270 bp DNA PRI 01-DEC-1997
DEFINITION Human HLA-B*15MD gene, exon 2.
ACCESSION U58315
VERSION U58315.1 GI:2654406
KEYWORDS
SEGMENT
SOURCE
1 of 2
human.
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE
1 (sites)
AUTHORS Gao,X. and Matheson,B.
TITLE A novel B15 variant found in oceanic populations

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alignment_scores:
  Quality: 50.00      Length: 10
  Ratio: 5.000        Gaps: 0
  Percent Similarity: 100.000  Percent Identity: 100.000

alignment_block:
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  Align seg 1/1 to: HSHLABSH1 from: 1 to: 270
      1 ArgGluAsnLeuArgThrAlaLeuArgTyr 10
      222 CGAGAGAACCTGCGACCGCGCTCGCTAC 251
  seq_name: gb_pr4:AF017316

seq_documentation_block:
  LOCUS AF017316 270 bp DNA PRI 26-MAR-1999
  DEFINITION Homo sapiens MHC class I antigen (HLA-B) gene, partial cds.
  ACCESSION AF017316
  VERSION AF017316.1 GI:2394335
  KEYWORDS
  SOURCE human.
  ORGANISM Homo sapiens
    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
    Eutheria; Primates; Catarrhini; Hominidae; Homo.
  REFERENCE
    1 (bases 1 to 270)
    Cao, K., Burdett, L., Zhang, G. and Fernandez-Vina, M.
    Direct Submission
    Submitted (07-AUG-1997) Nat. Histocompatibility Lab, Am Red Cross,
    box 173, 22 S. Greene St., Baltimore, MD 21201, USA
  JOURNAL
  FEATURES
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      /db_xref="GI:4521330"
      /translation="SXSRYFYTAMSRPGRPFRTVGVVDFTQVRFDSDATSPRM
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  BASE COUNT 59 a 92 c 83 g 36 t
  ORIGIN

alignment_scores:
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  Ratio: 5.000        Gaps: 0
  Percent Similarity: 100.000  Percent Identity: 100.000

alignment_block:
  US-08-653-294-25 x AF017316 ..
  Align seg 1/1 to: AF017316 from: 1 to: 270
      1 ArgGluAsnLeuArgThrAlaLeuArgTyr 10
      222 CGAGAGAACCTGCGACCGCGCTCGCTAC 251
  seq_name: gb_pr4:HB38021G1

seq_documentation_block:
  LOCUS HB38021G1 270 bp DNA PRI 23-SEP-1999
  DEFINITION Homo sapiens HLA-B MHC class I antigen (HLA-B) gene, HLA-B-*38021
  allele, exon 2.
  ACCESSION AF181857

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```

VERSION AF181857.1 GI:5919134
KEYWORDS
SEGMENT 1 of 2
SOURCE human.
ORGANISM Homo sapiens
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
  Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
  1 (bases 1 to 270)
  Pimtanothai, N. and Hurley, C.K.
  Novel HLA-B allele
  Unpublished
  JOURNAL
REFERENCE
  2 (bases 1 to 270)
  Pimtanothai, N. and Hurley, C.K.
  Direct Submission
  Submitted (30-AUG-1999) Microbiology & Immunology, Georgetown
  University, 3970 Reservoir Rd. N.W., Washington, D.C. 20007, USA
  JOURNAL
FEATURES
  source
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    /clone="49N-TA"
    <1..>270
    /gene="HLA-B"
    /number=2
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  ORIGIN

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  Ratio: 5.000        Gaps: 0
  Percent Similarity: 100.000  Percent Identity: 100.000

alignment_block:
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      1 ArgGluAsnLeuArgThrAlaLeuArgTyr 10
      222 CGAGAGAACCTGCGACCGCGCTCGCTAC 251
  seq_name: gb_pr4:HS44032S1

seq_documentation_block:
  LOCUS HS44032S1 270 bp DNA PRI 21-JUN-1999
  DEFINITION Human MHC class I antigen HLA-B (HLA-B*4410 allele) gene, exon 2.
  ACCESSION U63559
  VERSION U63559.1 GI:1488303
  KEYWORDS
  SEGMENT 1 of 2
  SOURCE human.
  ORGANISM Homo sapiens
    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
    Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
  1 (bases 1 to 270)
  Hurley, C.K. and Hoyer, R.J.
  Human MHC Class I Antigen HLA-B*4410
  Unpublished
  JOURNAL
REFERENCE
  2 (bases 1 to 270)
  Hurley, C.K. and Hoyer, R.J.
  Direct Submission
  Submitted (11-JUL-1996) Dept. of Microbiology and Immunology,
  Georgetown University, 3970 Reservoir Rd., NW, Washington, DC
  20007, USA
  JOURNAL
FEATURES
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    1..270
    /organism="Homo sapiens"
    /db_xref="taxon:9606"
    /chromosome="6"
    /cell_type="white blood cells from whole blood"
    1..270
    /gene="HLA-B"

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BASE COUNT 60 a 89 c 85 g 36 t
ORIGIN /number=2
alignment_scores: Quality: 50.00 Length: 10
Ratio: 5.000 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
US-08-653-294-25 x HS44032S1 ..

Align seg 1/1 to: HS44032S1 from: 1 to: 270

1 ArgGlusnLeuargThraLeuArgTyr 10
|||||
222 CGAGAGAACTGCGCACCGCTCCGCTAC 251

seq_name: gb_pr4:AF035648

seq_documentation_block: 395 bp DNA PRI 05-JAN-1999
LOCUS AF035648 Homo sapiens MHC class I antigen HLA-B gene (HLA-B*4402 variant allele), partial cds.
ACCESSION AF035648
VERSION AF035648.1 GI:4104422
KEYWORDS human.
SOURCE
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 395)
AUTHORS Holdsworth, R.
TITLE Direct Submission
JOURNAL Submitted (24-NOV-1997) Tissue Typing, Red Cross Blood Service, South Melbourne, Melbourne, Victoria 3205, Australia
FEATURES
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1..395
/organism="Homo sapiens"
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/chromosome="6"
<1..>395
/gene="HLA-B"
/product="MHC class I antigen"
/protein_id="AAD02035.1"
/db_xref="GI:4104423"
/translation="FSDATSPRKEPRAPWIEQGEPEYWDRETOISKNTNTQTYRENLR
TALRYNQSAGSHIQRMVGDVGPDRLLRGYDQDAYDKGYIALNEDLSWTAAD
TAAQITQRKEARVAEQDRAYLEGEVE"
BASE COUNT 89 a 120 c 141 g 45 t
ORIGIN

alignment_scores: Quality: 50.00 Length: 10
Ratio: 5.000 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:

US-08-653-294-25 x AF035648 ..

Align seg 1/1 to: AF035648 from: 1 to: 395

1 ArgGlusnLeuargThraLeuArgTyr 10
|||||

120 CGAGAGAACTGCGCACCGCTCCGCTAC 149
seq_name: gb_pr4:AF035649

seq_documentation_block: 395 bp DNA PRI 05-JAN-1999
LOCUS AF035649 Homo sapiens MHC class I antigen HLA-B gene (HLA-B*4403 variant allele), partial cds.
ACCESSION AF035649
VERSION AF035649.1 GI:4104424
KEYWORDS human.
SOURCE
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 395)
AUTHORS Holdsworth, R.
TITLE Direct Submission
JOURNAL Submitted (24-NOV-1997) Tissue Typing, Red Cross Blood Service, South Melbourne, Melbourne, Victoria 3205, Australia
FEATURES
source
1..395
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="6"
<1..>395
/gene="HLA-B"
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/protein_id="AAD02036.1"
/db_xref="GI:4104425"
/translation="FSDATSPRKEPRAPWIEQGEPEYWDPEITOISKNTNTQTYRENLR
TALRYNQSAGSHIQRMVGDVGPDRLLRGYDQDAYDKGYIALNEDLSWTAAD
TAAQITQRKEARVAEQDRAYLEGEVE"
BASE COUNT 87 a 122 c 139 g 47 t
ORIGIN

alignment_scores: Quality: 50.00 Length: 10
Ratio: 5.000 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:

US-08-653-294-25 x AF035649 ..

Align seg 1/1 to: AF035649 from: 1 to: 395

1 ArgGlusnLeuargThraLeuArgTyr 10
|||||

120 CGAGAGAACTGCGCACCGCTCCGCTAC 149

seq_name: gb_pr2:HUMBW44HLA

seq_documentation_block:
LOCUS HUMBW44HLA 404 bp DNA PRI 14-APR-1994
DEFINITION Homo sapiens HLA-B*44 variant.
ACCESSION L31798
VERSION L31798.1 GI:472361
KEYWORDS human leukocyte antigen.
SOURCE Homo sapiens blood DNA.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 404)
AUTHORS Petersdorf, E.W.
TITLE A Novel HLA-B*44 Variant

JOURNAL Unpublished (1994)
FEATURES
Location/Qualifiers
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/cell_type="leukocyte"
/tissue_type="blood"
/map="chromosome 6p"
misc_feature
1. .404
variation
203
/note="This is a report of an HLA-B*4402 variant
(HLA-B*4402v) that differs from the published sequence at
base 203 (nucleotide position 75 of exon 3)."
/phenotype="HLA-B*44"
/replace="t"
BASE COUNT 90 a 123 c 142 g 49 t
ORIGIN

alignment_scores:
Quality: 50.00 Length: 10
Ratio: 5.000 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
US-08-653-294-25 x HUMBW44HLA ..
Align seg 1/1 to: HUMBW44HLA from: 1 to: 404
1 ArgGluAsnLeuArgThrAlaLeuArgTyr 10
|||||
80 CGAGAGAACCTGCGCACCGCGCTCCGTAC 109

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OM of: US-08-653-294-25 to: N_Geneseq_36:* out_format : pfs
 Date: Feb 8, 2000 7:31 PM
 About: Results were produced by the GenCore software, version 4.5,
 Copyright (c) 1993-2000 CompuGen Ltd.

Command line parameters:

-MODEL=frame+ p2n.model -DEV=xlp
 -O=cnrl_1/USPTO.spool/US08653294/runat_04022000.160701_15807/app_query.fasta.2
 -DB=N_Geneseq_36 -QPMT=fastap -SUFFIX=mg -GAPOP=12.000
 -GAPEXT=4.000 -MINMATCH=0.100 -LOOPCL=0.000 -LOOPEXT=0.000
 -QGAPOP=4.500 -QGAPEXT=0.050 -XGAPOP=10.000 -XGAPEXT=0.500
 -FCGAPOP=6.000 -FCGAPEXT=7.000 -YGAPOP=10.000 -YGAPEXT=0.500
 -DELOP=6.000 -DELEXT=7.000 -START=1 -MATRIX=blossum62
 -TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR SCORE=pct
 -ALIGN=15 -MODE=LOCAL -OUTFMT=pfs -NORM=ext -MINLEN=0
 -MAXLEN=1000000 -USER=US08653294 -NCPU=6 -ICPU=3 -NO_XLPXY -WAIT
 -THREADS=1

Search information block:

Query: US-08-653-294-25
 Query length: 10
 Database: N_Geneseq_36:*
 Database sequences: 311585
 Database length: 125096042
 Search time (sec): 873.190000

score_list:

Sequence	Strid	Orig	zScore	EScore	Len	Documentation
N_Geneseq_36:Q29167	+	44.00	160.43	0.2460	270	HLA-B*52 exon 2 alpha-1 domain
N_Geneseq_36:Q01834	+	44.00	148.10	1.20	1086	Sequence encoding HLA-B*51 anti
N_Geneseq_36:Q01822	+	44.00	148.10	1.20	1086	Sequence encoding HLA-B*52 anti
N_Geneseq_36:Q005693	+	44.00	148.08	1.20	1089	HLA-B*51 gene for production of
N_Geneseq_36:Q05701	+	44.00	148.08	1.20	1089	HLA-B*52 gene for production of
N_Geneseq_36:Q12114	+	44.00	148.08	1.20	1089	HLA-B*53 exon. HLA-B*53 gene,
N_Geneseq_36:N70935	+	40.00	133.52	7.76	1026	Sequence encoding the human h
N_Geneseq_36:N70935	+	40.00	131.76	35.08	3874	Sequence of genomic DNA encodi
N_Geneseq_36:N70935	+	40.00	117.10	63.73	6553	HLA B*27 consensus sequence. De
N_Geneseq_36:V21209_16	-	37.00	85.47	3.7e+03	64976	Continuation (17 of 17) of
N_Geneseq_36:V22706	-	35.00	108.13	201.36	2147	Mouse recombinase hSREC2 gene
N_Geneseq_36:V35645	+	35.00	107.20	227.00	2386	Cladosporium oxysporum glucos
N_Geneseq_36:T70130	+	34.00	107.92	206.97	1437	Max-interacting protein coding
N_Geneseq_36:V73804	-	34.00	79.62	7.8e+03	35100	KSHV LTR DNA (nucleotides 70
N_Geneseq_36:V21209_00	+	34.00	69.50	2.8e+04	110000	Methanococcus jannaschii c
N_Geneseq_36:V19941	-	34.00	67.52	3.6e+04	137507	KSHV long unique coding regi
N_Geneseq_36:T47216	+	33.00	117.56	60.08	316	DNA sequence of IL33-C5a flank
N_Geneseq_36:T47217	+	33.00	115.95	73.87	379	DNA sequence of IL33-C5a flank
N_Geneseq_36:Q08098	+	33.00	109.14	177.00	818	PagC-pagD intergenic region. Sa
N_Geneseq_36:T70216	+	33.00	109.14	177.00	818	S. typhimurium pagC-pagD interg
N_Geneseq_36:Q90335	+	33.00	108.78	185.38	852	T.sergenti 33 kDa protein. New
N_Geneseq_36:Q055300	+	33.00	107.45	219.84	990	Theileria sergenti main piropl
N_Geneseq_36:X05748	+	33.00	105.82	270.95	1190	Nucleotide sequence of human H
N_Geneseq_36:V81737	+	33.00	104.62	315.85	1362	Spingomonas sp. strain AD109
N_Geneseq_36:X15191	+	33.00	104.62	315.85	1362	Nucleotide sequence of the Sph
N_Geneseq_36:Q26694	-	33.00	99.90	578.40	2320	Pag C. New anti-salmonella vac
N_Geneseq_36:Q27739	-	33.00	99.90	578.40	2320	PagC/AP fusion region. Detecti
N_Geneseq_36:Q085099	-	33.00	99.90	578.40	2320	PagC gene. Salmonella vaccine
N_Geneseq_36:T70212	-	33.00	99.90	578.40	2320	S. typhimurium pagC gene. Att
N_Geneseq_36:V95563	+	33.00	96.16	935.33	3542	Human secreted protein gene 53
N_Geneseq_36:X15190	+	33.00	94.77	1.1e+03	4144	Nucleotide sequence of the Sph
N_Geneseq_36:V22268	+	33.00	92.58	1.5e+03	5305	Streptococcus pneumoniae genom
N_Geneseq_36:T86375	+	33.00	73.88	1.6e+04	43804	Chicken embryo lethal orphan
N_Geneseq_36:X26690	+	33.00	73.88	1.6e+04	43804	Complete genome sequence of a
N_Geneseq_36:V30458_2	+	33.00	65.73	4.5e+04	110000	Continuation (3 of 6) of V3
N_Geneseq_36:V30459_2	+	33.00	65.73	4.5e+04	110000	Continuation (3 of 6) of V3
N_Geneseq_36:T60484	+	32.00	105.66	276.33	791	Rat calbindin cDNA sequence. En
N_Geneseq_36:T50947	+	32.00	102.04	439.86	1191	CAMP factor gene cfr. Nucleic
N_Geneseq_36:X14096	+	32.00	99.68	595.49	1555	H. pylori GHP1320 gene. New
N_Geneseq_36:X33945	+	32.00	97.20	817.81	2056	Human HCMV Inducible gene, SEQ
N_Geneseq_36:Q37687	+	32.00	95.33	1.0e+03	2540	Rat choline kinase gene. Rat d

N_Geneseq_36:X04639 + 32.00 93.90 1.2e+03 2985 ! Nucleic acid encoding an en
 N_Geneseq_36:X20565 - 32.00 93.23 1.4e+03 3219 ! Polynucleotide sequence fro
 N_Geneseq_36:V59714 - 32.00 91.79 1.6e+03 3791 ! Human secreted protein gene
 N_Geneseq_36:X20574 + 32.00 87.93 2.7e+03 5861 ! Polynucleotide sequence fro

seq_name: N_Geneseq_36:Q29167

seq_documentation_block:

ID Q29167 standard; DNA; 270 BP.
 AC Q29167:
 DT 09-MAR-1993 (first entry)
 DE HLA-B*52 exon 2 alpha-1 domain.
 KW Human leukocyte antigen; transgenic; germ cells; somatic cells;
 KW expression; ss.
 PN J04091731-A.
 PR 25-MAR-1992.
 PF 03-AUG-1990; 207329.
 PR 03-AUG-1990; JP-207329.
 PA (OLYU) OLYMPUS OPTICAL CO.
 DR WPI: 92-342893/42.
 PT Transgenic non-human mammalian HLA-B*52 gene - useful for
 PT analysis of expression of gene structure, and prodn. of
 PT mouse model of human disease
 PS Disclosure; Fig 1; 8pp; Japanese.
 CC The sequence shows the exon 2 alpha-1-domain of the human leukocyte
 CC antigen-B*52 gene. The complete gene may be introduced into non-
 CC human mammals, pref. rat or mouse, or their ancestors at the primary
 CC developmental biological step via transplantation into the zygote or
 CC embryo to generate transgenic non-human mammals incorporating the
 CC HLA-B*52 gene in both their germ cells and somatic cells. Transgenic
 CC non-human mammals contg. HLA-B*52 are useful for the analysis of
 CC expression of the gene, its structure, and prodn. of mouse models of
 CC human disease.
 SQ Sequence 270 BP; 59 A; 88 C; 86 G; 37 T;

alignment_scores:

Quality: 44.00 Length: 10
 Ratio: 4.889 Gaps: 0
 Percent Similarity: 90.000 Percent Identity: 90.000

alignment_block:

US-08-653-294-25 x Q29167 ..

Align seg 1/1 to: Q29167 from: 1 to: 270

1 ArgGluAsnLeuArgThrAlaLeuArgTyr 10
 |||||
 222 CGAGAGACCTCGCGATCGCGCTAC 251

seq_name: N_Geneseq_36:Q01834

seq_documentation_block:

ID Q01834 standard; DNA; 1086 BP.
 AC Q01834:
 DT 19-MAR-1991 (first entry)
 DE Sequence encoding HLA-B*51 antigen.
 KW Probe; HLA class I DNA; immunogen; ss.
 OS Homo sapiens.
 PN EP354580-A.
 PD 14-FEB-1990.
 PF 10-AUG-1989.
 PR 11-AUG-1988; JP-200758.
 PA (OLYU) Olympus Optical Co., Ltd.
 PI Kano K, Takiguchi;
 DR WPI: 90-046289/07.
 PT New DNA for class 1 human leukocyte antigens and derived probes and
 PT transformed cells, useful for DNA typing, as immunogens etc.
 PS Claim 1; Page 11: 23pp; English.
 CC The HLA class I DNA can be used as a source of probes for use in DNA
 CC typing. Transformed cells, which are useful as immunogens, can be
 CC obtained by introducing these DNAs into eucaryotic cells.
 SQ Sequence 1086 BP; 224 A; 334 C; 356 G; 172 T;

alignment_scores:
 Quality: 44.00 Length: 10
 Ratio: 4.889 Gaps: 0
 Percent Similarity: 90.000 Percent Identity: 90.000

alignment_block:

US-08-653-294-25 x Q01834

Align seg 1/1 to: Q01834 from: 1 to: 1086

1 ArgGluAsnLeuArgThrAlaLeuArgTyr 10

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 294 CGAGAGAACCTGCGGATCGGCTCGCTAC 323

seq_name: N_Geneseq_36:Q01822

seq_documentation_block:

ID Q01822 standard; DNA; 1086 BP.

AC Q01822;

DT 19-MAY-1991 (first entry)

DE Sequence encoding HLA-Bw52 antigen.

KW Probe: HLA class I DNA; immunogen; ss.

OS Homo sapiens.

FH Key Location/Qualifiers

FT cds 1..1086

FT /*tag= a

PN EP-354580-A.

PD 14-FEB-1990.

PF 10-AUG-1989.

PR 11-AUG-1988; JP-200758.

PA (OLVU) Olympus Optical Co., Ltd.

PI Kano K, Takiguchi;

DR WPI: 90-046289/07.

DR P-PSDB; R03142.

PT New DNA for class I human leucocyte antigens and transformed cells, useful for DNA typing, as immunogens etc.

PS Claim 2: p011-12: 23pp; English.

CC The HLA class I DNA can be used as a source of probes for use in DNA typing. Transformed cells, which are useful as immunogens, can be obtained by introducing these DNAs into eucaryotic cells.

SQ Sequence 1086 BP; 223 A; 335 C; 358 G; 170 T;

alignment_scores:
 Quality: 44.00 Length: 10
 Ratio: 4.889 Gaps: 0
 Percent Similarity: 90.000 Percent Identity: 90.000

alignment_block:

US-08-653-294-25 x Q01822

Align seg 1/1 to: Q01822 from: 1 to: 1086

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 294 CGAGAGAACCTGCGGATCGGCTCGCTAC 323

seq_name: N_Geneseq_36:Q05693

seq_documentation_block:

ID Q05693 standard; DNA; 1089 BP.

AC Q05693;

DT 03-JAN-1991 (first entry)

DE HLA-B51 gene for production of monoclonal antibodies.

KW Allotype specific monoclonal anti-HLA antibodies; hybridomas;

KW transgenic animals; HLA-B51 gene; ss.

FH Key Location/Qualifiers

FT exon 1..73

FT /*tag= a

FT /number=1

FT exon 74..343

FT /*tag= b

FT /number=2

FT /*tag= b
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 FT 344..619
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 FT 620..895
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 FT 896..1012
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 FT 1013..1042
 FT /*tag= f
 FT /number=6
 FT 1043..1089
 FT /*tag= g
 FT /number=7

EP-383183-A.

PD 22-AUG-1990.

PF 07-FEB-1990; 102424.

PR 08-FEB-1989; JP-Q29313.

PA (OLVU) OLYMPUS OPTICAL KK.

PI Takiguchi M;

DR WPI: 90-255479/34.

PT Allotype specific monoclonal anti- HLA antibodies prodn. - using hybridomas derived from transgenic animals carrying HLA gene and immunised with HLA antigen of different allotype

PS Disclosure; Fig 1 A-G; 20pp; English.

CC The human HLA-B51 gene was injected into fertilised mouse eggs and then these introduced into the uterus of a pseudo pregnant mouse. The young were tested to ensure incorporation of the gene into the chromosome, and one of them mated 3 times with a normal male to produce 16 young, seven of which carried the HLA-B51 gene.

CC The transgenic offspring were immunised with HLA antigen. The spleen lymphocytes were fused with myeloma cells. Hybridomas producing antibodies were selected.

CC See also Q05701.

SQ Sequence 1089 BP; 224 A; 335 C; 357 G; 173 T;

alignment_scores:
 Quality: 44.00 Length: 10
 Ratio: 4.889 Gaps: 0
 Percent Similarity: 90.000 Percent Identity: 90.000

alignment_block:

US-08-653-294-25 x Q05693

Align seg 1/1 to: Q05693 from: 1 to: 1089

1 ArgGluAsnLeuArgThrAlaLeuArgTyr 10

|||||
 295 CGAGAGAACCTGCGGATCGGCTCGCTAC 324

seq_name: N_Geneseq_36:Q05701

seq_documentation_block:

ID Q05701 standard; DNA; 1089 BP.

AC Q05701;

DT 03-JAN-1991 (first entry)

DE HLA-Bw52 gene for production of monoclonal antibodies.

KW Allotype specific monoclonal anti-HLA antibodies; hybridomas;

KW transgenic animals; HLA-Bw52 gene; ss.

FH Key Location/Qualifiers

FT exon 1..73

FT /*tag= a

FT /number=1

FT exon 74..343

FT /*tag= b

FT /number=2

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FT exon /note="alpha 1-domain"
FT 344..619
FT /*tag= c
FT /number=3
FT /note="alpha 2-domain"
FT 620..895
FT /*tag= d
FT /number=4
FT /note="alpha 3-domain"
FT 896..1012
FT /*tag= e
FT /number=5
FT 1013..1042
FT /*tag= f
FT /number=6
FT 1043..1089
FT /*tag= g
FT /number=7
FT
FT EP-383183-A.
PD 22-AUG-1990.
PF 07-FEB-1990; 102424.
PR 08-FEB-1989; JP-029313.
PA (OLYU ) OLYMPUS OPTICAL KK.
PI Takiguchi M;
DR WPI; 90-255479/34.
PT Allotype specific monoclonal anti- HLA antibodies prodn. - using
PT hybridomas derived from transgenic animals carrying HLA gene and
PT immunised with HLA antigen of different allotype
PS Disclosure; Fig 1 A-G; 20pp; English.
CC The human HLA-Bw52 gene was introduced into mouse L cells and
CC then these cells used to immunise one of the transgenic mice
CC (See Q05693).
CC The spleen lymphocytes were fused with myeloma cells (P3x63-Ag8.653).
CC Hybridomas producing antibodies were selected.
SQ Sequence 1089 BP; 223 A; 336 C; 359 G; 171 T;

alignment_scores:
  Quality: 44.00 Length: 10
  Ratio: 4.889 Gaps: 0
Percent Similarity: 90.000 Percent Identity: 90.000

alignment_block:
US-08-653-294-25 x Q05701 ..
Align seg 1/1 to: Q05701 from: 1 to: 1089

1 ArgGluAsnLeuArgThrAlaLeuArgTyr 10
|||||
295 CGAGAGACCTCGGATCGGCTCGCTAC 324

seq_name: N_Geneseq_36:Q12114

seq_documentation_block:
ID Q12114 standard; DNA; 1089 BP.
AC Q12114;
DT 29-AUG-1991 (first entry)
DE HLA-Bw53 exon.
KW Human leukocyte antigen; probe; major histocompatibility complex;
KW MHC; class I; ss.
OS Homo sapiens.
FH Key Location/Qualifiers
FT cds 1..1089
FT /*tag= a
FT
PN J03112487-A.
PD 14-MAY-1991.
PF 22-SEP-1989; 247697.
PR 22-SEP-1989; JP-247697.
PA (OLYU ) OLYMPUS OPTICAL KK.
DR WPI; 91-182991/25.
DR P-PSDB; R12463.
PT HLA-Bw53 gene, DNA probe and transformant cells - used for
immunisation, identifying specificity of antiserum etc.
```

```
PS Claim 1; Page 1; lipp; Japanese.
CC Probes comprising part of the sequence can be used to identify
CC Class I genes. The DNA can be expressed for immunisation of
CC animals and prodn. of monoclonal antibodies specific for the
CC HLA-Bw53 antigen. See also J03112485 and J03112486. 174 T;
SQ Sequence 1089 BP; 222 A; 337 C; 356 G; 174 T;

alignment_scores:
  Quality: 44.00 Length: 10
  Ratio: 4.889 Gaps: 0
Percent Similarity: 90.000 Percent Identity: 90.000

alignment_block:
US-08-653-294-25 x Q12114 ..
Align seg 1/1 to: Q12114 from: 1 to: 1089

1 ArgGluAsnLeuArgThrAlaLeuArgTyr 10
|||||
295 CGAGAGACCTCGGATCGGCTCGCTAC 324

seq_name: N_Geneseq_36:N70935

seq_documentation_block:
ID N70935 standard; DNA; 1026 BP.
AC N70935;
DT 10-APR-1991 (first entry)
DE Sequence encoding the human histocompatibility antigen HLA B27.
KW Rheumatic disorder; genetic screening; diagnosis;
KW ankylosing spondylitis; ss.
OS Homo sapiens.
FH Key Location/Qualifiers
FT cds 1..1026
FT
PN DE3542024-A.
PD 04-JUN-1987.
PF 28-NOV-1985; 542024.
PR 28-NOV-1985; DE-542024.
PR 21-DEC-1985; DE-545576.
PA (BEHW ) BEHRINGERWERKE AG.
PI Riethmuller G, Meo T, Weiss E, Szots H;
DR WPI; 87-157893/23.
DR P-PSDB; P70590.
PT DNA coding for antigen HLA B27 - and diagnostic reagents contg.
PT such DNA, antigen or antibody
PS Claim 2; Page 4; 5pp; German
CC The DNA may be used as a hybridisation probe for detecting the HLA
CC B27 gene, e.g. for assessing susceptibility to rheumatic disorders
CC such as ankylosis spondylitis, or may be used to transform cells
CC for prodn. of HLA B27. The HLA B27 may be used to detect HLA B27
CC antibody in human serum, or to produce mono- or polyclonal HLA B27
CC antibodies for use in immunoassay.
SQ Sequence 1026 BP; 213 A; 307 C; 344 G; 162 T;

alignment_scores:
  Quality: 40.00 Length: 10
  Ratio: 4.444 Gaps: 0
Percent Similarity: 90.000 Percent Identity: 80.000

alignment_block:
US-08-653-294-25 x N70935 ..
Align seg 1/1 to: N70935 from: 1 to: 1026

1 ArgGluAsnLeuArgThrAlaLeuArgTyr 10
|||||
223 CGAGAGACCTCGGACCTGCTCGCTAC 252

seq_name: N_Geneseq_36:N70225

seq_documentation_block:
ID N70225 standard; DNA; 3874 BP.
```

AC N70225;
 DT 03-APR-1991 (first entry)
 DE Sequence of genomic DNA encoding human histocompatibility antigen
 DE HLA-B 27.
 KW Ankylosing spondylitis; rheumatic disorder; diagnosis; ss.
 OS Homo sapiens.
 FH Key Location/Qualifiers
 FT intron 518..590
 FT intron /*tag= a
 FT intron 720..989
 FT intron /*tag= b
 FT intron 1090..1506
 FT intron /*tag= c
 FT intron 1932..2357
 FT intron /*tag= d
 FT intron 2450..2566
 FT intron /*tag= e
 FT intron 3009..3041
 FT intron /*tag= f
 FT intron 3148..3191
 FT intron /*tag= g
 PN EP-226069-A.
 PD 24-JUN-1987.
 PF 21-NOV-1986; 116139.
 PR 01-JAN-1985; DE-542024.
 PR 21-DEC-1985; DE-545576.
 PA (BEHW) BEHRINGERWERKE AG.
 PI Szotz H, Weiss E, Dorner C, Lang M, Meo T, Riethmuller G;
 DR WPI; 87-171469/25.
 DR P-PSDB; P70155.
 PT DNA coding for human histocompatibility antigen HLA-B 27 - useful
 PT for diagnosis and antigen and antibody prodn.
 PS Claim 1: p6; 13pp; German.
 CC The DNA may be used to detect the HLA-B 27 gene (opt. mutated) in
 CC human genetic material. The HLA-B 27 may be used to detect anti-HLA-
 CC B 27 antibodies in human serum. The antibodies may be used to
 CC determine HLA-B 27 levels in human serum, e.g. for diagnosis of
 CC rheumatic disorders, esp. ankylosing spondylitis.
 SQ Sequence 3874 BP; 751 A; 1094 C; 1171 G; 858 T;

alignment_scores:
 Quality: 40.00 Length: 10
 Ratio: 4.444 Gaps: 0
 Percent Similarity: 90.000 Percent Identity: 80.000

alignment_block:

US-08-653-294-25 x N70225 ..

Align seg 1/1 to: N70225 from: 1 to: 3874

1 ArgGluAsnLeuArgThrAlaLeuArgTyr 10
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 941 CGAGAGACCTCGGACCCCTCGCTCCGCTAC 970

seq_name: N_Geneseq_36:T61639

seq_documentation_block:

ID T61639 standard; DNA; 6553 BP.

AC T61639;

DT 05-JUN-1997 (first entry)

DE HLA B27 consensus sequence.

KW HLA B27; seronegative spondylarthropathy; ankylosing spondylitis;

KW Reiter's syndrome; arthritis; acute anterior uveitis; diagnosis;

KW ss; ds.

OS Homo sapiens.

FH Key Location/Qualifiers

FT mrna 3968..6653

FT intron /*tag= a

FT /*note= "HLA-B27 3' flanking region, downstream of

FT 3' untranslated region"

FT 4112..4556

FT intron /*tag= b

FT /*note= "3' flanking region diagnostic for genetic
 FT predisposition to SNSA"
 FT 4270..4556
 FT /*tag= b
 FT /*note= "3' flanking region diagnostic for genetic
 FT predisposition to SNSA"
 FT misc_difference 4495
 FT /*tag= d
 FT /*note= "absence of cytosine at this site is
 FT indicative of a predisposition to SNSA"

WO9709450-A1.

PN 13-MAR-1997.

PD 16-AUG-1996; U13256.

PF 01-SEP-1995; US-522942.

PR (CEDA-) CEDARS SINAI MEDICAL CENT.

PA Tyan DB;

PI WPI; 97-192924/17.

DR Detecting pre-disposition to seronegative spondylarthropathies -

PT from the absence of a C residue at a specific position in the

PT 3'-flanking region of the HLA B27 allele

PS Claim 1; Page 52-56; 68pp; English.

CC Genetic predisposition to seronegative spondylarthropathies (SNSA)

CC is detected by determining the absence of a cytosine nucleotide in

CC the 3' flanking region (see also T61647-48) of an HLA-B gene at a

CC position corresponding to nucleotide 4495 of the HLA-B27 consensus

CC sequence given in T61639. Probes and primers (see also T61640-46)

CC based on this region can be used in diagnostic assays to detect the

CC genetic predisposition to SNSA, and permit the distinction of B27+

CC individuals who are resistant to SNSA from B27+ normal individuals

CC who are susceptible (but as yet unaffected) to such diseases.

SQ Sequence 6553 BP; 1443 A; 1619 C; 2017 G; 1474 T;

alignment_scores:

Quality: 40.00 Length: 10
 Ratio: 4.444 Gaps: 0
 Percent Similarity: 90.000 Percent Identity: 80.000

alignment_block:

US-08-653-294-25 x T61639 ..

Align seg 1/1 to: T61639 from: 1 to: 6553

1 ArgGluAsnLeuArgThrAlaLeuArgTyr 10

|||||:::||||||| |||||

1102 CGAGAGACCTCGGACCCCTCGCTCCGCTAC 1131

seq_name: N_Geneseq_36:V21209_16

seq_documentation_block:

Continuation (17 of 17) of V21209 from base 1600001 (Methanococcus jannaschii circula

WP Sequence split into 17 fragments LOCUS V21209 Accession V21209

WP Fragment Name Begin End

WP V21209_00 1 110000

WP V21209_01 100001 210000

WP V21209_02 200001 310000

WP V21209_03 300001 410000

WP V21209_04 400001 510000

WP V21209_05 500001 610000

WP V21209_06 600001 710000

WP V21209_07 700001 810000

WP V21209_08 800001 910000

WP V21209_09 900001 1010000

WP V21209_10 1000001 1110000

WP V21209_11 1100001 1210000

WP V21209_12 1200001 1310000

WP V21209_13 1300001 1410000

WP V21209_14 1400001 1510000

WP V21209_15 1500001 1610000

WP V21209_16 1600001 1664976

alignment_scores:

FT misc_feature 1434.

name: N_Geneseq_36:V

name: N_Geneseq_36:V355645

name: N_Geneseq_36:V35645

PA (UYCO) UNIV COLUMBIA NEW YORK.
 PI Bohenzky RA, Chang Y, Edelman IS, Moore PS, Russo JJ;
 DR WPI: 99-069741/06.
 PT Kaposi's sarcoma-associated herpes virus nucleic acid - encodes
 PT di:hydrofolate reductase and is useful for treatment, prophylaxis
 PT or diagnosis of Kaposi's sarcoma
 PS Disclosure: Column 125-156; 109pp; English.
 CC This sequence is a fragment of the Kaposi's sarcoma-associated
 CC herpesvirus (KSHV) LUR (long unique region). This fragment contains
 CC coding regions for ORF48, ORF49, ORF50 which encodes a transactivator
 CC (LCTP), R8, ORF52, ORF53, ORF54 which encodes dUTPase, ORF55, ORF56
 CC which encodes DNA replication protein I, ORF57 which encodes immediate
 CC early protein II (IEP-II), K9 which encodes virF1 (ICSBP), K10, K11,
 CC ORF58 which encodes a phosphoprotein, ORF59 which encodes DNA replication
 CC protein II, ORF60 which encodes a small ribonucleotide reductase, ORF61
 CC which encodes a large ribonucleotide reductase, ORF62 which encodes an
 CC assembly/DNA maturation protein, ORF63 which encodes tegument protein
 CC II, ORF64 which encodes tegument protein III. KSHV is a new human
 CC Herpesvirus (HHV8) believed to cause Kaposi's sarcoma (KS) which is the
 CC most common form of neoplasm occurring in persons with acquired immune
 CC deficiency syndrome (AIDS). The DHFR protein is useful for vaccination,
 CC prophylaxis, diagnosis and treatment of a subject with Kaposi's sarcoma
 CC and for detecting expression of a DNA virus associated with Kaposi's
 CC sarcoma in a cell.
 SQ Sequence 35100 BP; 8632 A; 10010 C; 8650 G; 7808 T;

alignment_scores:
 Quality: 34.00 Length: 9
 Ratio: 4.250 Gaps: 0
 Percent Similarity: 88.889 Percent Identity: 77.778

alignment_block:
 US-08-653-294-25 x V73804/rev ..

Align seg 1/1 to reverse of: V73804 from: 1 to: 35100

1 ArgGluAsnLeuArgThrAlaLeuArg 9
 3575 CGGGAGATCTCCGGTGTCTCTGCGA 3549

seq_name: N_Geneseq_36:V21209_00

seq_documentation_block:

WP Sequence split into 17 fragments LOCUS V21209 Accession V21209

Fragment Name	Begin	End
WP V21209_00	1	110000
WP V21209_01	100001	210000
WP V21209_02	200001	310000
WP V21209_03	300001	410000
WP V21209_04	400001	510000
WP V21209_05	500001	610000
WP V21209_06	600001	710000
WP V21209_07	700001	810000
WP V21209_08	800001	910000
WP V21209_09	900001	1010000
WP V21209_10	1000001	1110000
WP V21209_11	1100001	1210000
WP V21209_12	1200001	1310000
WP V21209_13	1300001	1410000
WP V21209_14	1400001	1510000
WP V21209_15	1500001	1610000
WP V21209_16	1600001	1664976

ID V21209 standard; DNA; 1664976 BP.

AC V21209;
 DT 10-NOV-1998 (first entry)
 DE Methanococcus jannaschii circular chromosome.
 DE Methanococcus jannaschii: methanogenic archaeon; circular chromosome;
 KW genome; autotrophic; extrachromosomal element; identification; ds.
 OS Methanococcus jannaschii.
 PN W09807830-A2.
 PD 26-FEB-1998.
 PF 22-AUG-1997; U14900.

PR 22-AUG-1996; US-024428.
 PA (GENO-) INST GENOMIC RES.
 PA (UYII) UNIV ILLINOIS FOUND.
 PA (UYJO) UNIV JOHNS HOPKINS SCHOOL MEDICINE.
 PI Sult CJ, Smith HO, Venter JC, White OR, Woese CR;
 DR WPI: 98-169145/15.
 PT Complete genome sequence of methano-genic archaeon, Methanococcus
 PT jannaschii - useful in identification of M. jannaschii genome
 PT fragment
 PS Claim 13: Page 152-585; 614pp; English.
 CC The present sequence represents the complete 1.66-megabase pair genome
 CC sequence of the Methanococcus jannaschii circular chromosome. The
 CC present invention describes M. jannaschii open reading frames from the
 CC genome sequence. The invention also describes a computer based system
 CC for identifying fragments of the M. jannaschii genome that are
 CC homologous to target nucleotide sequences, comprising: (a) data storage
 CC means comprising the nucleotide sequence of the 1664976, 58407 or 16550
 CC bp sequence (see V21209, V21210 and V21211), or a nucleotide sequence at
 CC least 99.9% identical to it; (b) search means for comparing a target
 CC sequence to the nucleotide sequence of the data storage means to
 CC identify a homologous sequence, and (c) retrieval means for obtaining
 CC the homologous sequence. The method, which is based on whole genome
 CC random sequencing of an autotrophic archaeon M. jannaschii, the genome
 CC of which consists of 3 physically distinct elements, a large circular
 CC chromosome (the 1664976 bp sequence given in V21209), a large circular
 CC extra-chromosomal element (the 58407 bp sequence given in V21210), and a
 CC small circular extra-chromosomal element (the 16550 bp sequence given in
 CC V21211), can be used in the identification of M. jannaschii genome
 CC fragment.
 SQ Sequence 1664976 BP; 568133 A; 264649 C; 258701 G; 573392 T;

alignment_scores:
 Quality: 34.00 Length: 9
 Ratio: 4.250 Gaps: 0
 Percent Similarity: 88.889 Percent Identity: 66.667

alignment_block:
 US-08-653-294-25 x V21209_00 ..

Align seg 1/1 to: V21209_00 from: 1 to: 110000

2 GluAsnLeuArgThrAlaLeuArgTyr 10
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 94200 GAGAAATTTAAACCTCTACTAAATAT 94226

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 Date: Feb 8, 2000 6:23 AM
 About: Results were produced by the GenCore software, version 4.5,
 Copyright (c) 1993-2000 CompuGen Ltd.

Command line parameters:
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gb_est8:C03945	+ 44.00	167.16	1.52	232	AI03945 C03945 Human heart CDNA
gb_est10:AA151891	+ 44.00	166.30	1.70	255	AA151891 z001f06.r1 Stratagene
gb_est11:AA263158	+ 44.00	165.34	1.92	283	AA263158 PMY0534 KGI-a Lambda Z
gb_est6:D82221	+ 44.00	162.77	2.67	375	D82221 HUMHBC4626 Human pancrea
gb_est36:AI159260	+ 44.00	158.20	4.79	618	AI159260 qy27507.x1 NCI_CGAP_Br
gb_est31:AI169864	+ 44.00	156.45	6.00	748	AI169864 wC74h11.x1 NCI_CGAP_Pa
gb_est27:AA466429	+ 43.00	159.04	4.30	366	AA466429 vx35b04.y1 Stratagene
gb_est20:AA881004	+ 43.00	154.92	7.30	574	AA881004 vx35b04.y1 Stratagene
gb_gss7:AO894863	+ 41.00	148.17	17.35	506	AO894863 HS_3193_A2.D11.T7C CIT
gb_est38:AI035690	+ 40.00	144.14	8.06	171	AI035690 DKFp564D2463.r1 564 (
gb_est10:AA147151	+ 40.00	142.95	33.87	581	AA147151 z032d06.r1 Stratagene
gb_est37:AI197388	+ 39.00	142.76	34.69	385	AI197388 sd11c05.y1 Gm-cl020 GI
gb_est18:AA722000	+ 39.00	141.38	41.45	448	AA722000 zhl7e08.s1 Soares.pine
gb_est9:AA064631	+ 39.00	141.30	41.88	452	AA064631 zF72c03.s1 Soares.pine
gb_est9:AA064793	+ 39.00	141.02	43.41	466	AA064793 zF72c03.r1 Soares.pine
gb_est6:D82189	+ 38.00	138.12	62.90	415	D82189 HUMHBC4524 Human pancrea
gb_est44:AW212923	+ 38.00	136.17	80.85	514	AW212923 uo69c04.x1 NCI_CGAP_Ma
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gb_est32:AI007865	+ 37.00	136.41	78.38	325	AI007865 EST202316 Normalized r
gb_est14:AA445358	+ 37.00	135.30	90.40	367	AA445358 vF64d07.r1 Barstede ME
gb_est23:AI089530	+ 37.00	134.98	94.17	380	AI089530 z222a07.x1 Soares.tota
gb_est22:AI060602	+ 37.00	133.27	117.23	458	AI060602 BSMHFS209D7SK Brugia
gb_est3:RI3904	+ 37.00	133.25	117.53	459	RI3904 yf62c03.r1 Soares infant
gb_est16:AA570443	+ 37.00	132.94	122.36	475	AA570443 ga64a02.x1 Soares.feta
gb_gss11:AO275243	+ 37.00	132.78	124.78	483	AO275243 RPI1-1-1319T7 RPI1-1 H
gb_est21:AA910336	+ 37.00	132.75	125.38	485	AA910336 RPI1-1-1319T7 RPI1-1 H
gb_est26:AA817822	+ 37.00	131.95	140.69	535	AA817822 U1-rA0-aed-07-0-UI-8
gb_gss3:B60318	+ 37.00	131.76	142.23	540	AA817822 U1-rA0-aed-07-0-UI-8
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gb_gss8:AO20193	+ 37.00	130.97	157.49	589	AO20193 CIT-HSP-2306N22.TF CIT
gb_est42:AV324628	+ 36.00	134.71	97.45	698	AV324628 nbx0065M10f CUGI Rice
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gb_gss11:AO322213 + 36.00 126.94 264.07 594 ! AO322213 RPI11-96G8.TJ RPI1
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seq_name: gb_est23:AI124815

seq_documentation_block:
 LOCUS AI124815 414 bp mRNA EST 11-SEP-1998
 DEFINITION am5606.x1 Johnston frontal cortex Homo sapiens cDNA clone
 IMAGE:1539596 3' similar to gb:M24038.cdsl HLA CLASS I
 HISTOCOMPATIBILITY ANTIGEN, BW-44(B-12) B*4402 (HUMAN); contains
 MER20.t3 TARI repetitive element ; mRNA sequence.

ACCESSION AI124815
 VERSION AI124815
 KEYWORDS EST.

SOURCE
 ORGANISM Homo sapiens

REFERENCE
 1 (bases 1 to 414)
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 Eutheria; Primates; Catarrhini; Hominidae; Homo.

AUTHORS
 Hillier, L., Allen, M., Bowles, L., Dubuque, T., Geisel, G., Jost, S.,
 Krizman, D., Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M.,
 Martin, J., Moore, B., Schellenberg, K., Steptoe, M., Tan, F.,
 Theising, B., White, Y., Wylie, T., Waterston, R., and Wilson, R.
 WashU-NCI human EST Project
 Unpublished (1997)

TITLE
 JOURNAL
 COMMENT
 On Jan 17, 1998 this sequence version replaced gi:1899887.

Contact: Wilson RK
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810

Email: est@wustl.edu
 This clone is available royalty-free through LLNL : contact the
 IMAGE Consortium (info@image.llnl.gov) for further information.
 Seq primer: -40ml3 fwd. Et from Amersham.

FEATURES
 source
 1. 414

/organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:1539596"
 /clone_lib="Johnston frontal cortex"
 /sex="male"
 /tissue_type="pooled frontal lobe"
 /dev_stage="adult"
 /lab_host="SOLR (kanamycin resistant)"
 /note="Organ: brain; Vector: Bluescript SK-; Site:1:
 ECORI; Stanley Neurophatology Consortium
 (www.stanleylab.org) brains S-58, S-65, S-67, S-78.
 Random + oligo-gr primed into EORI site of ZAP II Vector.
 Mass excised. Avg insert length 1.9kb. Custom library
 provided by Dr. Nancy Johnston [(410) 614-3918,
 nj@welchlink.welch.jhu.edu].

BASE COUNT 80 a 140 c 136 g 58 t

ORIGIN

alignment_scores:
 Quality: 50.00 Length: 10
 Ratio: 5.000 Gaps: 0
 Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
 US-08-653-294-25 x AI124815 ..

Align seg 1/1 to AI124815 from: 1 to: 414

1 ArgGluAsnLeuArgThrAlaLeuArgTyr 10
 |||||

284 CGAGAGACCTGCGACCGCGCTCCGCTAC 313

seq_name: gb_est8:C03945

```

seq_documentation_block: 232 bp mRNA EST 30-JUL-1996
LOCUS C03945 Human heart cDNA (Ynakamura) Homo sapiens cDNA clone
DEFINITION 3NHC2454, mRNA sequence.
ACCESSION C03945
VERSION C03945.1 GI:1467196
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 232)
AUTHORS Tanaka,T., Ogiwara,A., Uchiyama,I., Takagi,T., Yazaki,Y. and Nakamura,Y.
TITLE Construction of a normalized directionally cloned cDNA library from adult heart and analysis of 3040 clones by partial sequencing
JOURNAL Genomics 35 (1), 231-235 (1996)
MEDLINE
COMMENT 96299762
On Oct 24, 1995 this sequence version replaced gi:1040105.
Contact: Yusuke Nakamura
Institute of Medical Science
University of Tokyo
4-6-1, Shirokanedai, Minato-ku, Tokyo 108, Japan
Tel: 81-3-5449-5372
Fax: 81-3-5449-5433
Email: yusuke@ims.u-tokyo.ac.jp.
FEATURES
Location/Qualifiers
source 1..232
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="3NHC2454"
/clone_lib="Human heart cDNA (Ynakamura)"
/dev_stage="adult"
/note="organ: heart; normalized directionally cloned cDNA from adult heart"
BASE COUNT 55 a 77 c 68 g 32 t
ORIGIN

alignment_scores:
Quality: 44.00 Length: 10
Ratio: 4.889 Gaps: 0
Percent Similarity: 90.000 Percent Identity: 90.000

alignment_block:
US-08-653-294-25 x C03945
Align seg 1/1 to: C03945 from: 1 to: 232

1 ArgGluAsnLeuArgThrAlaLeuArgTyr 10
|||||
40 CGAGAGAACCTGCGGATCGGCTCCGCTAC 69

seq_name: gb_est10:AA151891

seq_documentation_block: 255 bp mRNA EST 10-DEC-1996
LOCUS AA151891
DEFINITION z001f06.r1 Stratagene colon (#937204) Homo sapiens cDNA clone IMAGE:566435 5' similar to gb:M15497_cds1_HLA_CLASS_I HISTOCOMPATIBILITY ANTIGEN, A-24(A-9) A*2401 (HUMAN)), mRNA sequence.
ACCESSION AA151891
VERSION AA151891.1 GI:1720754
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 255)
AUTHORS Hillier,L., Lennon,G., Becker,M., Bonaldo,M.F., Chiapelli,B., Chissoe,S., Dietrich,N., Dubuque,T., Favell,A., Gish,W., Hawkins,M., Hultman,M., Kucaba,T., Lacy,M., Le,M., Le,N., Mardis,E., Moore,B., Morris,M., Parsons,J., Prange,C., Rifkin,L.,

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Rohlfing,T., Schellenberg,K., Soares,M.B., Tan,F., Thierry-Mieg,J.,
Trevaskis,E., Underwood,K., Wohldmann,P., Waterston,R., Wilson,R.
and Marra,M.
Generation and analysis of 280,000 human expressed sequence tags
Genome Res. 6 (9), 807-828 (1996)
97044478
On May 8, 1995 this sequence version replaced gi:800234.
Contact: Wilson RK
Washington University School of Medicine
4424 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Trace considered overall poor quality
Seq primer: -28M13 rev2 from Amersham
High quality sequence stop: 1.
Location/Qualifiers
source 1..255
/organism="Homo sapiens"
/db_xref="GDB:459088"
/db_xref="taxon:9606"
/clone="IMAGE:566435"
/clone_lib="Stratagene colon (#937204)"
/lab_host="SOLR cells (kanamycin resistant)"
/note="Organ: colon; Vector: pBluescript SK-; Site: 1: EcoRI; Site 2: XhoI; Cloned unidirectionally. Primer: Oligo dT. T-84 colonic epithelial cell line. Average insert size: 1.0 kb; Uni-ZAP XR Vector; -5' adaptor sequence: 5' GAATTCGGACGAG 3' -3' adaptor sequence: 5' CTCGAGTGTGTTTTTTTTTTT 3'"
BASE COUNT 57 a 70 c 75 g 44 t 9 others
ORIGIN

alignment_scores:
Quality: 44.00 Length: 10
Ratio: 4.889 Gaps: 0
Percent Similarity: 90.000 Percent Identity: 90.000

alignment_block:
US-08-653-294-25 x AA151891
Align seg 1/1 to: AA151891 from: 1 to: 255

1 ArgGluAsnLeuArgThrAlaLeuArgTyr 10
|||||
77 CGAGAGAACCTGCGGATCGCCTCCGCTAC 106

seq_name: gb_est11:AA263158

seq_documentation_block: 283 bp mRNA EST 02-JUL-1998
LOCUS AA263158
DEFINITION PMY0534 KGI-a Lambda zap Express cDNA library Homo sapiens CDNA 5', mRNA sequence.
ACCESSION AA263158
VERSION AA263158.1 GI:1898964
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 283)
AUTHORS Claudio,J.O., Liew,C.C., Dempsey,A.A., Cukerman,E., Stewart,A.K., Na,E., Atkins,H.I., Iscove,N.N. and Hawley,R.G.
TITLE Identification of sequence-tagged transcripts differentially expressed within the human hematopoietic hierarchy
JOURNAL Genomics 50 (1), 44-52 (1998)
MEDLINE 98292493
COMMENT On May 5, 1995 this sequence version replaced gi:797810.
Contact: Hawley RG
Oncology Research Laboratories

```

The Toronto Hospital
CRCS-424, 67 College St., Toronto, Ontario M5G 2M1, Canada
Tel: 416 3403834
Fax: 416 3403453
Email: r.hawley@utoronto.ca
Similar to M58636 MHC class I HLA-B* gene. Clone was randomly
picked from KGLA primary library.
Seq primer: 5' GAAATTAACCTCTACTAAAGG 3'
High quality sequence stop: 283.

FEATURES

source
1. 283
Location/Qualifiers
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="KGL-a Lambda Zap Express cDNA library"
/cell_type="promyeloblast"
/cell_line="KGL-a"
/note="Vector: Lambda Zap Express (Stratagene); Site_1:
EcoRI; Site_2: XhoI; Unidirectional cloning sites:
EcoRI-XhoI. mRNA was purified from KGL-a cell line, cDNA
was synthesized using an XhoI-OligodT linker primer. EcoRI
adaptors were ligated, followed by digestion with XhoI for
directional cloning into predigested Lambda Zap Express"

BASE COUNT

64 a 91 c 88 g 40 t

alignment_scores:

Quality: 44.00 Length: 10
Ratio: 4.889 Gaps: 0
Percent Similarity: 90.000 Percent Identity: 90.000

alignment_block:

US-08-653-294-25 x AA263158 ..

Align seg 1/1 to: AA263158 from: 1 to: 283

1 ArgGluAsnLeuArgThrAlaLeuArgTyr 10
|||||
120 CGAGAGAACCTCGGATCGCGTCCGCTAC 149

seq_name: gb_est6:D82221

seq_documentation_block:

LOCUS D82221 375 bp mRNA EST 09-FEB-1996
DEFINITION HUMHBC4626 Human pancreatic islet Homo sapiens cDNA similar to
HLA-B, mRNA sequence.

ACCESSION

D82221

VERSION

D82221.1 GI:1183739

KEYWORDS

EST.

SOURCE

human.

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;

Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 375)

Human pancreatic islet ESTs

Unpublished (1995)

On Apr 14, 1993 this sequence version replaced gi:785255.

Contact: Jun Takeda

Institute for Molecular and Cellular Regulation, Gunma University

3-39-15 Shova-machi, Maebashi Gunma 371, Japan

Tel: 272-20-8856

Fax: 272-20-8896

Email: jtakeda@sb.gunma-u.ac.jp.

Location/Qualifiers

1. 375

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone_lib="Human pancreatic islet"

/note="Vector: Lambda ZAPII; Site_1: Eco RI; Site_2: Xho

BASE COUNT

75 a 124 c 118 g 55 t 3 others

ORIGIN

alignment_scores:

Quality: 44.00 Length: 10
Ratio: 4.889 Gaps: 0
Percent Similarity: 90.000 Percent Identity: 90.000

alignment_block:

US-08-653-294-25 x D82221 ..

Align seg 1/1 to: D82221 from: 1 to: 375

1 ArgGluAsnLeuArgThrAlaLeuArgTyr 10

|||||

306 CGAGAGAACCTCGGATCGCGTCCGCTAC 335

seq_name: gb_est6:AI359260

seq_documentation_block:

LOCUS AI359260 618 bp mRNA EST 15-FEB-1999
DEFINITION QY27B07.x1 NCI_CGAP_Brn23 Homo sapiens cDNA clone IMAGE:2013205 3'
similar to gb:D32129 HLA CLASS I HISTOCOMPATIBILITY ANTIGEN,
AW-66(A-10) A*6601 ALPHA (HUMAN);, mRNA sequence.

ACCESSION

AI359260

VERSION

AI359260.1 GI:4110881

KEYWORDS

EST.

SOURCE

human.

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;

Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 618)

NCI/NCI-NDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute / National Institute of Neurological

Disorders and Stroke, Brain Tumor Genome Anatomy Project

(CGAP/BTGP), Tumor Gene Index

Unpublished (1998)

Contact: Robert Strausberg, Ph.D.

Tel: (301) 496-1550

Email: Robert_Strausberg@nih.gov

Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D.,

Ph.D.

cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima

Bonaldo, Ph.D.

cDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

www-bio.llnl.gov/bbrp/image/image.html

Insert Length: 691 Std Error: 0.00

Seq primer: -400P from Gibco

High quality sequence stop: 458.

FEATURES

Location/Qualifiers

1. 618

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone_image="IMAGE:2013205"

/clone_lib="NCI_CGAP_Brn23"

/tissue_type="glioblastoma (pooled)"

/lab_host="DH10B"

/note="Organ: brain; Vector: pT7T3D-Pac (Pharmacia) with a

modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st

strand cDNA was primed with a Not I - oligo(dT) primer [5'

TGTTACCAATCTGAGTGGCGGCATATCTTTTTTTTTTTTTTTTTTTT

T 3']; double-stranded cDNA was ligated to Eco RI

adaptors (Pharmacia), digested with Not I and cloned into

the Not I and Eco RI sites of the modified pT7T3 vector.

Library is normalized, and was constructed by Bento

Soares and M.Fatima Bonaldo."

BASE COUNT 128 a 171 c 182 g 137 t

ORIGIN

alignment_scores:
 Quality: 44.00 Length: 10
 Ratio: 4.889 Gaps: 0
 Percent Similarity: 90.000 Percent Identity: 90.000

alignment_block:

US-08-653-294-25 x AI359260/rev ..
 Align seg 1/1 to reverse of: AI359260 from: 1 to: 618

1 ArgGlusnLeuArgThralaLeuArgTyr 10

|||||
 319 CGAGAGACCTCGGATCGGCTCCGCTAC 290

seq_name: gb_est31:AI696864

seq_documentation_block: 748 bp mRNA EST 03-JUN-1999
 LOCUS AI696864 wc74h11.x1 NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2324421 3'
 DEFINITION similar to gb:M28205 HLA CLASS I HISTOCOMPATIBILITY ANTIGEN,
 B-51(B-5) B*5101 ALPHA (HUMAN);, mRNA sequence.

ACCESSION AI696864

VERSION AI696864.1 GI:4984764

KEYWORDS EST.

SOURCE human.

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

1 (bases 1 to 748)

AUTHORS NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.

TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

Tumor Gene Index

JOURNAL Unpublished (1997)

COMMENT

On Mar 16, 1998 this sequence version replaced gi:2961758.
 Contact: Robert Strausberg, Ph.D.
 Tel: (301) 496-1550
 Email: Robert.Strausberg@nih.gov
 Life Technologies catalog #: 11548-013
 DNA Sequencing by: Washington University Genome Sequencing Center
 Clone distribution: NCI-CGAP clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html

Seq primer: -40UP from Gibco

High quality sequence stop: 424.

FEATURES

source

1..748
 Location/Qualifiers
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:2324421"
 /clone_lib="NCI_CGAP_Pan1"
 /tissue_type="adenocarcinoma"
 /lab_host="DH10B"
 /note="Organ: pancreas; Vector: pCMV-SPORT6; Site:1; salI;
 Site:2: NotI; Cloned unidirectionally. Primer: Oligo dT.
 Average insert size 1.72 kb. Life technologies catalog #:
 11548-013"

BASE COUNT 169 a 227 c 237 g 108 t 7 others

ORIGIN

alignment_scores:
 Quality: 44.00 Length: 10
 Ratio: 4.889 Gaps: 0
 Percent Similarity: 90.000 Percent Identity: 90.000

alignment_block:

US-08-653-294-25 x AI696864 ..

Align seg 1/1 to: AI696864 from: 1 to: 748

1 ArgGlusnLeuArgThralaLeuArgTyr 10
 |||||
 137 CGAGAGACCTCGGATCGGCTCCGCTAC 166

seq_name: gb_est27:AI466429

seq_documentation_block:

LOCUS AI466429 366 bp mRNA EST 09-MAR-1999

DEFINITION vx35b04.y1 Stratagene mouse lung 937302 Mus musculus cDNA clone
 IMAGE:1277167 5' similar to gb:L11570 H1A CLASS I
 HISTOCOMPATIBILITY ANTIGEN, BW-72(BW-70) B*1503 (HUMAN); gb:M69073
 Mus musculus mRNA, complete cds (MOUSE);, mRNA sequence.

ACCESSION AI466429

VERSION AI466429.1 GI:4315048

KEYWORDS EST.

SOURCE house mouse.

ORGANISM

Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE

1 (bases 1 to 366)

AUTHORS Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T.,
 Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,F.,
 Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R.,
 Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R.,
 Waterston,R. and Willson,R.
 The WashU-NCI Mouse EST Project 1999

TITLE The WashU-NCI Mouse EST Project 1999

JOURNAL Unpublished (1999)

COMMENT On Feb 17, 1998 this sequence version replaced gi:2889763.

Contact: Marra M/WashU-NCI Mouse EST Project 1999

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA

Tel: 314 286 1800

Fax: 314 286 1810

Email: mouseest@watson.wustl.edu

This clone is available royalty-free through LLNL; contact the
 IMAGE Consortium (info@image.llnl.gov) for further information.
 MGI:668967

This read is a RESEQUENCE of a previously sequenced mouse clone
 correct orientation)

Seq primer: -40RP from Gibco

High quality sequence stop: 243.

FEATURES

Location/Qualifiers

1..366
 /organism="Mus musculus"
 /strain="C57BL/6 x CBA"
 /db_xref="taxon:10090"
 /clone="IMAGE:1277167"
 /clone_lib="Stratagene mouse lung 937302"
 /sex="female"
 /tissue_type="lung"
 /dev_stage="6-8 month old"
 /lab_host="SOLR (kanamycin resistant)"
 /note="Organ: lung; Vector: pBluescript SK-; Site:1;
 EcoRI; Site:2: XhoI; Cloned unidirectionally. Primer:
 Oligo dT. 6-8 month old female lung and 1.5 year old male
 lung were source of mRNA. Average insert size: 1.5 kb.
 Uni-ZAP XR Vector; -5' adaptor sequence: 5' GAATTCGACGAG
 3' -3' adaptor sequence: 5' CTCGAGTTTTTTTTTTTTTTT 3'.

BASE COUNT 65 a 115 c 124 g 62 t

ORIGIN

alignment_scores:
 Quality: 43.00 Length: 10
 Ratio: 4.778 Gaps: 0
 Percent Similarity: 90.000 Percent Identity: 90.000

alignment_block:

US-08-653-294-25 x AI466429 ..

Align seg 1/1 to: AI466429 from: 1 to: 366

100

SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 448)
AUTHORS Hillier, L., Allen, M., Bowles, L., Dubucque, T., Geisels, G., Jost, S.,
Krizman, D., Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M.,
Martin, J., Moore, B., Schellenberg, K., Steptoe, M., Tan, F.,
Therasing, B., Whittier, J., Wyllie, J., Waterston, R. and Wilson, R.
TITLE WashU-NCI human EST Project
JOURNAL Unpublished (1997)
COMMENT On Sep 19, 1997 this sequence version replaced qi:1520503.

```

Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu

This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -40ml3 fwd. Et from Amersham
High quality sequence stop: 443.

Location/Qualifiers
1. .448
/organism="Homo sapiens"
/db_xref="GDB:1304052"
/db_xref="taxon:9606"
/clone="IMAGE:412358"
/clone_lib="Soares-pineal_gland_N3HPG"
/lab_host="PH10B (ampicillin resistant)"
/note="Organ: pineal gland; Vector: pT73D (Pharmacia)
with a modified polylinker; Site_1: Not I; Site_2: Eco RI;
1st strand cDNA was primed with a Not I - oligo(dT) primer
[5'- TGTTACCAATCTGAAGTGGAGCGCGCCGTTTTTTTTTTTTTTT
3'], double-stranded cDNA was size selected, ligated to
Eco RI adapters (Pharmacia), digested with Not I and
cloned into the Not I and Eco RI sites of a modified pT73
vector (Pharmacia). Library constructed by Bento Soares
and M.Fatima Bonaldo."

BASE COUNT      92 a      89 c      87 g      180 t
ORIGIN

alignment_scores:
Quality:      39.00
Ratio:        3.900
Percent Similarity: 100.00 Percent Identity: 70.00

```

RATIO: 3.900 Gaps: 0
 Percent Similarity: 100.000 Percent Identity: 70.000

Align seg 1/1 to reverse of: AA722000 from: 1 to: 448

303 AGAGAAAGCCTGAGAACCCAGCCTAAATAT 274

seq_name: gb_est9:AA064631

seq_documentation_block:					
LOCUS	AA064631	452 bp	mRNA	EST	02-FEB-1997
DEFINITION	zif72c03: s1 pineal_gland_N3HPG Homo sapiens cDNA clone IMAGE:382468 3', mRNA sequence.				

ACCESSION AA064631
VERSION AA064631.1 GI:1558875

ESL.	human.	Homo sapiens	Chordata; Craniata; Vertebrata; Mammalia;
KEYWORDS	ORGANISM	Eukaryota; Metazoa;	
		Eutheria; Primates;	
		Catarrhini; Hominoidea; Homo.	
	REFERENCE	1 (bases 1 to 452)	
	AUTHORS	Hillier, L., Lennon, G., Becker, M., Bonaldo, M.F., Chiapelli, B., Chisnoe, S., Dietrich, N., Dubuque, T., Favello, A., Gish, W.,	

Hawkins, M., Hultman, M., Kucaba, T., Lacy, M., Le, N., Mardis, E., Moore, B., Morris, M., Parsons, J., Prange, C., Rifkin, L., Rohlfing, T., Schellenberg, K., Soares, M. B., Tan, F., Thierry-Mieg, J., Trevaskis, E., Underwood, K., Wohlmann, P., Waterston, R., Wilson, R., and Marra, M.

Generation and analysis of 280,000 human expressed sequence tags

Genome Res. 6 (9), 807-828 (1996)

97044478

On Nov 29, 1993 this sequence version replaced gi:429994.

Contact: Wilson RK

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800

Fax: 314 286 1810

Email: estewartson.wustl.edu

This clone is available royalty-free through LNL; contact the

IMAGE Consortium (info@image.llnl.gov) for further information.

Insert Length: 633 Std Error: 0.00

Seq primer: -40M13 fwd. from Amersham

High quality sequence stop: 290.

FEATURES

Location/Qualifiers

1..452

/organism="Homo sapiens"

/db_xref="GDB:1290725"

/db_xref="taxon:9606"

/clone="IMAGE:382468"

/clone_lib="Soares_pineal_gland_N3HPG"

/lab_host="DH10B (ampicillin resistant)"

/note="Organ: pineal gland; Vector: pT73D (Pharmacia)

with a modified polylinker; Site_1: Not I; Site_2: Eco RI;

1st strand cDNA was primed with a Not I - oligo(dT) primer

[5' TGTTACCAATCTGAAGTGGAGCGCGCGTTTTTTTTTTTTTTT

3'], double-stranded cDNA was size selected, ligated to

Eco RI adapters (Pharmacia), digested with Not I and

cloned into the Not I and Eco RI sites of a modified pT73

vector (Pharmacia). Library constructed by Bento Soares

and M. Fatima Bonaldo."

BASE COUNT 98 a 88 c 91 g 174 t 1 others

ORIGIN

alignment_scores:

Quality: 39.00 Length: 10

Ratio: 3.900 Gaps: 0

Percent Similarity: 100.000 Percent Identity: 70.000

alignment_block:

US-08-653-294-25 x AA064631/rev ..

Align seg 1/1 to reverse of: AA064631 from: 1 to: 452

1 ArgGluAsnLeuArgThrAlaLeuArgTyr 10

|||||:|||||:|||||:|||||:|||||

303 AGAGAAAGCCTGAGAACCCAGCCTAAATAT 274

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: February 8, 2000, 04:05:43 ; Search time 133.56 Seconds
(without alignments)
3.547 Million cell updates/sec

Title: US-08-653-294-26

Perfect score: 98

Sequence: 1 YRLAIRLNRERENLRALRY 20

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 188963 segs, 23686106 residues

Total number of hits satisfying chosen parameters: 188963

Minimum DB seq length: 0

Maximum DB seq length: 1000000

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database : A_Geneseq_36.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	98	100.0	20	1 R92907	HLA-B2702 CTL modu
2	98	100.0	20	1 R95428	HLA-B2702 84-75-84
3	98	100.0	20	1 R33778	Immunomodulating d
4	93	94.9	20	1 R92909	HLA-B2702 CTL modu
5	93	94.9	20	1 R92908	HLA-B2702 CTL modu
6	93	94.9	20	1 W33791	Peptide B2702.84-7
7	93	94.9	20	1 W33792	Peptide B2702.84-7
8	88	89.8	20	1 R92910	HLA-B2702 CTL modu
9	88	89.8	20	1 W33793	Peptide B2702.84-7
10	85	86.7	20	1 R95430	HLA-B2702 84-75T/7
11	54.5	55.6	20	1 R92911	HLA-B2702 CTL modu
12	54.5	55.6	20	1 W33779	Immunomodulating d
13	49	50.0	10	1 R41208	Peptide fragment o
14	49	50.0	10	1 R33062	HLA-B2702 CTL modu
15	49	50.0	10	1 R95413	Alpha1-helix of HL
16	49	50.0	10	1 W07512	T-cell modulating
17	49	50.0	10	1 W47265	Immunomodulatory p
18	49	50.0	10	1 W47266	Immunomodulatory p
19	49	50.0	10	1 W33784	Peptide B2702.75-8
20	49	50.0	15	1 R92912	HLA-B2702 CTL modu
21	49	50.0	15	1 W33795	Peptide B2702.70-8
22	49	50.0	25	1 R41205	Peptide fragment o
23	49	50.0	25	1 R48286	Peptide fragment o
24	49	50.0	25	1 R83090	HLA-B2702 CTL modu
25	49	50.0	25	1 R83093	HLA-B2702 CTL modu
26	49	50.0	25	1 R95416	HLA-B2702.60-84. C
27	49	50.0	25	1 R95422	HLA-B2702.60-84. C
28	49	50.0	25	1 W33794	Peptide B2702.60-8
29	49	50.0	184	1 Y06801	Peptide Seq ID No:
30	49	50.0	362	1 R03142	Sequence of HLA-Bw
31	49	50.0	362	1 R03144	Sequence of HLA-B5
32	49	50.0	362	1 R12463	HLA-Bw53 exon. HLA
33	46	46.9	326	1 W79969	Methanococcus jann
34	44	44.9	10	1 R83094	HLA-B2702 CTL modu

HLA-B2702 CTL modu
HLA-B2702 CTL modu
HLA-B2702.75-84(D)
HLA-B2702.75-84(T)
T-cell modulating
Immunomodulatory p
Immunomodulatory p
Immunomodulatory p
Immunomodulatory p
Peptide B2702.75-8
Peptide B2702.75-8

35 44 44.9 10 1 R83095
36 44 44.9 10 1 R83096
37 44 44.9 10 1 R95425
38 44 44.9 10 1 R95426
39 44 44.9 10 1 W07513
40 44 44.9 10 1 W47267
41 44 44.9 10 1 W47268
42 44 44.9 10 1 W47269
43 44 44.9 10 1 W47270
44 44 44.9 10 1 W33788
45 44 44.9 10 1 W33787

ALIGNMENTS

RESULT 1

R92907 ID R92907 standard; peptide; 20 AA.
AC R92907;
DT 16-MAY-1996 (first entry)
DE HLA-B2702 CTL modulating peptide (B2702.84-75/75-84).
KW Cytotoxic T lymphocyte; CTL; major histocompatibility complex; MHC;
KW Immunosuppressant; graft versus host disorder; transplantation; therapy;
KW class I MHC; HLA-B2702.
OS Synthetic.
PN W09526979-A1.
PD 12-OCT-1995.
PF 05-APR-1995; U04349.
PR 05-APR-1994; US-222851.
PA (STRD) UNIV LELAND STANFORD JUNIOR.
PI Clayberger C, Krensky AM, Parham P;
DR WPI; 95-358582/46.
PT Extension of acceptance period of transplants from MHC unmatched
PT donor hosts - using Class I B75-84 MHC antigen of the recipient
PT host
PS Example 15; Page 36; 80pp; English.
CC R83061-R83085, R83090-R83096 and R92907-R92914 represent fragments of
CC class I major histocompatibility complex (MHC) antigens. This sequence
CC is an inverted dimer of residues 75-84 of the alpha-1 domain of the class
CC I MHC HLA-B2702. These sequences can be used to extend the period of
CC acceptance by a recipient of a transplant from an MHC unmatched donor.
CC The peptides are administered to a patient in conjunction with a
CC subtherapeutic amount of an immunosuppressant. This is administered to
CC the patient for a limited period of time (compared to the lifetime
CC administration for current treatments). The peptides particularly
CC modulate (or inhibit) the activity of the cytotoxic T lymphocytes (CTLs)
CC of the patient.
SQ Sequence 20 AA;

Query Match 100.0%; Score 98; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 3.9e-10;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YRLAIRLNRERENLRALRY 20

DB 1 YRLAIRLNRERENLRALRY 20

RESULT 2

R95428 ID R95428 standard; peptide; 20 AA.
AC R95428;
DT 12-NOV-1996 (first entry)
DE HLA-B2702 84-75-84 palindrome.
KW HLA; p74; alpha1-helix; human-leucocyte-associated antigen; inhibitor;
KW T-cell lysate; membrane protein; mammal; heat shock protein; Hsc70; APC;
KW B cell; calcium influx; cytotoxic T lymphocyte; CTL; differentiation;
KW cytolysis; antigen presenting cell.
OS Synthetic.
PN W09513288-A1.
PD 18-MAY-1995.

PF 10-NOV-1994; U12985.
 PR 10-NOV-1993; US-150493.
 PA (STRD) UNIV LELAND STANFORD JUNIOR.
 PI Clayberger C. Krensky AM;
 DR WPI: 95-194027/25.
 PT Compsns. comprising lymphoid surface membrane proteins - which may
 PT inhibit cytolytic activity and differentiation of CTLs.
 PS Example; Page 12; 29pp; English.
 CC R95413, and R95415-R95431 represent palindromes and fragments of
 CC human-leucocyte-associated antigens. This sequence represents the
 CC the protein p74 from a T-cell lysate. p74 is a T-cell surface membrane
 CC protein associated with T-cell activation in mammalian T-cells, and is
 CC also immunologically cross reactive with the heat shock protein Hsc70.
 CC p74 is found in a limited number of cell types, but is particularly
 CC expressed on B and T cells. p74 can be isolated by lysis of a suitable
 CC cell with an amphoteric detergent, and then passed through an affinity
 CC column containing a covalently bound HLA-B2702 palindromic peptide.
 CC Compositions comprising the extracellular fragment of p74 combined with
 CC HLA-B2702-60-84 (see R95416), induces calcium influx, and inhibits
 CC cytotoxic T lymphocyte (CTL) differentiation or cytotoxicity. Candidate
 CC compounds can be screened for their effect on the cytolytic activity of
 CC T-cells, by combining them with the extracellular portion of p74 and
 CC determining the amount of binding between the candidate compound and p74.
 CC Modulation of CTL activity can be inhibited in a cellular composition
 CC containing T-cells and antigen presenting cells (APCs), by adding to the
 CC mix the extracellular portion of p74, in an amount sufficient to compete
 CC with p74 for the binding of the p74 ligand.
 CC Sequence 20 AA;
 SQ

Query Match 100.0%; Score 98; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 3.9e-10;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YRLAIRLNERENRIALRY 20
 Db 1 YRLAIRLNERENRIALRY 20
 |||||

RESULT 3
 W33778 19-JUN-1998 (first entry)
 ID W33778 standard; peptide; 20 AA.
 AC W33778;
 DE Immunomodulating dimer peptide #1.
 DE Immunomodulating dimer; immunosuppressant drug; CTL activation;
 KW transplantation; autoimmune disease; Class I HLA-B alpha-1 domain;
 KW rejection.
 OS Synthetic.
 OS Homo sapiens.
 PN W09744351-A1.
 PD 27-NOV-1997.
 PF 22-MAY-1997; U08689.
 PR 24-MAY-1996; US-653294.
 PA (STRD) UNIV LELAND STANFORD JUNIOR.
 PI Beulow R, Clayberger C, Krensky AM;
 DR WPI: 98-086530/08.
 PT New immunomodulating dimer peptide(s) - based on a Class I HLA-B
 PT alpha-1 domain, used for preventing rejection of transplants or
 PT treating autoimmune diseases
 PS Claim 16; Page 35; 41pp; English.
 CC This sequence represents a specifically claimed immunomodulating
 CC dimer peptide of the invention. A peptide-type compound or variant is
 CC amino acids, where the peptide-type compound comprises the formula: A-B,
 CC where A, B = (R aa76-77L) (aa79-84) or (aa84-79) (Laa77-76R); aa76 = E or
 CC V; aa77 = D, S or R; aa79 = R or G; aa80 = I or N; aa81, aa84 = a
 CC hydrophobic or small amino acid; aa82 = R or L; aa83 = G or R; and aa
 CC represents amino acid. The sequence in the brackets may optionally be
 CC absent or truncated at any peptide type bond within the brackets. The
 CC compounds comprise amino acid sequences related to a Class I HLA-B

CC alphas domain (positions 79-84). They can be used to inhibit cytotoxic
 CC T-lymphocytes (CTL) from undesirably attacking cells in a host or in
 CC vitro. They can also be used in combination with antigenic peptides or
 CC proteins of interest to activate CTLs. They can also inhibit the
 CC proliferation of T cells in response to anti-CD3. The peptide can be
 CC used for preventing rejection of transplants or for treating autoimmune
 CC diseases, e.g. diabetes, rheumatoid arthritis and lupus erythematosus.
 CC The products can also be used for detection and diagnosis.
 CC Sequence 20 AA;
 SQ

Query Match 100.0%; Score 98; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 3.9e-10;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YRLAIRLNERENRIALRY 20
 Db 1 YRLAIRLNERENRIALRY 20
 |||||

RESULT 4
 R92909 standard; peptide; 20 AA.
 ID R92909;
 AC R92909;
 DE 16-MAY-1996 (first entry)
 DE HLA-B2702 CTL modulating peptide (B2702.84-75/75-84(T)).
 DE Cytotoxic T lymphocyte; CTL; major histocompatibility complex; MHC;
 KW immunosuppressant; graft versus host disorder; transplantation; therapy;
 KW class I MHC; HLA-B2702.
 OS Synthetic.
 PN W09526979-A1.
 PD 12-OCT-1995.
 PF 05-APR-1995; U04349.
 PR 05-APR-1994; US-222851.
 PA (STRD) UNIV LELAND STANFORD JUNIOR.
 PI Clayberger C, Krensky AM, Farham P;
 DR WPI: 95-358582/46.
 PT Extension of acceptance period of transplants from MHC unmatched
 PT donor hosts - using Class I B75-84 MHC antigen of the recipient
 PT host
 PS Example 15; Page 36; 80pp; English.
 CC R83061-R83085, R83090-R83096 and R92907-R92913 represent fragments of
 CC class I major histocompatibility complex (MHC) antigens. This sequence
 CC is an inverted dimer of residues 75-84 of the alpha-1 domain of the class
 CC I MHC HLA-B2702. These sequences can be used to extend the period of
 CC acceptance by a recipient of a transplant from an MHC unmatched donor.
 CC The peptides are administered to a patient in conjunction with a
 CC subtherapeutic amount of an immunosuppressant. This is administered to
 CC the patient for a limited period of time (compared to the lifetime
 CC administration for current treatments). The peptides particularly
 CC modulate (or inhibit) the activity of the cytotoxic T lymphocytes (CTLs)
 CC of the patient.
 CC Sequence 20 AA;
 SQ

Query Match 94.9%; Score 93; DB 1; Length 20;
 Best Local Similarity 95.0%; Pred. No. 2.6e-09;
 Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 YRLAIRLNERENRIALRY 20
 Db 1 YRLAIRLNERENRIALRY 20
 |||||

RESULT 5
 R92908 standard; peptide; 20 AA.
 ID R92908;
 AC R92908;
 DE 16-MAY-1996 (first entry)
 DE HLA-B2702 CTL modulating peptide (B2702.84-75(T)/75-84).
 DE Cytotoxic T lymphocyte; CTL; major histocompatibility complex; MHC;
 KW immunosuppressant; graft versus host disorder; transplantation; therapy;
 KW class I MHC; HLA-B2702.

OS Synthetic.
 PN W09526979-A1.
 PD 12-OCT-1995.
 PF 05-APR-1995; U04349.
 PR 05-APR-1994; US-222851.
 PA (STRD) UNIV LELAND STANFORD JUNIOR.
 PI Clayberger C, Krensky AM, Parham P;
 DR WPI; 95-358582/46.
 PT Extension of acceptance period of transplants from MHC unmatched
 PT donor hosts - using Class I B75-84 MHC antigen of the recipient
 PT host
 PS Example 15; Page 36; 80pp; English.
 CC R83061-R83085, R83090-R83096 and R92907-R92914 represent fragments of
 CC class I major histocompatibility complex (MHC) antigens. This sequence
 CC is an inverted dimer of residues 75-84 of the alpha-1 domain of the class
 CC I MHC HLA-B*2702. These sequences can be used to extend the period of
 CC acceptance by a recipient of a transplant from an MHC unmatched donor.
 CC The peptides are administered to a patient in conjunction with a
 CC subtherapeutic amount of an immunosuppressant. This is administered to
 CC the patient for a limited period of time (compared to the lifetime
 CC administration for current treatments). The peptides particularly
 CC modulate (or inhibit) the activity of the cytotoxic T lymphocytes (CTLs)
 CC of the patient.
 SQ Sequence 20 AA;

Query Match 94.9%; Score 93; DB 1; Length 20;
 Best Local Similarity 95.0%; Pred. No. 2.6e-09;
 Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YRLAIRLNRRERENLRALRY 20
 DB 1 YRLAIRLNRRERENLRALRY 20

RESULT 6

ID W33791 standard; peptide; 20 AA.
 AC W33791;
 DT 19-JUN-1998 (first entry)
 DE Peptide B2702.84-75/75-84 tested for immunomodulating activity.
 KW Immunomodulating dimer; immunosuppressant drug; CTL activation;
 KW transplantation; autoimmune disease; Class I HLA-B alpha-1 domain;
 KW rejection.
 OS Synthetic.
 OS Homo sapiens.
 PN W09744351-A1.
 PD 27-NOV-1997.
 PF 22-MAY-1997; U08689.
 PR 24-MAY-1996; US-653294.
 PA (STRD) UNIV LELAND STANFORD JUNIOR.
 PI Beulow R, Clayberger C, Krensky AM;
 DR WPI; 98-086530/08.
 PT New immunomodulating dimer peptide(s) - based on a Class I HLA-B
 PT alpha-1 domain, used for preventing rejection of transplants or
 PT treating autoimmune diseases
 PS Example 1; Page 19; 41pp; English.
 CC Peptides W33784-98 and W33778-9 were assayed for their immunomodulating
 CC activity. A peptide-type compound or variant is claimed which has
 CC c-terminal amidated or esterified forms of up to 60 amino acids, where
 CC the peptide-type compound comprises the formula: A-B, where A, B =
 CC (R aa76-77L) (aa79-84) or (aa84-79) (Laa77-76R); aa76 = E or V; aa77 =
 CC D, S or N; aa79 = R or G; aa80 = I or N; aa81, aa84= a hydrophobic or
 CC small amino acid; aa82 = R or L; aa83 = G or R; and aa represents amino
 CC acid. The sequence in the brackets may optionally be absent or truncated
 CC at any peptide type bond within the brackets. The compounds comprise
 CC amino acid sequences related to a Class I HLA-B alpha1 domain (positions
 CC 79-84). They can be used to inhibit cytotoxic T-lymphocytes (CTL) from
 CC undesirably attacking cells in a host or in vitro. They can also be
 CC used in combination with antigenic peptides or proteins of interest to
 CC activate CTLs. They can also inhibit the proliferation of T cells in
 CC response to anti-CD3. The peptide can be used for preventing rejection

CC of transplants or for treating autoimmune diseases, e.g. diabetes,
 CC rheumatoid arthritis and lupus erythematosus. The products can also be
 CC used for detection and diagnosis.
 SQ Sequence 20 AA;

Query Match 94.9%; Score 93; DB 1; Length 20;
 Best Local Similarity 95.0%; Pred. No. 2.6e-09;
 Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YRLAIRLNRRERENLRALRY 20
 DB 1 YRLAIRLNRRERENLRALRY 20

RESULT 7

ID W33792 standard; peptide; 20 AA.
 AC W33792;
 DT 19-JUN-1998 (first entry)
 DE Peptide B2702.84-75/75-84 tested for immunomodulating activity.
 KW Immunomodulating dimer; immunosuppressant drug; CTL activation;
 KW transplantation; autoimmune disease; Class I HLA-B alpha-1 domain;
 KW rejection.
 OS Synthetic.
 OS Homo sapiens.
 PN W09744351-A1.
 PD 27-NOV-1997.
 PF 22-MAY-1997; U08689.
 PR 24-MAY-1996; US-653294.
 PA (STRD) UNIV LELAND STANFORD JUNIOR.
 PI Beulow R, Clayberger C, Krensky AM;
 DR WPI; 98-086530/08.
 PT New immunomodulating dimer peptide(s) - based on a Class I HLA-B
 PT alpha-1 domain, used for preventing rejection of transplants or
 PT treating autoimmune diseases
 PS Example 1; Page 19; 41pp; English.
 CC Peptides W33784-98 and W33778-9 were assayed for their immunomodulating
 CC activity. A peptide-type compound or variant is claimed which has
 CC immunomodulating activity, including the N-terminal acylated and/or
 CC c-terminal amidated or esterified forms of up to 60 amino acids, where
 CC the peptide-type compound comprises the formula: A-B, where A, B =
 CC (R aa76-77L) (aa79-84) or (aa84-79) (Laa77-76R); aa76 = E or V; aa77 =
 CC D, S or N; aa79 = R or G; aa80 = I or N; aa81, aa84= a hydrophobic or
 CC small amino acid; aa82 = R or L; aa83 = G or R; and aa represents amino
 CC acid. The sequence in the brackets may optionally be absent or truncated
 CC at any peptide type bond within the brackets. The compounds comprise
 CC amino acid sequences related to a Class I HLA-B alpha1 domain (positions
 CC 79-84). They can be used to inhibit cytotoxic T-lymphocytes (CTL) from
 CC undesirably attacking cells in a host or in vitro. They can also be
 CC used in combination with antigenic peptides or proteins of interest to
 CC activate CTLs. They can also inhibit the proliferation of T cells in
 CC response to anti-CD3. The peptide can be used for preventing rejection
 CC of transplants or for treating autoimmune diseases, e.g. diabetes,
 CC rheumatoid arthritis and lupus erythematosus. The products can also be
 CC used for detection and diagnosis.
 SQ Sequence 20 AA;

Query Match 94.9%; Score 93; DB 1; Length 20;
 Best Local Similarity 95.0%; Pred. No. 2.6e-09;
 Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YRLAIRLNRRERENLRALRY 20
 DB 1 YRLAIRLNRRERENLRALRY 20

RESULT 8

ID R92910 standard; peptide; 20 AA.
 AC R92910;
 DT 16-MAY-1996 (first entry)

HLA-B2702 CTL modulating peptide (B2702.84-75(T)/75-84(T)).
Cytotoxic T lymphocyte; CTL; major histocompatibility complex; MHC;
Immunosuppressant; graft versus host disorder; transplantation; therapy;
Class I MHC; HLA-B2702.
Synthetic.
PN WO9526979-A1.
PD 12-OCT-1995.
PF 05-APR-1995; U04349.
PR 05-APR-1994; US-222851.
PA (STRD) UNIV LELAND STANFORD JUNIOR.
PI Clayberger C, Krensky AM, Parham P;
DR WPI; 95-358582/46.
PT Extension of acceptance period of transplants from MHC unmatched
PT donor hosts - using Class I B75-84 MHC antigen of the recipient
PT host
PS Example 15; Page 36; 80pp; English.
CC R33081-R33085, R83090-R83096 and R92907-R92913 represent fragments of
CC Class I major histocompatibility complex (MHC) antigens. This sequence
CC is an inverted dimer of residues 75-84 of the alpha-1 domain of the class
CC I MHC HLA-B2702. These sequences can be used to extend the period of
CC acceptance by a recipient of a transplant from an MHC unmatched donor.
CC The peptides are administered to a patient in conjunction with a
CC subtherapeutic amount of an immunosuppressant. This is administered to
CC the patient for a limited period of time (compared to the lifetime
CC administration for current treatments). The peptides particularly
CC modulate (or inhibit) the activity of the cytotoxic T lymphocytes (CTLs)
CC of the patient.
CC Sequence 20 AA;

Query Match 89.8%; Score 88; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 1.7e-08;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 YRLAIRLNERRENRLRY 20
DB 1 YRLATRLNERRENRLRY 20

RESULT 9
W33793
ID W33793 standard; peptide; 20 AA.
AC W33793;
DE 19-JUN-1998 (first entry)
DT Peptide B2702.84-75(T)/75-84(T) tested for immunomodulating activity.
KW Immunomodulating dimer; immunosuppressant drug; CTL activation;
KW transplantation; autoimmune disease; Class I HLA-B alpha-1 domain;
KW rejection.
OS Synthetic.
OS Homo sapiens.
PN WO9744351-A1.
PD 27-NOV-1997.
PF 22-MAY-1997; U08689.
PR 24-MAY-1996; US-653294.
PA (STRD) UNIV LELAND STANFORD JUNIOR.
PI Beulow R, Clayberger C, Krensky AM;
DR WPI; 98-086530/08.
PT New immunomodulating dimer peptide(s) - based on a Class I HLA-B
PT alpha-1 domain, used for preventing rejection of transplants or
PT treating autoimmune diseases
PS Example 1; Page 19; 41pp; English.
CC Peptides W33784-98 and W33778-9 were assayed for their immunomodulating
CC activity. A peptide-type compound or variant is claimed which has
CC immunomodulating activity, including the N-terminal acylated and/or
CC C-terminal amidated or esterified forms of up to 60 amino acids, where
CC the peptide-type compound comprises the formula: A-B, where A, B =
CC (R aa76-77L) (aa79-84) or (aa84-79) (Laa77-76R); aa76 = E or V; aa77 =
CC D, S or N; aa79 = R or G; aa80 = I or N; aa81, aa84 = a hydrophobic or
CC small amino acid; aa82 = R or L; aa83 = G or R; and aa represents amino
CC acid. The sequence in the brackets may optionally be absent or truncated
CC at any peptide type bond within the brackets. The compounds comprise
CC amino acid sequences related to a Class I HLA-B alpha-1 domain (positions
CC 79-84). They can be used to inhibit cytotoxic T-lymphocytes (CTL) from

undesirably attacking cells in a host or in vitro. They can also be
used in combination with antigenic peptides or proteins of interest to
activate CTLs. They can also inhibit the proliferation of T cells in
response to anti-CD3. The peptide can be used for preventing rejection
of transplants or for treating autoimmune diseases, e.g. diabetes, be
rheumatoid arthritis and lupus erythematosus. The products can also be
used for detection and diagnosis.

Sequence 20 AA;

Query Match 89.8%; Score 88; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 1.7e-08;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 YRLAIRLNERRENRLRY 20
DB 1 YRLATRLNERRENRLRY 20

RESULT 10

R95430
ID R95430 standard; peptide; 20 AA.
AC R95430;
DT 12-NOV-1996 (first entry)
DE HLA-B2702.84-75(T)/75-84(T) palindromic.
KW HLA; p74; alpha1-helix; human-leucocyte-associated antigen; inhibitor;
KW T-cell lysate; membrane protein; mammal; heat shock protein; Hsc70; APC;
KW B cell; calcium influx; cytotoxic T lymphocyte; CTL; differentiation;
KW cytolysis; antigen presenting cell.
OS Synthetic.
OS WO9513288-A1.
PD 18-MAY-1995.
PF 10-NOV-1994; U12985.
PR 10-NOV-1993; US-150493.
PA (STRD) UNIV LELAND STANFORD JUNIOR.
PI Clayberger C, Krensky AM;
DR WPI; 95-194027/25.
PT Compens. comprising lymphoid surface membrane proteins - which may
PT inhibit cytolytic activity and differentiation of CTLs.
PS Example; Page 12; 29pp; English.
CC R95413, and R95415-R95431 represent palindromes and fragments of
CC human-leucocyte-associated antigens. This sequence represents the
CC HLA-B2702.84-75(T)/75-84(T) palindromic. These sequences can be used to
CC isolate the protein p74 from a T-cell lysate. p74 is a T-cell surface
CC membrane protein associated with T-cell activation in mammalian T-cells,
CC and is also immunologically cross reactive with the heat shock protein
CC Hsc70. p74 is found in a limited number of cell types, but is
CC particularly expressed on B and T cells. p74 can be isolated by lysis of
CC a suitable cell with an amphoteric detergent, and then passed through an
CC affinity column containing a covalently bound HLA-B2702 palindromic
CC peptide. Compositions comprising the extracellular fragment of p74
CC combined with HLA-B2702.60-84 (see R95416), induces calcium influx, and
CC inhibits cytotoxic T lymphocyte (CTL) differentiation or cytolysis.
CC Candidate compounds can be screened for their effect on the cytolytic
CC activity of T-cells, by combining them with the extracellular portion of
CC p74 and determining the amount of binding between the candidate compound
CC and p74. Modulation of CTL activity can be inhibited in a cellular
CC composition containing T-cells and antigen presenting cells (APCs), by
CC adding to the mix the extracellular portion of p74, in an amount
CC sufficient to compete with p74 for the binding of the p74 ligand.
CC Sequence 20 AA;

Query Match 86.7%; Score 85; DB 1; Length 20;
Best Local Similarity 94.7%; Pred. No. 5.4e-08;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YRLAIRLNERRENRLRY 19
DB 1 YRLAIRLNERRENRLRY 19

RESULT 11

R92911
 ID R92911 standard; peptide; 20 AA.
 AC R92911;
 DT 16-MAY-1996 (first entry)
 DE HLA-B*2702 CTL modulating peptide (B2702.84-75/84-75).
 KW Cytotoxic T lymphocyte; CTL; major histocompatibility complex; MHC;
 KW immunosuppressant; graft versus host disorder; transplantation; therapy;
 KW class I MHC; HLA-B*2702.
 OS Synthetic.
 PN WO9526979-A1.
 PD 12-OCT-1995.
 PF 05-APR-1995; U04349.
 PR 05-APR-1994; US-222851.
 PA (STRD) UNIV LELAND STANFORD JUNIOR.
 PI Clayberger C, Krensky AM, Parham P;
 DR WPI: 95-358582/46.
 PT Extension of acceptance period of transplants from MHC unmatched
 PT donor hosts - using Class I B*75-84 MHC antigen of the recipient
 PT host
 PS Example 15; Page 36; 80pp; English.
 CC R83061-R83085, R83090-R83096 and R92907-R92914 represent fragments of
 CC class I major histocompatibility complex (MHC) antigens. This sequence
 CC is a dimer of residues 75-84 of the alpha-1 domain of the class I MHC
 CC HLA-B*2702. These sequences can be used to extend the period of
 CC acceptance by a recipient of a transplant from an MHC unmatched donor.
 CC The peptides are administered to a patient in conjunction with a
 CC subtherapeutic amount of an immunosuppressant. This is administered to
 CC the patient for a limited period of time (compared to the lifetime
 CC administration for current treatments). The peptides particularly
 CC modulate (or inhibit) the activity of the cytotoxic T lymphocytes (CTLs)
 CC of the patient.
 CC Sequence 20 AA;
 SQ

Query Match 55.6%; Score 54.5; DB 1; Length 20;
 Best Local Similarity 68.4%; Pred. No. 0.0058;
 Matches 13; Conservative 2; Mismatches 1; Indels 3; Gaps 1;
 QY 1 YRLAIRLNERRLRLRL 19
 Db 1 YRLAIRLNER--YRLAIR 16
 |||||
 RESULT 13
 ID R41208 standard; peptide; 10 AA.
 AC R41208;
 DT 15-MAR-1994 (first entry)
 DE Peptide fragment of Class I HLA peptide.
 KW Human leukocyte antigen; HLA; peptide; transplantation; neoplasia;
 KW parasitic disease; cytotoxic T lymphocyte; modulation.
 OS Synthetic.
 PN WO9317699-A.
 PD 16-SEP-1993.
 PF 25-FEB-1993; U01758.
 PR 02-MAR-1992; US-844716.
 PA (STRD) UNIV LELAND STANFORD JUNIOR.
 PI Clayberger CA, Krensky AM;
 DR WPI: 93-303134/38.
 PT New peptide(s) based on Class I HLA antigen domains - used for
 PT modulating cytotoxic T-lymphocyte activity towards targets
 PS Claim 11; Page 54; 61pp; English.
 CC The peptide is used to modulate cytotoxic T-lymphocyte (CTL)
 CC activity, either by inhibition or stimulation. It can be used
 CC for inhibiting CTL toxicity in transplantations, for inducing CTL
 CC activity in parasitic diseases and neoplasia and in studies on viral
 CC infection. The peptide can also be used for identifying CTLs which
 CC bind to it and removing subsets of CTLs from a T-cell composition.
 CC This peptide sequence is more commonly found within larger peptide
 CC compounds of not more than 30 amino acids in length.
 CC Sequence 10 AA;
 SQ

Query Match 50.0%; Score 49; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.022;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 11 RNLRLRLRY 20
 Db 1 RNLRLRLRY 10
 |||||
 RESULT 14
 ID R83062 standard; peptide; 10 AA.
 AC R83062;
 DT 16-MAY-1996 (first entry)
 DE HLA-B*2702 CTL modulating peptide (B2702.75-84).
 KW Cytotoxic T lymphocyte; CTL; major histocompatibility complex; MHC;
 KW immunosuppressant; graft versus host disorder; transplantation; therapy;
 KW class I MHC; HLA-B*2702.
 OS Synthetic.
 PN WO9526979-A1.

R92911
 ID R92911 standard; peptide; 20 AA.
 AC R92911;
 DT 16-MAY-1996 (first entry)
 DE HLA-B*2702 CTL modulating peptide (B2702.84-75/84-75).
 KW Cytotoxic T lymphocyte; CTL; major histocompatibility complex; MHC;
 KW immunosuppressant; graft versus host disorder; transplantation; therapy;
 KW class I MHC; HLA-B*2702.
 OS Synthetic.
 PN WO9526979-A1.
 PD 12-OCT-1995.
 PF 05-APR-1995; U04349.
 PR 05-APR-1994; US-222851.
 PA (STRD) UNIV LELAND STANFORD JUNIOR.
 PI Clayberger C, Krensky AM, Parham P;
 DR WPI: 95-358582/46.
 PT Extension of acceptance period of transplants from MHC unmatched
 PT donor hosts - using Class I B*75-84 MHC antigen of the recipient
 PT host
 PS Example 15; Page 36; 80pp; English.
 CC R83061-R83085, R83090-R83096 and R92907-R92914 represent fragments of
 CC class I major histocompatibility complex (MHC) antigens. This sequence
 CC is a dimer of residues 75-84 of the alpha-1 domain of the class I MHC
 CC HLA-B*2702. These sequences can be used to extend the period of
 CC acceptance by a recipient of a transplant from an MHC unmatched donor.
 CC The peptides are administered to a patient in conjunction with a
 CC subtherapeutic amount of an immunosuppressant. This is administered to
 CC the patient for a limited period of time (compared to the lifetime
 CC administration for current treatments). The peptides particularly
 CC modulate (or inhibit) the activity of the cytotoxic T lymphocytes (CTLs)
 CC of the patient.
 CC Sequence 20 AA;
 SQ

Query Match 55.6%; Score 54.5; DB 1; Length 20;
 Best Local Similarity 68.4%; Pred. No. 0.0058;
 Matches 13; Conservative 2; Mismatches 1; Indels 3; Gaps 1;
 QY 1 YRLAIRLNERRLRLRL 19
 Db 1 YRLAIRLNER--YRLAIR 16
 |||||
 RESULT 12
 ID W33779 standard; peptide; 20 AA.
 AC W33779;
 DT 19-JUN-1998 (first entry)
 DE Immunomodulating dimer peptide #2.
 KW Immunomodulating dimer; immunosuppressant drug; CTL activation;
 KW transplantation; autoimmune disease; Class I HLA-B alpha-1 domain;
 KW rejection.
 OS Synthetic.
 OS Homo sapiens.
 PN WO9744351-A1.
 PD 27-NOV-1997.
 PF 22-MAY-1997; U08689.
 PR 24-MAY-1996; US-653294.
 PA (STRD) UNIV LELAND STANFORD JUNIOR.
 PI Beulow R, Clayberger C, Krensky AM;
 DR WPI: 98-086530/08.
 PT New immunomodulating dimer peptide(s) - based on a Class I HLA-B
 PT alpha-1 domain, used for preventing rejection of transplants or
 PT treating autoimmune diseases
 PS Claim 16; Page 35; 41pp; English.
 CC This sequence represents a specifically claimed immunomodulating
 CC dimer peptide of the invention. A peptide-type compound or variant is
 CC claimed which has immunomodulating activity, including the N-terminal
 CC acylated and/or C-terminal amidated or esterified forms of up to 60
 CC amino acids, where the peptide-type compound comprises the formula: A-B,
 CC where A, B = (R aa76-77L) (aa79-84) or (aa84-79) (Laa77-76R); aa76 = E or
 CC V; aa77 = D, S or N; aa79 = R or G; aa80 = I or N; aa81, aa84 = a
 CC hydrophobic or small amino acid; aa82 = R or L; aa83 = G or R; and aa

PD 12-OCT-1995.
 PF 05-APR-1995; U04349.
 PR 05-APR-1994; US-222851.
 PA (STRD) UNIV LELAND STANFORD JUNIOR.
 PI Clayberger C, Krensky AM, Farham P;
 DR WPI: 95-358582/46.
 PT Extension of acceptance period of transplants from MHC unmatched
 PT donor hosts - using Class I B75-84 MHC antigen of the recipient
 PT host
 PS Claim 15: Page 9: 80pp: English.
 CC R83061-R83085, R83090-R83096 and R92907-R92913 represent fragments of
 CC class I major histocompatibility complex (MHC) antigens. This sequence
 CC corresponds to residues 75-84 of the alpha-1 domain of the class I MHC
 CC HLA-B*2702. These sequences can be used to extend the period of
 CC acceptance by a recipient of a transplant from an MHC unmatched donor.
 CC The peptides are administered to a patient in conjunction with a
 CC subtherapeutic amount of an immunosuppressant. This is administered to
 CC the patient for a limited period of time (compared to the lifetime
 CC administration for current treatments). The peptides particularly
 CC modulate (or inhibit) the activity of the cytotoxic T lymphocytes (CTLs)
 CC of the patient.
 SQ Sequence 10 AA;

CC with p74 for the binding of the p74 ligand.
 SQ Sequence 10 AA;

Query Match 50.0%; Score 49; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.022;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 RENVRLALRY 20
 Db 1 RENVRLALRY 10
 |||||

Search completed: February 8, 2000, 04:05:43
 Job time: 9360 sec

Query Match 50.0%; Score 49; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.022;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 RENVRLALRY 20
 Db 1 RENVRLALRY 10
 |||||

RESULT 15

R95413
 ID R95413 standard; peptide; 10 AA.
 AC R95413;
 DT 12-NOV-1996 (first entry)
 DE Alpha-helix of HLA-B*2702.
 KW HLA; p74; alpha-helix; human-leucocyte-associated antigen; inhibitor;
 KW T-cell lysate; membrane protein; mammal; heat shock protein; Hsc70; APC;
 KW B cell; calcium influx; cytotoxic T lymphocyte; CTL; differentiation;
 KW cytolysis; antigen presenting cell.
 OS Synthetic.
 PN WO9513288-A1.
 PD 18-MAY-1995.
 PF 10-NOV-1994; U12985.
 PR 10-NOV-1993; US-150493.
 PA (STRD) UNIV LELAND STANFORD JUNIOR.
 PI Clayberger C, Krensky AM;
 DR WPI: 95-194027/25.
 PT Compns. comprising lymphoid surface membrane proteins - which may
 PT inhibit cytolytic activity and differentiation of CTLs.
 PS Example; Page 11; 29pp: English.
 CC This sequence represents the alpha-helix of the
 CC human-leucocyte-associated antigen B2702 (HLA-B*2702). This sequence,
 CC epitopes, and palindromes of it (such as R95428) can be used to isolate
 CC the protein p74 from a T-cell lysate. p74 is a T-cell surface membrane
 CC protein associated with T-cell activation in mammalian T-cells, and is
 CC also immunologically cross reactive with the heat shock protein Hsc70.
 CC p74 is found in a limited number of cell types, but is particularly
 CC expressed on B and T cells. p74 can be isolated by lysis of a suitable
 CC cell with an amphoteric detergent, and then passed through an affinity
 CC column containing a covalently bound HLA-B*2702 palindromic peptide.
 CC Compositions comprising the extracellular fragment of p74 combined with
 CC HLA-B*2702.60-84 (see R95416), induces calcium influx, and inhibits
 CC cytotoxic T lymphocyte (CTL) differentiation or cytolysis. Candidate
 CC compounds can be screened for their effect on the cytolytic activity of
 CC T-cells, by combining them with the extracellular portion of p74 and
 CC determining the amount of binding between the candidate compound and p74.
 CC Modulation of CTL activity can be inhibited in a cellular composition
 CC containing T-cells and antigen presenting cells (APCs), by adding to the
 CC mix the extracellular portion of p74, in an amount sufficient to compete

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: February 7, 2000, 18:04:37 ; Search time 111.22 Seconds
(without alignments)
8.482 Million cell updates/sec

Title: US-08-653-294-26

Perfect score: 98
Sequence: 1 YRLAIRLRRENRLRY 20

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 142080 seqs, 47169319 residues

Total number of hits satisfying chosen parameters: 142080

Minimum DB seq length: 0

Maximum DB seq length: 1000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : PIR.62.*

1: Pirl.*

2: Pirl.*

3: Pirl.*

4: Pirl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	49	50.0	273	I38509	MHC class I histoc
2	49	50.0	274	I54463	MHC HLA-B38 chain
3	49	50.0	354	I59308	class I histocompa
4	49	50.0	354	I80168	class I histocompa
5	49	50.0	354	I80167	class I histocompa
6	49	50.0	355	I80169	class I histocompa
7	49	50.0	355	I80171	class I histocompa
8	49	50.0	359	IHLHU12	MHC class I histoc
9	49	50.0	362	IHLHU8	MHC class I histoc
10	49	50.0	362	I30345	MHC class I histoc
11	49	50.0	362	I30341	class I histocompa
12	49	50.0	362	I30339	class I histocompa
13	49	50.0	362	I30340	class I histocompa
14	49	50.0	362	I45834	MHC class I histoc
15	49	50.0	362	I84486	transmembrane glyc
16	49	50.0	362	I62045	gene HLA B-1517 pr
17	49	50.0	362	I84490	lymphocyte antigen
18	49	50.0	362	I37521	HLA-Bw57.2 antigen
19	49	50.0	362	I30345	MHC class I histoc
20	49	50.0	362	I59633	MHC HLA-B transmem
21	49	50.0	362	I24434	class I histocompa
22	49	50.0	362	I37120	MHC class I histoc
23	49	50.0	363	I307113	class I histocompa
24	49	50.0	363	I30337	class I histocompa
25	49	50.0	364	I30337	MHC class I histoc
26	49	50.0	365	I577963	MHC class I histoc
27	49	50.0	365	I54416	HLA-AW24 protein -
28	49	50.0	365	I54493	MHC class I histoc
29	44	44.9	274	IHLHU32	MHC class I histoc
30	44	44.9	355	I37516	HLA-B alpha-chain

class I histocompa
MHC class I histoc
MHC HLA-B44.2 chai
MHC class I histoc
MHC class I histoc
NADH dehydrogenase
240K tegument prot
tegument protein -
conserved hypothet
gene COX1 intron 4
glucosamine-fructo
hypothetical prote
rRNA (adenine-N6,N
hypothetical prote
probable serine/th

ALIGNMENTS

RESULT 1

I38509

MHC class I histocompatibility antigen - human (fragment)

C:Species: Homo sapiens (man)

C:Date: 08-Sep-1996 #sequence_revision 06-Sep-1996 #text_change 23-Jul-1999

C:Accession: I38509

R:Cereb, N.; Chol, J.W.; Riu, K.Z.; Yang, S.Y.

Tissue Antigens 44, 271-273, 1994

A:Title: HLA-B*5105, a newly identified B51 IEF variant.

A:Reference number: I38509; MUID:95176331

A:Accession: I38509

A:Status: preliminary; translated from GB/EMBL/DDBJ

A:Molecule type: mRNA

A:Residues: 1-273 <RES>

A:Cross-references: EMBL:U06697; NID:g469544; PIDN:AAA92997.1; PID:g469545

C:Genetics:

A:Gene: GDB:HLA-B

A:Cross-references: GDB:120048; OMIM:142830

A:Map position: 6p21.3-6p21.3

C:Superfamily: class I histocompatibility antigen; immunoglobulin homology

Query Match 50.0%; Score 49; DB 2; Length 273;
Best Local Similarity 100.0%; Pred. No. 1.3;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 RENLRYALRY 20

Db 74 RENLRYALRY 83

RESULT 2

I54463

MHC HLA-B38 chain - human (fragment)

C:Species: Homo sapiens (man)

C:Date: 07-Jun-1996 #sequence_revision 07-Jun-1996 #text_change 23-Jul-1999

C:Accession: I54463

R:Mueller, C.A.; Engler-Blum, G.; Gekeler, V.; Steiert, I.; Weiss, E.; Schmidt, H.

Immunogenetics 30, 200-207, 1989

A:Title: Genetic and serological heterogeneity of the supertypic HLA-B locus specific

A:Reference number: I54463; MUID:89379286

A:Accession: I54463

A:Status: preliminary; translated from GB/EMBL/DDBJ

A:Molecule type: DNA

A:Residues: 1-274 <RES>

A:Cross-references: GB:M29864; NID:g187674; PIDN:AAA36222.1; PID:g187675

C:Superfamily: class I histocompatibility antigen; immunoglobulin homology

Query Match 50.0%; Score 49; DB 2; Length 274;
Best Local Similarity 100.0%; Pred. No. 1.3;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 RENLIRALRY 20
| | | | | | | |
Db 75 RENLIRALRY 84

RESULT 3

class I histocompatibility antigen - pygmy chimpanzee (fragment)
C:Species: Pan paniscus (pygmy chimpanzee, bonobo)
C:Date: 31-May-1996 #sequence_revision 31-May-1996 #text_change 23-Jul-1999
C:Accession: I59308
R:McAdam, S.N.; Boyson, J.E.; Liu, X.; Garber, T.L.; Hughes, A.L.; Bontrop, R.E.; Watkin
Proc. Natl. Acad. Sci. U.S.A. 91, 5893-5897, 1994
A:Title: A uniquely high level of recombination at the HLA-B locus.
A:Reference number: I59308; MUID:94286544
A:Accession: I59308
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-354 <RES>
A:Cross-references: EMBL:U05575; NID:g454767; PIDN:AAA50178.1; PID:g454768
C:Superfamily: class I histocompatibility antigen; immunoglobulin homology

Query Match 50.0%; Score 49; DB 2; Length 354;
Best Local Similarity 100.0%; Pred. No. 1.7;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 RENLIRALRY 20
| | | | | | | |
Db 91 RENLIRALRY 100

RESULT 4

class I histocompatibility antigen - chimpanzee (fragment)
C:Species: Pan troglodytes (chimpanzee)
C:Date: 24-May-1996 #sequence_revision 24-May-1996 #text_change 23-Jul-1999
C:Accession: I80168
R:McAdam, S.N.; Boyson, J.E.; Liu, X.; Garber, T.L.; Hughes, A.L.; Bontrop, R.E.; Watkin
Proc. Natl. Acad. Sci. U.S.A. 91, 5893-5897, 1994
A:Title: A uniquely high level of recombination at the HLA-B locus.
A:Reference number: I59308; MUID:94286544
A:Accession: I80168
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-354 <RES>
A:Cross-references: EMBL:U05579; NID:g454775; PIDN:AAA50182.1; PID:g454776
C:Superfamily: class I histocompatibility antigen; immunoglobulin homology

Query Match 50.0%; Score 49; DB 2; Length 354;
Best Local Similarity 100.0%; Pred. No. 1.7;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 RENLIRALRY 20
| | | | | | | |
Db 91 RENLIRALRY 100

RESULT 5

class I histocompatibility antigen - pygmy chimpanzee (fragment)
C:Species: Pan paniscus (pygmy chimpanzee, bonobo)
C:Date: 24-May-1996 #sequence_revision 24-May-1996 #text_change 23-Jul-1999
C:Accession: I80167
R:McAdam, S.N.; Boyson, J.E.; Liu, X.; Garber, T.L.; Hughes, A.L.; Bontrop, R.E.; Watkin
Proc. Natl. Acad. Sci. U.S.A. 91, 5893-5897, 1994
A:Title: A uniquely high level of recombination at the HLA-B locus.
A:Reference number: I59308; MUID:94286544
A:Accession: I80167
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-354 <RES>

A:Cross-references: EMBL:U05578; NID:g454773; PIDN:AAA50181.1; PID:g454774
C:Superfamily: class I histocompatibility antigen; immunoglobulin homology

Query Match 50.0%; Score 49; DB 2; Length 354;
Best Local Similarity 100.0%; Pred. No. 1.7;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 RENLIRALRY 20
| | | | | | | |
Db 91 RENLIRALRY 100

RESULT 6

class I histocompatibility antigen - chimpanzee (fragment)
C:Species: Pan troglodytes (chimpanzee)
C:Date: 24-May-1996 #sequence_revision 24-May-1996 #text_change 23-Jul-1999
C:Accession: I80169
R:McAdam, S.N.; Boyson, J.E.; Liu, X.; Garber, T.L.; Hughes, A.L.; Bontrop, R.E.; Watkin
Proc. Natl. Acad. Sci. U.S.A. 91, 5893-5897, 1994
A:Title: A uniquely high level of recombination at the HLA-B locus.
A:Reference number: I59308; MUID:94286544
A:Accession: I80169
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-355 <RES>

Query Match 50.0%; Score 49; DB 2; Length 355;
Best Local Similarity 100.0%; Pred. No. 1.7;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 RENLIRALRY 20
| | | | | | | |
Db 91 RENLIRALRY 100

RESULT 7

class I histocompatibility antigen - chimpanzee (fragment)
C:Species: Pan troglodytes (chimpanzee)
C:Date: 24-May-1996 #sequence_revision 24-May-1996 #text_change 23-Jul-1999
C:Accession: I80171
R:McAdam, S.N.; Boyson, J.E.; Liu, X.; Garber, T.L.; Hughes, A.L.; Bontrop, R.E.; Watkin
Proc. Natl. Acad. Sci. U.S.A. 91, 5893-5897, 1994
A:Title: A uniquely high level of recombination at the HLA-B locus.
A:Reference number: I59308; MUID:94286544
A:Accession: I80171
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-355 <RES>
A:Cross-references: EMBL:U05582; NID:g454781; PIDN:AAA50185.1; PID:g454782
C:Superfamily: class I histocompatibility antigen; immunoglobulin homology

Query Match 50.0%; Score 49; DB 2; Length 355;
Best Local Similarity 100.0%; Pred. No. 1.7;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 RENLIRALRY 20
| | | | | | | |
Db 91 RENLIRALRY 100

RESULT 8

MHC class I histocompatibility antigen HLA alpha chain precursor (clone pHLA 12.4) -
C:Species: Homo sapiens (man)
C:Date: 05-Apr-1983 #sequence_revision 05-Apr-1983 #text_change 22-Jun-1999
C:Accession: A02189

R:Malissen, M.; Malissen, B.; Jordan, B.R.
Proc. Natl. Acad. Sci. U.S.A. 79, 893-897, 1982
A:Title: Exon/intron organization and complete nucleotide sequence of an HLA gene.
A:Reference number: A02189; MUID:82151002
A:Accession: A02189
A:Molecule type: DNA
A:Residues: 1-359 <MAL>
A:Cross-references: GB:J00191; GB:V00526; NID:g187600; PIDN:AAA36218.1; PID:g386873
C:Comment: The seven exons correspond approximately to the domain structure of this chain
C:Genetics:
A:Map position: 6p21.3
A:Introns: 22/1; 112/1; 204/1; 296/1; 335/1; 346/1
C:Superfamily: class I histocompatibility antigen; immunoglobulin homology
C:Keywords: duplication; glycoprotein; heterodimer; transmembrane protein; transplantat

F:1-21/Domain: signal sequence #status predicted <SIG>
F:22-359/Product: class I histocompatibility antigen HLA alpha chain #status predicted <EXT>
F:22-304/Domain: extracellular #status predicted <EXT>
F:22-111/Domain: alpha-1 <EX1>
F:112-203/Domain: alpha-2 <EX2>
F:217-282/Domain: immunoglobulin homology <IMM>
F:305-329/Domain: transmembrane #status predicted <TM>
F:335-359/Domain: intracellular #status predicted <INT>
F:107/Binding site: carbohydrate (Asn) (covalent) #status predicted
F:224-280/Disulfide bonds: #status predicted

Query Match 50.0%; Score 49; DB 1; Length 359;
Best Local Similarity 100.0%; Pred. No. 1.7;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 RENLRIALRY 20
Db 96 RENLRIALRY 105

RESULT 9

HLH088
MHC class I histocompatibility antigen HLA-B*58 alpha chain precursor - human
C:Species: Homo sapiens (man)
C:Date: 31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change 05-Sep-1997
C:Accession: A23895
R:Ways, J.P.; Coppin, H.L.; Parham, P.
J. Biol. Chem. 260, 11924-11933, 1985
A:Title: The complete primary structure of HLA-B*58.
A:Reference number: A23895; MUID:86008247
A:Accession: A23895
A:Molecule type: DNA
A:Residues: 1-362 <WAY>
A:Note: The authors translated the codon GCC for residue 349 as Ser
C:Comment: This protein is a subtype of the HLA-B17 family.
C:Genetics:
A:Gene: GDB:HLA-B

A:Cross-references: GDB:120048; OMTM:142830
A:Map position: 6p21.3-6p21.3
A:Introns: 25/1; 115/1; 207/1; 299/1; 338/1; 349/1
C:Superfamily: class I histocompatibility antigen; immunoglobulin homology
C:Keywords: duplication; glycoprotein; heterodimer; transmembrane protein; transplantat
F:1-24/Domain: signal sequence #status predicted <SIG>
F:25-362/Product: class I histocompatibility antigen HLA-B*58 alpha chain #status predic
F:25-307/Domain: extracellular #status predicted <EXT>
F:25-114/Domain: alpha-1 <EX1>
F:115-206/Domain: alpha-2 <EX2>
F:220-285/Domain: immunoglobulin homology <IMM>
F:308-331/Domain: transmembrane #status predicted <TM>
F:332-362/Domain: intracellular #status predicted <INT>
F:110/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 50.0%; Score 49; DB 1; Length 362;
Best Local Similarity 100.0%; Pred. No. 1.7;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 RENLRIALRY 20

Db 99 RENLRIALRY 108

RESULT 10

B30345
MHC class I histocompatibility antigen HLA-B*52 precursor - human
C:Species: Homo sapiens (man)
C:Date: 29-Jan-1990 #sequence_revision 29-Jan-1990 #text_change 16-Feb-1997
C:Accession: B30345
R:Hayashi, H.; Ennis, P.D.; Ariga, H.; Salter, R.D.; Parham, P.; Kano, K.; Takiguchi, J.
Immunol. 142, 306-311, 1989
A:Title: HLA-B*51 and HLA-B*52 differ by only two amino acids which are in the helical
A:Reference number: A30345; MUID:89080265
A:Accession: B30345
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-362 <HAY>
C:Superfamily: class I histocompatibility antigen; immunoglobulin homology
C:Keywords: transmembrane protein
F:220-285/Domain: immunoglobulin homology <IMM>

Query Match 50.0%; Score 49; DB 2; Length 362;
Best Local Similarity 100.0%; Pred. No. 1.7;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 RENLRIALRY 20
Db 99 RENLRIALRY 108

RESULT 11

JH0541
Class I histocompatibility antigen Gogo-B0103 heavy chain precursor - lowland gorilla
C:Species: Gorilla gorilla gorilla (lowland gorilla)
C:Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 23-Jul-1999
C:Accession: JH0541
R:Lawlor, D.A.; Warren, E.; Taylor, P.; Parham, P.
J. Exp. Med. 174, 1491-1509, 1991
A:Title: Gorilla class I major histocompatibility complex alleles: comparison to huma
A:Reference number: JH0534; MUID:92078860
A:Accession: JH0541
A:Molecule type: DNA
A:Residues: 1-362 <LAW>
A:Cross-references: EMBL:X60254; NID:g22869; PIDN:CAA42806.1; PID:g22870
A:Experimental source: EBV-transformed B cell
C:Genetics:
A:Introns: 25/1; 115/1; 207/1; 299/1; 338/1; 349/1
C:Superfamily: class I histocompatibility antigen; immunoglobulin homology
C:Keywords: transmembrane protein
F:1-24/Domain: signal sequence #status predicted <SIG>
F:25-362/Product: class I histocompatibility antigen heavy chain, Gogo-B0103 #status

Query Match 50.0%; Score 49; DB 2; Length 362;
Best Local Similarity 100.0%; Pred. No. 1.7;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 RENLRIALRY 20
Db 99 RENLRIALRY 108

RESULT 12

JH0539
Class I histocompatibility antigen Gogo-B0101 heavy chain precursor - lowland gorilla
C:Species: Gorilla gorilla gorilla (lowland gorilla)

C:Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 23-Jul-1999
C:Accession: JH0539
R:Lawlor, D.A.; Warren, E.; Taylor, P.; Parham, P.
J. Exp. Med. 174, 1491-1509, 1991
A:Title: Gorilla class I major histocompatibility complex alleles: comparison to human a
A:Reference number: JH0534; MUID:92078860
A:Accession: JH0539
A:Molecule type: DNA
A:Residues: 1-362 <LAW>
A:Cross-references: EMBL:X60255; NID:g22865; PIDN:CAA42807.1; PID:g22866
A:Experimental source: EBV-transformed B cell
C:Genetics:
A:Introns: 25/1; 115/1; 207/1; 299/1; 338/1; 349/1
C:Superfamily: class I histocompatibility antigen; immunoglobulin homology
C:Keywords: transmembrane protein
F:1-24/Domain: signal sequence #status predicted <SIG>
F:25-362/Product: class I histocompatibility antigen heavy chain, Gogo-B0101 #status pre
F:25-114/Domain: alpha-1 <AL1>
F:115-206/Domain: alpha-2 <AL2>
F:207-298/Domain: alpha-3 <AL3>
F:220-285/Domain: immunoglobulin homology <IMM>
F:299-362/Domain: intracellular #status predicted <INT>

Query Match 50.0%; Score 49; DB 2; Length 362;
Best Local Similarity 100.0%; Pred. No. 1.7;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 RNLRIALRY 20
|||||
DB 99 RNLRIALRY 108

RESULT 13
JH0540
class I histocompatibility antigen Gogo-B0102 heavy chain precursor - lowland gorilla
C:Species: Gorilla gorilla gorilla (lowland gorilla)
C:Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 23-Jul-1999
C:Accession: JH0540
R:Lawlor, D.A.; Warren, E.; Taylor, P.; Parham, P.
J. Exp. Med. 174, 1491-1509, 1991
A:Title: Gorilla class I major histocompatibility complex alleles: comparison to human a
A:Reference number: JH0534; MUID:92078860
A:Accession: JH0540
A:Molecule type: DNA
A:Residues: 1-362 <LAW>
A:Cross-references: EMBL:X60693; NID:g22867; PIDN:CAA43101.1; PID:g22868
A:Experimental source: EBV-transformed B cell
C:Genetics:
A:Introns: 25/1; 115/1; 207/1; 299/1; 338/1; 349/1
C:Superfamily: class I histocompatibility antigen; immunoglobulin homology
C:Keywords: transmembrane protein
F:1-24/Domain: signal sequence #status predicted <SIG>
F:25-362/Product: class I histocompatibility antigen heavy chain, Gogo-B0102 #status pre
F:25-114/Domain: alpha-1 <AL1>
F:115-206/Domain: alpha-2 <AL2>
F:207-298/Domain: alpha-3 <AL3>
F:220-285/Domain: immunoglobulin homology <IMM>
F:299-362/Domain: intracellular #status predicted <INT>

Query Match 50.0%; Score 49; DB 2; Length 362;
Best Local Similarity 100.0%; Pred. No. 1.7;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 RNLRIALRY 20
|||||
DB 99 RNLRIALRY 108

RESULT 14
A45834
MHC Class I histocompatibility antigen HLA-B53 alpha chain precursor - human

C:Species: Homo sapiens (man)
C:Date: 03-Jun-1993 #sequence_revision 03-Jun-1993 #text_change 23-Jul-1999
C:Accession: A45834
R:Havashi, H.; Ooba, T.; Nakayama, S.; Sekimata, M.; Kano, K.; Takiguchi, M.
Immunogenetics 32, 195-199, 1990
A:Title: Allotopes specificities between HLA-B*53 and HLA-B*35 are generated by substitution
A:Reference number: A45834; MUID:91033941
A:Accession: A45834
A:Molecule type: DNA
A:Residues: 1-362 <HAY>
A:Cross-references: GB:M58636; NID:g187756; PIDN:AAA36228.1; PID:g187757; GB:M33574
A:Note: this allele is designated B*5301
C:Genetics:
A:Gene: GDB:HLA-B
A:Map position: 6p21.3-6p21.3
C:Superfamily: class I histocompatibility antigen; immunoglobulin homology
C:Keywords: glycoprotein; heterodimer; transmembrane protein
F:1-24/Domain: signal sequence #status predicted <SIG>
F:220-285/Domain: immunoglobulin homology <IMM>
F:110/Binding site: carbohydrate (asn) (covalent) #status predicted

Query Match 50.0%; Score 49; DB 2; Length 362;
Best Local Similarity 100.0%; Pred. No. 1.7;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 RNLRIALRY 20
|||||
DB 99 RNLRIALRY 108

RESULT 15
I84486
transmembrane glycoprotein - human
C:Species: Homo sapiens (man)
C:Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 23-Jul-1999
C:Accession: I84486
R:Hildebrand, W.H.; Domena, J.D.; Shen, S.Y.; Lau, M.; Terasaki, P.I.; Bunce, M.; Mar
Tissue Antigens 43, 209-218, 1994
A:Title: HLA-B*15: a widespread and diverse family of HLA-B alleles.
A:Reference number: I38421; MUID:94367483
A:Accession: I84486
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-362 <RES>
A:Cross-references: GB:LI5005; NID:g493154; PIDN:AAA56832.1; PID:g493155
C:Genetics:
A:Gene: HLA-B*1513
C:Superfamily: class I histocompatibility antigen; immunoglobulin homology
C:Keywords: glycoprotein

Query Match 50.0%; Score 49; DB 2; Length 362;
Best Local Similarity 100.0%; Pred. No. 1.7;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 RNLRIALRY 20
|||||
DB 99 RNLRIALRY 108

Search completed: February 7, 2000, 18:04:38
Job time: 22204 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: February 8, 2000, 01:25:58 ; Search time 68.63 Seconds
(without alignments)
8.703 Million cell updates/sec

Title: US-08-653-294-26

Perfect score: 98

Sequence: 1 YRLAIRLNERENLRALRY 20

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 82229 seqs, 29864866 residues

Total number of hits satisfying chosen parameters: 82229

Minimum DB seq length: 0

Maximum DB seq length: 1000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : SwissProt_38.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query	Score	Match	Length	DB	ID	Description
1	49	50.0	359	1	1B01_PANTR	1	P13750 pan troglod
2	49	50.0	362	1	1B01_GORGO	1	P30379 gorilla gor
3	49	50.0	362	1	1B02_GORGO	1	P30380 gorilla gor
4	49	50.0	362	1	1B03_GORGO	1	P30381 gorilla gor
5	49	50.0	362	1	1B15_HUMAN	1	P10317 homo sapien
6	49	50.0	362	1	1B47_HUMAN	1	P30487 homo sapien
7	49	50.0	362	1	1B49_HUMAN	1	P18464 homo sapien
8	49	50.0	362	1	1B52_HUMAN	1	P30489 homo sapien
9	49	50.0	362	1	1B53_HUMAN	1	P30490 homo sapien
10	49	50.0	362	1	1B54_HUMAN	1	P30491 homo sapien
11	49	50.0	362	1	1B60_HUMAN	1	P18465 homo sapien
12	49	50.0	362	1	1B61_HUMAN	1	P30497 homo sapien
13	49	50.0	362	1	1B62_HUMAN	1	P10319 homo sapien
14	49	50.0	362	1	1B63_HUMAN	1	P01893 homo sapien
15	49	50.0	365	1	1A23_HUMAN	1	P30447 homo sapien
16	49	50.0	365	1	1A24_HUMAN	1	P05534 homo sapien
17	44	44.9	362	1	1B05_HUMAN	1	P30461 homo sapien
18	44	44.9	362	1	1B41_HUMAN	1	P30481 homo sapien
19	44	44.9	362	1	1B42_HUMAN	1	P30482 homo sapien
20	44	44.9	365	1	1A25_HUMAN	1	P18462 homo sapien
21	44	44.9	365	1	1A32_HUMAN	1	P10314 homo sapien
22	44	44.9	400	1	NUCM_PROWI	1	Q37619 prototheca
23	44	44.9	2077	1	TEGU_HSV6G	1	P30002 herpes simp
24	44	44.9	2077	1	TEGU_HSV6U	1	P52340 herpes simp
25	43	43.9	924	1	ORC1_DROME	1	O16810 drosophila
26	42	42.9	591	1	GLMS_AQUAE	1	O65648 a glucosami
27	41	41.8	287	1	KSGA_HAEIN	1	P44749 h dimethyla
28	41	41.8	394	1	NUCM_ARATH	1	P93306 arabidopsis
29	40	40.8	433	1	HEM2_SPIOL	1	P24493 spinacia ol
30	40	40.8	525	1	LAC3_HUMAN	1	P18627 homo sapien
31	40	40.8	3712	1	ACVS_CEPAC	1	P25464 cephalospor
32	39.5	40.3	406	1	YACH_YEAST	1	P38953 saccharomyc
33	39	39.8	117	1	YCHN_ECOLI	1	P39164 escherichia
34	39	39.8	162	1	PUR6_BACSU	1	P12044 bacillus su

RESULT 1

ID	1B01_PANTR	STANDARD;	PRT;	359 AA.
AC	P13750;			
DT	01-JAN-1990 (Rel. 13, Created)			
DT	01-JAN-1990 (Rel. 13, Last sequence update)			
DT	01-APR-1993 (Rel. 25, Last annotation update)			
DE	CHLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-1 ALPHA CHAIN PRECURSOR (FRAGMENT).			
DE	Pan troglodytes (Chimpanzee).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;			
OC	Eutheria; Primates; Catarrhini; Hominiidae; Pan.			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE; 89030641.			
RA	MAYER W.E., JONKER M., KLEIN D., IVANYI P., VAN SEVENTER G.,			
RA	KLEIN J.			
RT	"Nucleotide sequences of chimpanzee MHC class I alleles: evidence for trans-species mode of evolution."			
RL	EMBO J. 7:2765-2774(1988).			
RN	[2]			
RP	REVISIONS.			
RA	MAYER W.			
RL	Submitted (FEB-1989) to the EMBL/GenBank/DBJ databases.			
CC	-!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO THE IMMUNE SYSTEM.			
CC	-!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-MICROGLOBULIN).			
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CC	EMBL; X13115; CAA31507.1; .			
DR	PIR; S03537; S03537.			
DR	HSSP; P03989; IHSa.			
DR	PROSITE; PS00290; IG_MHC; 1.			
DR	PFAM; PF00047; Ig; 1.			
DR	PFAM; PF00129; MHC_I; 1.			
KW	MHC I; Transmembrane; Glycoprotein; Signal.			
FT	NON_TER	1		
FT	SIGNAL	<1	20	
FT	CHAIN	21	359	
FT	DOMAIN	21	110	
FT	DOMAIN	111	202	
FT	DOMAIN	203	294	
FT	DOMAIN	295	305	
FT	TRANSMEM	306	329	
FT	DOMAIN	330	359	
FT	DISULFID	121	184	
FT	DISULFID	223	279	
FT	CARBOHYD	106	106	

CHLA CLASS I HISTOCOMPATIBILITY ANTIGEN,
B-1 ALPHA CHAIN.
EXTRACELLULAR ALPHA-1.
EXTRACELLULAR ALPHA-2.
EXTRACELLULAR ALPHA-3.
CONNECTING PEPTIDE.
CYTOPLASMIC TAIL.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.

OC Eutheria; Primates; Catarrhini; Hominidae; Gorilla.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 92078860.
 RA LAWLOR D.A., WARREN E., TAYLOR P., PARHAM P.;
 RT "Gorilla class I major histocompatibility complex alleles: comparison
 to human and chimpanzee class I.";
 RL J. Exp. Med. 174:1491-1509(1991).
 CC -!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
 THE IMMUNE SYSTEM.
 CC -!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
 MICROGLOBULIN).
 CC -----
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 or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: X60254; CAA42806.1; -.
 DR PIR: JH0541; JH0541.
 DR HSP: P03989; IHSA.
 DR PROSITE: PS00290; IG_MHC; 1.
 DR PFAM: PF00047; Ig; 1.
 DR PFAM: PF00129; MHC_I; 1.
 KW MHC I; Transmembrane; Glycoprotein; Signal.
 FT SIGNAL 1 24
 FT CHAIN 25 362
 FT CLASS I HISTOCOMPATIBILITY ANTIGEN,
 FT GOGO-B0103 ALPHA CHAIN.
 FT DOMAIN 25 114
 FT DOMAIN 115 206
 FT DOMAIN 207 298
 FT DOMAIN 299 308
 FT TRANSMEM 309 332
 FT DOMAIN 333 362
 FT DISULFID 125 188
 FT DISULFID 227 283
 FT CARBOHYD 110 110
 SQ SEQUENCE 362 AA; 40248 MW; FEA6A941 CRC32;
 Query Match 50.0%; Score 49; DB 1; Length 362;
 Best Local Similarity 100.0%; Pred. No. 0.62;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 11 RENLIRALRY 20
 Db |||||
 Db 99 RENLIRALRY 108
 RESULT 5
 ID IB15_HUMAN STANDARD; PRT; 362 AA.
 AC P10317;
 DT 01-MAR-1989 (Rel. 10; Created)
 DT 01-MAR-1989 (Rel. 10; Last sequence update)
 DT 01-APR-1993 (Rel. 25; Last annotation update)
 DE HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-27 B*2702 ALPHA CHAIN
 DE PRECURSOR (B-27K) (B27.2).
 GN HLA-B OR HLAB.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia;
 OC Eutheria; Primates; Catarrhini; Hominidae; Homo.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 86220133.
 RA SEEMANN G.H.A., REIN R.S., BROWN C.S., PLOEGH H.L.;
 RT "Gene conversion-like mechanisms may generate polymorphism in human
 class I genes.";
 RL EMBO J. 5:547-552(1986).
 RN [2]

RP SEQUENCE FROM N.A.
 RA PARHAM P., ARNETT K.L., ADAMS E.J.;
 RL Submitted (JUL-1995) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE OF 86-107 AND 171-181.
 RX MEDLINE: 86042671.
 RA VEGA M.A., EQUERRA A., ROJO S., APARICIO P., BRAGADO R.,
 RA LOPEZ DE CASTRO J.A.;
 RT "Structural analysis of an HLA-B27 functional variant: identification
 of residues that contribute to the specificity of recognition by
 cytolytic T lymphocytes.";
 RT Proc. Natl. Acad. Sci. U.S.A. 82:7394-7398(1985).
 RL CC -!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
 THE IMMUNE SYSTEM.
 CC -!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
 MICROGLOBULIN).
 CC -----
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 or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: X03664; CAA27301.1; -.
 DR EMBL: X03667; CAA27301.1; JOINED.
 DR EMBL: L38504; AAA69724.1; -.
 DR PIR: B25092; HLHUBK.
 DR HSP: P03989; IHSA.
 DR MIM: I42830; -.
 DR PROSITE: PS00290; IG_MHC; 1.
 DR PFAM: PF00047; Ig; 1.
 DR PFAM: PF00129; MHC_I; 1.
 KW MHC I; Transmembrane; Glycoprotein; Signal.
 FT SIGNAL 1 24
 FT CHAIN 25 362
 FT CLASS I HISTOCOMPATIBILITY ANTIGEN,
 FT B-27 B*2702 ALPHA CHAIN.
 FT DOMAIN 25 114
 FT DOMAIN 115 206
 FT DOMAIN 207 298
 FT DOMAIN 299 308
 FT TRANSMEM 309 332
 FT DOMAIN 333 362
 FT CARBOHYD 110 110
 FT DISULFID 125 188
 FT DISULFID 227 283
 SQ SEQUENCE 362 AA; 40397 MW; 9798F0BB CRC32;
 Query Match 50.0%; Score 49; DB 1; Length 362;
 Best Local Similarity 100.0%; Pred. No. 0.62;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 11 RENLIRALRY 20
 Db |||||
 Db 99 RENLIRALRY 108
 RESULT 6
 ID IB47_HUMAN STANDARD; PRT; 362 AA.
 AC P30487;
 DT 01-APR-1993 (Rel. 25; Created)
 DT 01-FEB-1996 (Rel. 33; Last sequence update)
 DT 01-FEB-1996 (Rel. 33; Last annotation update)
 DE HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-49(B-21) B*4901 ALPHA CHAIN
 DE PRECURSOR.
 GN HLA-B OR HLAB.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Eutheria; Primates; Catarrhini; Hominidae; Homo.
 RN [1]

RP SEQUENCE FROM N.A.
 RX MEDLINE: 89235215.
 RA PARHAM P., LANIOR D.A., LOMEN C.E., ENNIS P.D.;
 RT "Diversity and diversification of HLA-A,B,C alleles."
 RL J. Immunol. 142:3937-3950(1989).
 RN [2]
 RP REVISION TO 78.
 RX MEDLINE: 93056529.
 RA HILDEBRAND W.H., MADRIGAL J.A., BELICH M.P., ZEMMOUR J., WARD F.E.,
 RA WILLIAMS R.C., PARHAM P.;
 RT "Serologic cross-reactivities poorly reflect allelic relationships in
 RT the HLA-B*12 and HLA-B*21 groups. Dominant epitopes of the alpha 2
 RT helix."
 RL J. Immunol. 149:3563-3568(1992).
 CC -1- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
 CC THE IMMUNE SYSTEM.
 CC -1- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
 CC MICROGLOBULIN).
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL: M24037; AAA02950.1;
 DR HSSP: P30491; IALM.
 DR MIM: 142830;
 DR PROSITE: PS00290; IG_MHC; 1.
 DR PFAM: PF00047; Ig; 1.
 DR PFAM: PF00129; MHC_I; 1.
 DR MHC I: Transmembrane; Glycoprotein; Signal.
 KW SIGNAL 1 24
 FT CHAIN 25 362
 FT FT HLA CLASS I HISTOCOMPATIBILITY ANTIGEN,
 FT B-49(B-21) B*4901 ALPHA CHAIN.
 FT DOMAIN 25 114
 FT DOMAIN 115 206
 FT DOMAIN 207 298
 FT DOMAIN 299 309
 FT TRANSMEM 310 333
 FT DOMAIN 334 362
 FT CARBOHYD 110 110
 FT DISULFID 125 188
 FT DISULFID 227 283
 FT SEQUENCE 362 AA; 40581 MW; E996F82F CRC32;

Query Match 50.0%; Score 49; DB 1; Length 362;
 Best Local Similarity 100.0%; Pred. No. 0.62;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 RENLIRALRY 20
 DB 99 RENLIRALRY 108

RESULT 7
 1B49 HUMAN STANDARD; PRT; 362 AA.
 ID 1B49 HUMAN
 AC P18464;
 DT 01-NOV-1990 (Rel. 16, Created)
 DT 01-NOV-1990 (Rel. 16, Last sequence update)
 DT 01-FEB-1996 (Rel. 33, Last annotation update)
 DE HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-51(B-5) B*5101 ALPHA CHAIN
 DE PRECURSOR.
 GN HLA-B OR HLA-B.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Eutheria; Primates; Catarrhini; Hominidae; Homo.
 RN [1]
 RP SEQUENCE FROM N.A.

RX MEDLINE: 90207291.
 RA ENNIS P.D., ZEMMOUR J., SALTER R.D., PARHAM P.;
 RT "Rapid cloning of HLA-A,B CDNA by using the polymerase chain
 RT reaction: frequency and nature of errors produced in amplification."
 RL Proc. Natl. Acad. Sci. U.S.A. 87:2833-2837(1990).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 89080265.
 RA HAYASHI H., ENNIS P.D., ARIGA H., SALTER R.D., PARHAM P., KANO K.,
 RA TAKIGUCHI M.;
 RT "HLA-B*51 and HLA-B*52 differ by only two amino acids which are in the
 RT helical region of the alpha 1 domain."
 RL J. Immunol. 142:306-311(1989).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 89233295.
 RA POHLA H., KUON W., TABACZEWSKI P., DOERNER C., WEISS E.H.;
 RT "Allelic variation in HLA-B and HLA-C sequences and the evolution of
 RT the HLA-B alleles."
 RL Immunogenetics 29:297-307(1989).
 CC -1- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
 CC THE IMMUNE SYSTEM.
 CC -1- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
 CC MICROGLOBULIN).
 CC -----
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 CC -----
 CC EMBL: M23219; AAA36232.1;
 DR EMBL: M22792; AAA59620.1; ALT_SEQ.
 DR EMBL: M22786; AAA59620.1; JOINED.
 DR EMBL: M22787; AAA59620.1; JOINED.
 DR EMBL: M22788; AAA59620.1; JOINED.
 DR EMBL: M22789; AAA59620.1; JOINED.
 DR EMBL: M22790; AAA59620.1; JOINED.
 DR EMBL: M22791; AAA59620.1; JOINED.
 DR EMBL: L41087; AAA64513.1;
 DR EMBL: L41086; AAA64513.1; JOINED.
 DR PIR: A30345; A30345.
 DR PIR: A30548; A30548.
 DR HSSP: P30491; IALM.
 DR MIM: 142830;
 DR PROSITE: PS00290; IG_MHC; 1.
 DR PFAM: PF00047; Ig; 1.
 DR PFAM: PF00129; MHC_I; 1.
 DR MHC I: Transmembrane; Glycoprotein; Signal.
 KW SIGNAL 1 24
 FT CHAIN 25 362
 FT FT HLA CLASS I HISTOCOMPATIBILITY ANTIGEN,
 FT B-51(B-5) B*5101 ALPHA CHAIN.
 FT DOMAIN 25 114
 FT DOMAIN 115 206
 FT DOMAIN 207 298
 FT DOMAIN 299 308
 FT TRANSMEM 309 332
 FT DOMAIN 333 362
 FT CARBOHYD 110 110
 FT DISULFID 125 188
 FT DISULFID 227 283
 FT SEQUENCE 362 AA; 40566 MW; 4D846F30 CRC32;

Query Match 50.0%; Score 49; DB 1; Length 362;
 Best Local Similarity 100.0%; Pred. No. 0.62;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 RENLIRALRY 20
 DB 99 RENLIRALRY 108

```

DE DE HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, BW-52(B-5) B*5201 ALPHA CHAIN
DE DE PRECURSOR.
GN HLA-B OR HLAB.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Primates; Catarrhini; Homiidae; Homo.
RN [1]
RN SEQUENCE FROM N.A.
RX MEDLINE; 89080265.
RA HAYASHI H., ENNIS P.D., ARIGA H., SALTER R.D., PARHAM P., KANO K.,
RA TAKIGUCHI M.;
RT "HLA-B*51 and HLA-B*52 differ by only two amino acids which are in the
RT helical region of the alpha 1 domain.";
RL J. Immunol. 142:306-311(1989).
CC -!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
CC THE IMMUNE SYSTEM.
CC -!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
CC MICROGLOBULIN).
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; M22799; AAA59645.1; ALT-SEQ.
CC EMBL; M22793; AAA59645.1; JOINED.
CC EMBL; M22794; AAA59645.1; JOINED.
CC EMBL; M22795; AAA59645.1; JOINED.
CC EMBL; M22796; AAA59645.1; JOINED.
CC EMBL; M22797; AAA59645.1; JOINED.
CC EMBL; M22798; AAA59645.1; JOINED.
CC PIR; B30345; B30345.
CC PIR; B30548; B30548.
CC HSSP; P30491; IALM.
CC MIM; 142830;
CC PROSITE; PS00290; IG_MHC; 1.
CC PFAM; PF00047; ig; 1.
CC PFAM; PF00129; MHC_I; 1.
CC MHC I; transmembrane; Glycoprotein; Signal.
CC SIGNAL
CC CHAIN 25 362 HLA CLASS I HISTOCOMPATIBILITY ANTIGEN,
CC B*51(B-5) B*5104 ALPHA CHAIN.
CC DOMAIN 25 114 EXTRACELLULAR ALPHA-1.
CC DOMAIN 115 206 EXTRACELLULAR ALPHA-2.
CC DOMAIN 207 298 EXTRACELLULAR ALPHA-3.
CC DOMAIN 299 308 CONNECTING PEPTIDE.
CC TRANSMEM 309 332
CC DOMAIN 333 362 CYTOPLASMIC TAIL.
CC CARBOHYD 110 110 BY SIMILARITY.
CC DISULFID 125 188 BY SIMILARITY.
CC DISULFID 227 283 BY SIMILARITY.
CC SEQUENCE 362 AA; 40560 MW; F22F08AB CRC32;
SQ

DE DE HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, BW-52(B-5) B*5201 ALPHA CHAIN
DE DE PRECURSOR.
GN HLA-B OR HLAB.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Primates; Catarrhini; Homiidae; Homo.
RN [1]
RN SEQUENCE FROM N.A.
RX MEDLINE; 89080265.
RA HAYASHI H., ENNIS P.D., ARIGA H., SALTER R.D., PARHAM P., KANO K.,
RA TAKIGUCHI M.;
RT "HLA-B*51 and HLA-B*52 differ by only two amino acids which are in the
RT helical region of the alpha 1 domain.";
RL J. Immunol. 142:306-311(1989).
CC -!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
CC THE IMMUNE SYSTEM.
CC -!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
CC MICROGLOBULIN).
CC
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CC
CC EMBL; M22799; AAA59645.1; ALT-SEQ.
CC EMBL; M22793; AAA59645.1; JOINED.
CC EMBL; M22794; AAA59645.1; JOINED.
CC EMBL; M22795; AAA59645.1; JOINED.
CC EMBL; M22796; AAA59645.1; JOINED.
CC EMBL; M22797; AAA59645.1; JOINED.
CC EMBL; M22798; AAA59645.1; JOINED.
CC PIR; B30345; B30345.
CC PIR; B30548; B30548.
CC HSSP; P30491; IALM.
CC MIM; 142830;
CC PROSITE; PS00290; IG_MHC; 1.
CC PFAM; PF00047; ig; 1.
CC PFAM; PF00129; MHC_I; 1.
CC MHC I; transmembrane; Glycoprotein; Signal.
CC SIGNAL
CC CHAIN 25 362 HLA CLASS I HISTOCOMPATIBILITY ANTIGEN,
CC B*51(B-5) B*5104 ALPHA CHAIN.
CC DOMAIN 25 114 EXTRACELLULAR ALPHA-1.
CC DOMAIN 115 206 EXTRACELLULAR ALPHA-2.
CC DOMAIN 207 298 EXTRACELLULAR ALPHA-3.
CC DOMAIN 299 308 CONNECTING PEPTIDE.
CC TRANSMEM 309 332
CC DOMAIN 333 362 CYTOPLASMIC TAIL.
CC CARBOHYD 110 110 BY SIMILARITY.
CC DISULFID 125 188 BY SIMILARITY.
CC DISULFID 227 283 BY SIMILARITY.
CC SEQUENCE 362 AA; 40560 MW; F22F08AB CRC32;
SQ

Query Match 50.0%; Score 49; DB 1; Length 362;
Best Local Similarity 100.0%; Pred. No. 0.62;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 RENLIRALRY 20
Db 99 RENLIRALRY 108
|||||
RENRIRALRY 108

RESULT 10
ID 1B54_HUMAN STANDARD; PRT; 362 AA.
AC P30491;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)

Query Match 50.0%; Score 49; DB 1; Length 362;
Best Local Similarity 100.0%; Pred. No. 0.62;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 RENLIRALRY 20
Db 99 RENLIRALRY 108
|||||
RENRIRALRY 108

RESULT 9
ID 1B53_HUMAN STANDARD; PRT; 362 AA.
AC P30490;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 01-APR-1993 (Rel. 25, Last annotation update)

```

DE HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, BW-53 B*5301 ALPHA CHAIN
DE PRECURSOR.

GN HLA-B OR HLAB.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;

OC Eutheria; Primates; Catarrhini; Homiidae; Homo.

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE; 91033941.

RA HAYASHI H., Ooba T., NAKAYAMA S., SEKIMATA M., KANO K.,

RA TAKIGUCHI M.;

RT "Allopecificities between HLA-Bw53 and HLA-B35 are generated by

RT substitution of the residues associated with HLA-Bw4/Bw6 public

RT epitopes.";

RL Immunogenetics 32:195-199(1990).

RN [2]

RP X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF 25-302.

RX MEDLINE; 96209672.

RA SMITH K.J., REID S.W., HARLOS K., MCMICHAEL A.J., STUART D.I.,

RA BELL J.I., JONES E.Y.;

RT "Bound water structure and polymorphic amino acids act together to

RT allow the binding of different peptides to MHC class I HLA-B53.";

RL Immunity 4:215-228(1996).

CC -!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO

CC THE IMMUNE SYSTEM.

CC -!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-

CC MICROGLOBULIN).

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DR EMBL; M58636; AAA36228.1; -

DR PIR; A45834; A45834

DR PDB; 1A1M; 08-APR-98.

DR PDB; 1A1O; 08-APR-98.

DR MIM; 142830; -

DR PROSITE; PS00290; IG_MHC; 1.

DR PFAM; PF00047; ig; 1.

DR PFAM; PF00129; MHC_I; 1.

KW MHC I; Transmembrane; Glycoprotein; Signal; 3D-structure.

FT SIGNAL

FT CHAIN

FT HLA CLASS I HISTOCOMPATIBILITY ANTIGEN,

FT BW-53 B*5301 ALPHA CHAIN.

FT DOMAIN 25 114

FT DOMAIN 115 206

FT DOMAIN 207 298

FT DOMAIN 299 308

FT DOMAIN 309 332

FT TRANSMEM 333 362

FT DOMAIN 110 110

FT CARBOHYD 125 188

FT DISULFID 227 283

FT DISULFID 227 283

FT SEQUENCE 362 AA; 40495 MW; 2BDC746E CRC32;

Query Match 50.0%; Score 49; DB 1; Length 362;

Best Local Similarity 100.0%; Pred. No. 0.62;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 RENLIRALRY 20

Db 99 RENLIRALRY 108

|||||

RESULT 11

1B60_HUMAN

ID 1B60_HUMAN

AC P18465;

STANDARD; PRT; 362 AA.

DT

DT

DT

DE

DE

GN

GN

OS

OC

OC

Eutheria; Primates; Catarrhini; Homiidae; Homo.

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE; 90207291.

RA ENNIS P.D., ZEMMOUR J., SALTER R.D., PARHAM P.;

RT "Rapid cloning of HLA-A,B CDNA by using the polymerase chain

RT reaction; frequency and nature of errors produced in amplification.";

RL Proc. Natl. Acad. Sci. U.S.A. 87:2833-2837(1990).

RN [2]

RP SEQUENCE FROM N.A.

RX MEDLINE; 91067476.

RA ISAMAT M., GIRDLESTONE J., MILSTEIN C.;

RT "Nucleotide sequence of an HLA-Bw57 gene.";

RL Nucleic Acids Res. 18:6702-6702(1990).

CC -!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO

CC THE IMMUNE SYSTEM.

CC -!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-

CC MICROGLOBULIN).

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DR EMBL; M32318; AAA36231.1; -

DR EMBL; X55711; CAA39244.1; -

DR PIR; S12622; S12622

DR PIR; D35997; D35997.

DR HSP; P30491; 1A1M.

DR MIM; 142830; -

DR PROSITE; PS00290; IG_MHC; 1.

DR PFAM; PF00047; ig; 1.

DR PFAM; PF00129; MHC_I; 1.

KW MHC I; Transmembrane; Glycoprotein; Signal.

FT SIGNAL

FT CHAIN

FT HLA CLASS I HISTOCOMPATIBILITY ANTIGEN,

FT B-57(B-17) B*5701 ALPHA CHAIN.

FT DOMAIN 25 114

FT DOMAIN 115 206

FT DOMAIN 207 298

FT DOMAIN 299 308

FT DOMAIN 309 332

FT TRANSMEM 333 362

FT DOMAIN 110 110

FT CARBOHYD 125 188

FT DISULFID 227 283

FT DISULFID 227 283

FT SEQUENCE 362 AA; 40224 MW; D91DF8DD CRC32;

Query Match 50.0%; Score 49; DB 1; Length 362;

Best Local Similarity 100.0%; Pred. No. 0.62;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 RENLIRALRY 20

Db 99 RENLIRALRY 108

|||||

RESULT 12

1B61_HUMAN

ID 1B61_HUMAN

AC P30497;

STANDARD; PRT; 362 AA.

RESULT	13	
1B62_HUMAN		
ID	1B62_HUMAN	STANDARD: PRT; 362 AA.
AC	P10319;	
DT	01-MAR-1989	(Rel. 10, Created)
DT	01-MAR-1989	(Rel. 10, Last sequence update)
DT	15-JUL-1998	(Rel. 36, Last annotation update)
DE	HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, BW-58(B-17) B*5801 ALPHA	
DE	DE ϵ -1 CHAIN PRECURSOR.	
GN	HLA-B OR HLAB.	

QY 11 RENLRY 20
db 99 RENLRY 108

RESULT	14
HLAH_HUMAN	
ID	HLAH_HUMAN
STANDARD;	PRT; 362 AA.
AC	P01893;
DT	21-JUL-1986 (Rel. 01, Created)
DT	01-APR-1993 (Rel. 25, Last sequence update)
DT	15-DEC-1999 (Rel. 39, Last annotation update)
DE	HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, ALPHA CHAIN H PRECURSOR
DE	(HLA-A*) (HLA-12.4).
GN	HLA-H OR HLAH.
OS	Homo sapiens (Human).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC	Eutheria; Primates; Catarrhini; Hominoidea; Homo.

RN SEQUENCE FROM N.A.
RX MEDLINE; 82151002.
RA MALISSEN M., MALISSEN B., JORDAN B.R.;
RT "Exon/intron organization and complete nucleotide sequence of an HLA
gene.";
RL Proc. Natl. Acad. Sci. U.S.A. 79:893-897(1982).
CC -!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
CC THE IMMUNE SYSTEM. COULD BE THE PRODUCT OF A PSEUDOGENE.
CC -!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
CC MICROGLOBULIN).
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CC
CC EMBL; J00191; AAA36218.1; ALT_INIT.
CC PIR; A02189; HLH12.
CC HSP; P03989; IHS.
CC MIM; 142800; -.
CC PROSITE; PS00290; IG_MHC; 1.
CC PFAM; PF00047; Ig; 1.
CC PFAM; PF00129; MHC_I; 1.
CC MHC I; Transmembrane; Glycoprotein; Signal.
CC SIGNAL 1 24
CC CHAIN 25 362 HLA CLASS I HISTOCOMPATIBILITY ANTIGEN,
CC DOMAIN 25 114 ALPHA CHAIN H.
CC DOMAIN 115 206 EXTRACELLULAR ALPHA-1.
CC DOMAIN 207 298 EXTRACELLULAR ALPHA-2.
CC DOMAIN 299 308 EXTRACELLULAR ALPHA-3.
CC TRANSMEM 309 332 CONNECTING PEPTIDE.
CC DOMAIN 333 362 CYTOPLASMIC TAIL.
CC CARBOHYD 110 110 BY SIMILARITY.
CC DISULFID 227 283 BY SIMILARITY.
CC SEQUENCE 362 AA; 40850 MW; 5E610F63 CRC32;

Query Match 50.0%; Score 49; DB 1; Length 362;
Best Local Similarity 100.0%; Pred. No. 0.62;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 RENLRALRY 20
DB 99 RENLRALRY 108

RESULT 15
1A23_HUMAN
ID 1A23_HUMAN STANDARD; PRT; 365 AA.
AC P30447;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, A-23(A-9) ALPHA CHAIN
DE PRECURSOR.
GN HLA-A OR HLA-A.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Primates; Catarrhini; Hominidae; Homo.
RN [1]
RP SEQUENCE FROM N.A. (A*2301).
RX MEDLINE; 92104637.
RA LITTLE A.-M., MADRIGAL J.A., PARHAM P.;
RT "Molecular definition of an elusive third HLA-A9 molecule: HLA-A9.3.";
RL Immunogenetics 35:41-45(1992).
CC -!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
CC THE IMMUNE SYSTEM.
CC -!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-

CC MICROGLOBULIN).
CC -!- POLYMORPHISM: THE ONLY ALLELE OF A-23 KNOWN IS A*2301 WHICH IS
CC SHOWN HERE.
CC
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CC
CC EMBL; M64742; AAA03662.1; -.
CC HSP; P01892; IAQD.
CC MIM; 142800; -.
CC PROSITE; PS00290; IG_MHC; 1.
CC PFAM; PF00047; Ig; 1.
CC PFAM; PF00129; MHC_I; 1.
CC MHC I; Transmembrane; Glycoprotein; Signal.
CC SIGNAL 1 24
CC CHAIN 25 365 HLA CLASS I HISTOCOMPATIBILITY ANTIGEN,
CC DOMAIN 25 114 A-23(A-9) ALPHA CHAIN.
CC DOMAIN 115 206 EXTRACELLULAR ALPHA-1.
CC DOMAIN 207 298 EXTRACELLULAR ALPHA-2.
CC DOMAIN 299 308 EXTRACELLULAR ALPHA-3.
CC TRANSMEM 309 332 CONNECTING PEPTIDE.
CC DOMAIN 333 365 CYTOPLASMIC TAIL.
CC CARBOHYD 110 110 BY SIMILARITY.
CC DISULFID 125 188 BY SIMILARITY.
CC DISULFID 227 283 BY SIMILARITY.
CC SEQUENCE 365 AA; 40732 MW; BIC21094 CRC32;

Query Match 50.0%; Score 49; DB 1; Length 365;
Best Local Similarity 100.0%; Pred. No. 0.62;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 RENLRALRY 20
DB 99 RENLRALRY 108

Search completed: February 8, 2000, 01:25:59
Job time: 1559 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: February 8, 2000, 19:16:13 ; Search time 176.54 Seconds
(without alignments)
7.855 Million cell updates/sec

Title: US-08-653-294-26

Perfect score: 98
Sequence: 1 YRLAIRLNERENLRALRY 20

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 225878 seqs, 69334122 residues

Total number of hits satisfying chosen parameters: 225878

Minimum DB seq length: 0

Maximum DB seq length: 1000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

SPTREMBL_12.*
1: sp-archaea.*
2: sp-bacteria.*
3: sp-fungi.*
4: sp-human.*
5: sp-invertebrate.*
6: sp-mammal.*
7: sp-mhc.*
8: sp-organelle.*
9: sp-phage.*
10: sp-plant.*
11: sp-rodent.*
12: sp-virus.*
13: sp-vertebrate.*
14: sp-unclassified.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	49	50.0	89	7 019569	019569 homo sapien
2	49	50.0	90	7 046697	046697 gorilla gor
3	49	50.0	133	7 019189	019189 homo sapien
4	49	50.0	138	7 078209	078209 homo sapien
5	49	50.0	172	7 019770	019770 homo sapien
6	49	50.0	172	7 019774	019774 homo sapien
7	49	50.0	172	7 019775	019775 homo sapien
8	49	50.0	172	7 019780	019780 homo sapien
9	49	50.0	172	7 095364	Q95364 homo sapien
10	49	50.0	172	7 019771	019771 homo sapien
11	49	50.0	172	7 019772	019772 homo sapien
12	49	50.0	172	7 019773	019773 homo sapien
13	49	50.0	175	7 029694	Q29694 homo sapien
14	49	50.0	180	7 019607	019607 homo sapien
15	49	50.0	180	7 019608	019608 homo sapien
16	49	50.0	180	7 019609	019609 homo sapien
17	49	50.0	180	7 019610	019610 homo sapien
18	49	50.0	180	7 019611	019611 homo sapien
19	49	50.0	180	7 019612	019612 homo sapien
20	49	50.0	180	7 019613	019613 homo sapien

21	49	50.0	181	7 046703	046703 homo sapien
22	49	50.0	181	7 062917	062917 homo sapien
23	49	50.0	181	7 062892	062892 homo sapien
24	49	50.0	181	7 062899	062899 homo sapien
25	49	50.0	181	7 062920	062920 homo sapien
26	49	50.0	181	7 062922	062922 homo sapien
27	49	50.0	181	7 062923	062923 homo sapien
28	49	50.0	181	7 019623	019623 homo sapien
29	49	50.0	181	7 019747	019747 homo sapien
30	49	50.0	181	7 029667	029667 homo sapien
31	49	50.0	181	7 030198	Q30198 homo sapien
32	49	50.0	181	7 029708	Q29708 homo sapien
33	49	50.0	181	7 019631	019631 homo sapien
34	49	50.0	181	7 019769	019769 homo sapien
35	49	50.0	181	7 029724	Q29724 homo sapien
36	49	50.0	181	7 029910	Q29910 homo sapien
37	49	50.0	181	7 079559	P79559 homo sapien
38	49	50.0	181	7 029679	Q29679 homo sapien
39	49	50.0	181	7 019521	019521 homo sapien
40	49	50.0	181	7 019597	019597 homo sapien
41	49	50.0	181	7 029909	Q29909 homo sapien
42	49	50.0	181	7 029701	Q29701 homo sapien
43	49	50.0	181	7 029841	Q29841 homo sapien
44	49	50.0	181	7 019354	019354 gorilla gor
45	49	50.0	181	7 029765	Q29765 homo sapien

ALIGNMENTS

RESULT 1
019569 PRELIMINARY; PRT; 89 AA.
AC 019569;
DT 01-JAN-1998 (TRENBLrel. 05, Created)
DT 01-MAY-1999 (TRENBLrel. 10, Last sequence update)
DT 01-MAY-1999 (TRENBLrel. 10, Last annotation update)
DE MHC CLASS I ANTIGEN (FRAGMENT).
GN HLA-B.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Primates; Catarrhini; Hominidae; Homo.
RN [1]
RP SEQUENCE FROM N.A.
RA CAO K., BURDETT L., ZHANG G., FERNANDEZ-VINA M.;
RL Submitted (AUG-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF017320; AAB70286.2;
KW MHC.
FT NON_TER 1
FT NON_TER 89
SQ SEQUENCE 89 AA; 10606 MW; 99D11089 CRC32;

Query Match 50.0%; Score 49; DB 7; Length 89;
Best Local Similarity 100.0%; Pred. No. 1.1;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 RENLRALRY 20
DB 74 RENLRALRY 83

RESULT 2
046697 PRELIMINARY; PRT; 90 AA.
AC 046697;
DT 01-JUN-1998 (TRENBLrel. 06, Created)
DT 01-JUN-1998 (TRENBLrel. 06, Last sequence update)
DT 01-MAY-1999 (TRENBLrel. 10, Last annotation update)
DE MHC CLASS I ANTIGEN HLA-H ORTHOLOG (FRAGMENT).
GN HLA-H.
OS Gorilla gorilla gorilla (Lowland gorilla).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;

OC Eutheria; Primates; Catarrhini; Hominidae; Gorilla.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-SHABRA;
 RA GRIMSLEY C., MATHER K.A., OBER C.;
 RL Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF022172; AAC99794.1; -;
 DR PFAM; PF00129; MHC_I; 1.
 KW MHC.
 FT NON_TER 1 1
 FT NON_TER 90 90
 SQ SEQUENCE 90 AA; 10689 MW; 555F2495 CRC32;

Query Match 50.0%; Score 49; DB 7; Length 90;
 Best Local Similarity 100.0%; Pred. No. 1.1;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 RENLIRALRY 20
 DB 75 RENLIRALRY 84
 |||||

RESULT 3
 OI9189 PRELIMINARY; PRT; 133 AA.
 AC OI9189;
 DT 01-JAN-1998 (TREMREL. 05, Created)
 DT 01-JAN-1998 (TREMREL. 05, Last sequence update)
 DT 01-NOV-1999 (TREMREL. 12, Last annotation update)
 DE MHC CLASS I HISTOCOMPATIBILITY ANTIGEN-B (HLA-B-27KSH) (FRAGMENT).
 GN HLA-B.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Eutheria; Primates; Catarrhini; Hominidae; Homo.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-LEUKOCYTE;
 RA PETERSDORF E.;
 RL Submitted (DEC-1994) to the EMBL/GenBank/DBJ databases.
 DR EMBL; U18659; AAB60357.1; -;
 DR MIM; 142830; -;
 DR PFAM; PF00129; MHC_I; 1.
 KW MHC I.
 FT NON_TER 1 1
 FT NON_TER 133 133
 SQ SEQUENCE 133 AA; 15491 MW; 3A3BC802 CRC32;

Query Match 50.0%; Score 49; DB 7; Length 133;
 Best Local Similarity 100.0%; Pred. No. 1.7;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 RENLIRALRY 20
 DB 27 RENLIRALRY 36
 |||||

RESULT 4
 OI78209 PRELIMINARY; PRT; 138 AA.
 AC OI78209;
 DT 01-NOV-1998 (TREMREL. 08, Created)
 DT 01-NOV-1998 (TREMREL. 08, Last sequence update)
 DT 01-MAY-1999 (TREMREL. 10, Last annotation update)
 DE HUMAN LEUKOCYTE ANTIGEN PRECURSOR (FRAGMENT).
 GN HLA-A.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Eutheria; Primates; Catarrhini; Hominidae; Homo.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 98007772.

RA LAFORET M., FROELICH N., PARISSIADIS A., BAUSINGER H., PFEIFFER B.,
 RA TONGIO M.M.;
 RT "An intronic mutation responsible for a low level of expression of an
 RT HLA-A*24 allele.";
 RL Tissue Antigens 50:340-346(1997).
 DR EMBL; Z72423; CAA96533.1; -;
 DR PFAM; PF00129; MHC_I; 1.
 KW Signal; MHC.
 FT SIGNAL 1 24
 FT NON_TER 138 138
 SQ SEQUENCE 138 AA; 15610 MW; B8417FA0 CRC32;

Query Match 50.0%; Score 49; DB 7; Length 138;
 Best Local Similarity 100.0%; Pred. No. 1.7;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 RENLIRALRY 20
 DB 99 RENLIRALRY 108
 |||||

RESULT 5
 OI9770 PRELIMINARY; PRT; 172 AA.
 AC OI9770;
 DT 01-JAN-1998 (TREMREL. 05, Created)
 DT 01-JAN-1998 (TREMREL. 05, Last sequence update)
 DT 01-NOV-1998 (TREMREL. 08, Last annotation update)
 DE MHC CLASS I HLA-B (FRAGMENT).
 GN HLA-B.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Eutheria; Primates; Catarrhini; Hominidae; Homo.
 RN [1]
 RP SEQUENCE FROM N.A.
 RA CHANDANAYINGYONG D., SIRIKONG M., LONGTA K., SRINAK D., RUNGROUNG E.,
 RA BEJCHANDRA S., JUJI T., TOKUNAGA K.;
 RL Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.
 DR EMBL; U90421; AAB50144.1; -;
 DR EMBL; U90420; AAB50144.1; JOINED.
 DR PFAM; PF00129; MHC_I; 1.
 KW MHC.
 FT NON_TER 1 1
 FT NON_TER 172 172
 SQ SEQUENCE 172 AA; 19909 MW; CAAE5641 CRC32;

Query Match 50.0%; Score 49; DB 7; Length 172;
 Best Local Similarity 100.0%; Pred. No. 2.2;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 RENLIRALRY 20
 DB 68 RENLIRALRY 77
 |||||

RESULT 6
 OI9774 PRELIMINARY; PRT; 172 AA.
 AC OI9774;
 DT 01-JAN-1998 (TREMREL. 05, Created)
 DT 01-JAN-1998 (TREMREL. 05, Last sequence update)
 DT 01-NOV-1998 (TREMREL. 08, Last annotation update)
 DE MHC CLASS I HLA-B (FRAGMENT).
 GN HLA-B.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Eutheria; Primates; Catarrhini; Hominidae; Homo.
 RN [1]
 RP SEQUENCE FROM N.A.
 RA CHANDANAYINGYONG D., SIRIKONG M., LONGTA K., SRINAK D., RUNGROUNG E.,
 RA BEJCHANDRA S., BLASCZYK R., GROSSE-WILDE H.;

RL Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.
 DR EMBL; U90423; AAB50145.1; -
 DR EMBL; U90422; AAB50145.1; JOINED.
 DR PFAM; PF00129; MHC_I; 1.
 KW MHC.
 FT NON_TER 1 1
 FT NON_TER 172 172
 SQ SEQUENCE 172 AA; 19909 MW; CAAE5641 CRC32;

Query Match 50.0%; Score 49; DB 7; Length 172;
 Best Local Similarity 100.0%; Pred. No. 2.2;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 RENLRIALRY 20
 Db 68 RENLRIALRY 77

RESULT 7

O19775 PRELIMINARY; PRT; 172 AA.
 AC O19775;
 DT 01-JAN-1998 (TRENBLrel. 05, Created)
 DT 01-JAN-1998 (TRENBLrel. 05, Last sequence update)
 DT 01-NOV-1998 (TRENBLrel. 08, Last annotation update)
 DE MHC CLASS I HLA-B (FRAGMENT).
 GN HLA-B.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Eutheria; Primates; Catarrhini; Hominidae; Homo.
 RN [1]
 RP SEQUENCE FROM N.A.
 RA CHANDANAYONG D., SIRIKONG M., LONGTA K., SRINAK D., RUNGROUNG E.,
 RA BEJCHANDRA S.;
 RL Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.
 DR EMBL; U90425; AAB50146.1; -
 DR EMBL; U90424; AAB50146.1; JOINED.
 DR PFAM; PF00129; MHC_I; 1.
 KW MHC.
 FT NON_TER 1 1
 FT NON_TER 172 172
 SQ SEQUENCE 172 AA; 19909 MW; CAAE5641 CRC32;

Query Match 50.0%; Score 49; DB 7; Length 172;
 Best Local Similarity 100.0%; Pred. No. 2.2;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 RENLRIALRY 20
 Db 68 RENLRIALRY 77

RESULT 8

O19780 PRELIMINARY; PRT; 172 AA.
 AC O19780;
 DT 01-JAN-1998 (TRENBLrel. 05, Created)
 DT 01-JAN-1998 (TRENBLrel. 05, Last sequence update)
 DT 01-NOV-1998 (TRENBLrel. 08, Last annotation update)
 DE MHC CLASS I HLA-B (FRAGMENT).
 GN HLA-B.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Eutheria; Primates; Catarrhini; Hominidae; Homo.
 RN [1]
 RP SEQUENCE FROM N.A.
 RA CHANDANAYONG D., SIRIKONG M., LONGTA K., SRINAK D., RUNGROUNG E.,
 RA BEJCHANDRA S., JUJI T., TOKUNAGA K.;
 RL Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.
 DR EMBL; U90419; AAB50143.1; -
 DR EMBL; U90418; AAB50143.1; JOINED.

DR PFAM; PF00129; MHC_I; 1.
 KW MHC.
 FT NON_TER 1 1
 FT NON_TER 172 172
 SQ SEQUENCE 172 AA; 19909 MW; CAAE5641 CRC32;

Query Match 50.0%; Score 49; DB 7; Length 172;
 Best Local Similarity 100.0%; Pred. No. 2.2;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 RENLRIALRY 20
 Db 68 RENLRIALRY 77

RESULT 9

Q95364 PRELIMINARY; PRT; 172 AA.
 ID Q95364;
 AC Q95364;
 DT 01-FEB-1997 (TRENBLrel. 02, Created)
 DT 01-FEB-1997 (TRENBLrel. 02, Last sequence update)
 DT 01-NOV-1998 (TRENBLrel. 08, Last annotation update)
 DE MHC HLA-B*51 PROTEIN (FRAGMENT).
 GN HLA-B*51FA.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Eutheria; Primates; Catarrhini; Hominidae; Homo.
 RN [1]
 RP SEQUENCE FROM N.A.
 RA BLASCZYK R.;
 RL Submitted (MAR-1996) to the EMBL/GenBank/DBJ databases.
 DR EMBL; X96473; CAA65327.1; -
 DR PFAM; PF00129; MHC_I; 1.
 KW MHC.
 FT NON_TER 1 1
 FT NON_TER 172 172
 SQ SEQUENCE 172 AA; 19942 MW; 1A73E47D CRC32;

Query Match 50.0%; Score 49; DB 7; Length 172;
 Best Local Similarity 100.0%; Pred. No. 2.2;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 RENLRIALRY 20
 Db 65 RENLRIALRY 74

RESULT 10

O19771 PRELIMINARY; PRT; 172 AA.
 ID O19771;
 AC O19771;
 DT 01-JAN-1998 (TRENBLrel. 05, Created)
 DT 01-JAN-1998 (TRENBLrel. 05, Last sequence update)
 DT 01-NOV-1998 (TRENBLrel. 08, Last annotation update)
 DE MHC CLASS I HLA-B (FRAGMENT).
 GN HLA-B.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Eutheria; Primates; Catarrhini; Hominidae; Homo.
 RN [1]
 RP SEQUENCE FROM N.A.
 RA CHANDANAYONG D., SIRIKONG M., LONGTA K., SRINAK D.,
 RA SIRIBOONRIT U., RUNGROUNG E., BEJCHANDRA S.;
 RL Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.
 DR EMBL; U90612; AAB50151.1; -
 DR EMBL; U90611; AAB50151.1; JOINED.
 DR PFAM; PF00129; MHC_I; 1.
 KW MHC.
 FT NON_TER 1 1
 FT NON_TER 172 172
 SQ SEQUENCE 172 AA; 20026 MW; 4D9A1043 CRC32;

Query Match 50.0%; Score 49; DB 7; Length 172;
Best Local Similarity 100.0%; Pred. No. 2.2;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 RENLRIALRY 20
DB 68 RENLRIALRY 77

RESULT 11

O19772 PRELIMINARY; PRT; 172 AA.
AC O19772;
DT 01-JAN-1998 (TREMBlrel. 05, Created)
DT 01-JAN-1998 (TREMBlrel. 05, Last sequence update)
DT 01-NOV-1998 (TREMBlrel. 08, Last annotation update)
DE MHC CLASS I HLA-B (FRAGMENT).
GN HLA-B.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Primates; Catarrhini; Hominidae; Homo.
RN [1]
RP SEQUENCE FROM N.A.
RA CHANDANAYINGYONG D., SIRIKONG M., LONGTA K., SRINAK D.,
RA SIRIBOONRIT U., RUNGRONG E., BEJCHANDRA S.;
RL Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; U90614; AAB50244.1; -
DR EMBL; U90615; AAB50245.1; JOINED.
DR PFAM; PF00129; MHC_I; 1.
KW MHC.
FT NON_TER 1 1
FT NON_TER 172 172
SQ SEQUENCE 172 AA; 20026 MW; 4D9A1043 CRC32;

Query Match 50.0%; Score 49; DB 7; Length 172;
Best Local Similarity 100.0%; Pred. No. 2.2;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 RENLRIALRY 20
DB 68 RENLRIALRY 77

RESULT 12

O19773 PRELIMINARY; PRT; 172 AA.
AC O19773;
DT 01-JAN-1998 (TREMBlrel. 05, Created)
DT 01-JAN-1998 (TREMBlrel. 05, Last sequence update)
DT 01-NOV-1998 (TREMBlrel. 08, Last annotation update)
DE MHC CLASS I HLA-B (FRAGMENT).
GN HLA-B.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Primates; Catarrhini; Hominidae; Homo.
RN [1]
RP SEQUENCE FROM N.A.
RA CHANDANAYINGYONG D., SIRIKONG M., LONGTA K., SRINAK D.,
RA SIRIBOONRIT U., RUNGRONG E., BEJCHANDRA S.;
RL Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; U90614; AAB50244.1; -
DR EMBL; U90615; AAB50245.1; JOINED.
DR PFAM; PF00129; MHC_I; 1.
KW MHC.
FT NON_TER 1 1
FT NON_TER 172 172
SQ SEQUENCE 172 AA; 20052 MW; F6214671 CRC32;

Query Match 50.0%; Score 49; DB 7; Length 172;

Best Local Similarity 100.0%; Pred. No. 2.2;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 RENLRIALRY 20
DB 68 RENLRIALRY 77

RESULT 13

O29694 PRELIMINARY; PRT; 175 AA.
AC Q29694;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-NOV-1999 (TREMBlrel. 12, Last annotation update)
DE MHC CLASS I HLA-B ANTIGEN (FRAGMENT).
GN HLA-B.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Primates; Catarrhini; Hominidae; Homo.
RN [1]
RP SEQUENCE FROM N.A.
RA PETERSDORF E.;
RL Submitted (JUN-1995) to the EMBL/GenBank/DBJ databases.
DR EMBL; U28759; AAB60367.1; -
DR HSSP; P10318; 1ROC.
DR PFAM; PF00129; MHC_I; 1.
KW MHC.
FT NON_TER 1 1
FT VARIANT 67 67 Y -> D.
FT VARIANT 73 73 I -> T.
FT NON_TER 175 175
SQ SEQUENCE 175 AA; 20332 MW; 83A0C5C3 CRC32;

Query Match 50.0%; Score 49; DB 7; Length 175;
Best Local Similarity 100.0%; Pred. No. 2.2;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 RENLRIALRY 20
DB 68 RENLRIALRY 77

RESULT 14

O19607 PRELIMINARY; PRT; 180 AA.
AC O19607;
DT 01-JAN-1998 (TREMBlrel. 05, Created)
DT 01-JAN-1998 (TREMBlrel. 05, Last sequence update)
DT 01-NOV-1999 (TREMBlrel. 12, Last annotation update)
DE MHC CLASS I HLA-A (FRAGMENT).
GN HLA-A.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Primates; Catarrhini; Hominidae; Homo.
RN [1]
RP SEQUENCE FROM N.A.
RA CHANDANAYINGYONG D., SIRIKONG M., LUANGTRAKOOL K., SRINAK D.,
RA RUNGRONG E., BEJCHANDRA S.;
RL Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF030920; AAB87056.1; -
DR EMBL; AF030919; AAB87056.1; JOINED.
DR HSSP; P01891; 1TMC.
DR PFAM; PF00129; MHC_I; 1.
KW MHC.
FT NON_TER 1 1
FT NON_TER 180 180
SQ SEQUENCE 180 AA; 20811 MW; CECC3537 CRC32;

Query Match 50.0%; Score 49; DB 7; Length 180;

Best Local Similarity 100.0%; Pred. No. 2.3;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 RENLIRALRY 20
|||||
Db 74 RENLIRALRY 83

RESULT 15

O19608
ID O19608 PRELIMINARY; PRT; 180 AA.
AC O19608; 1998 (TREMBlrel. 05, Created)
DT 01-JAN-1998 (TREMBlrel. 05, Last sequence update)
DT 01-NOV-1999 (TREMBlrel. 12, Last annotation update)
DE MHC CLASS I HLA-A (FRAGMENT).
GN HLA-A.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Primates; Catarrhini; Hominidae; Homo.
RN [1]
RP SEQUENCE FROM N.A.
RA CHANDANAYONG D., SIRIKONG M., LUANGTRAKOOL K., SRINAK D.,
RA RUNGROUNG E., BEJCHANDRA S.;
RL Submitted (OCT-1997) to the EMBL/genBank/DBJ databases.
DR EMBL; AF030922; AAB87057.1; -.
DR EMBL; AF030921; AAB87057.1; JOINED.
DR HSP; P01891; 1TMC.
DR PFAM; PF00129; MHC_I; 1.
KW MHC.
FT NON_TER 1
FT NON_TER 180
SQ SEQUENCE 180 AA; 20811 MW; CECC3537 CRC32;

Query Match 50.0%; Score 49; DB 7; Length 180;

Best Local Similarity 100.0%; Pred. No. 2.3;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 RENLIRALRY 20
|||||
Db 74 RENLIRALRY 83

Search completed: February 8, 2000, 19:16:13
Job time: 21500 sec

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OM of: US-08-653-294-26 to: GenEmbl:* out_format : pfs
Date: Feb 8, 2000 10:22 PM
About: Results were produced by the GenCore software, version 4.5.
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Command line parameters:
-MODEL=frame+p2n.model -DEV=xlp
-O=Cgml_1/USPTO.spool/US08653294/runat_04022000_160701_15779/app_query.fasta.2
-DB=GenEmbl -OFMT=fastap -SUFFIX=rge -GAPOP=12.000 -GAPEXT=4.000
-MINMATCH=0.100 -LOPEXT=0.000 -LOPEXT=0.000 -GAPOP=4.500
-GAPEXT=0.050 -GAPOP=10.000 -GAPEXT=0.500 -DELOP=6.000
-DELEXT=7.000 -START=1 -MATRIX=blomsum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR SCORE=pct -ALIGN=15 -MODE=LOCAL
-OUTFMT=pfs -NORW=ext -MINLEN=0 -MAXLEN=100000 -USER=US08653294
-NCPU=6 -ICPU=3 -NO_XLPHY -WAIT -THREADS=1

Search information block:

Query: US-08-653-294-26
Query length: 20
Database: GenEmbl:*
Database sequences: 821193
Database length: -1518192014
Search time (sec): 10176.920000

score_list:

Sequence	Strd	Orig	Zscore	Escore	Len	Documentation
gb_in1:CEVITELA	+	55.00	142.44	6.54	5562	! X56212 C.elegans gene for vitellogenin
gb_in1:CELC42D8	+	55.00	123.90	70.49	42801	! U56966 Caenorhabditis elegans
gb_pr1:SHSLABHBA	+	49.00	151.08	2.16	250	! Y08692 H.sapiens HLA-B gene, ex
gb_pr1:SHSLABHBB	+	49.00	151.08	2.16	250	! Y08693 H.sapiens HLA-B gene, ex
gb_pr1:SHSLABHBD	+	49.00	151.08	2.16	250	! Y08694 H.sapiens HLA-B gene, ex
gb_pr2:SHSLABD1	+	49.00	151.08	2.16	250	! U90420 Human cell line THAI DCH
gb_pr2:SHSLABD2	+	49.00	151.08	2.16	250	! U90611 Human cell line THAI DCH
gb_pr2:SHSLABD3	+	49.00	151.08	2.16	250	! U90613 Human cell line THAI DCH
gb_pr2:SHSLABD4	+	49.00	151.08	2.16	250	! U90615 Human cell line THAI DCH
gb_pr2:SHSLABD5	+	49.00	151.08	2.16	250	! U90432 Human cell line THAI DCH
gb_pr2:SHSLABD6	+	49.00	151.08	2.16	250	! U90434 Human cell line THAI DCH
gb_pr2:SHSLABD7	+	49.00	151.08	2.16	250	! U90418 Human cell line THAI DCH
gb_pr2:SHSLABD8	+	49.00	151.08	2.16	250	! U90418 Human cell line THAI DCH
gb_pr2:SHSLABD9	+	49.00	151.08	2.16	250	! U90418 Human cell line THAI DCH
gb_pr2:SHSLABD10	+	49.00	151.08	2.16	250	! U90418 Human cell line THAI DCH
gb_pr2:SHSLABD11	+	49.00	151.08	2.16	250	! U90418 Human cell line THAI DCH
gb_pr2:SHSLABD12	+	49.00	151.08	2.16	250	! U90418 Human cell line THAI DCH
gb_pr2:SHSLABD13	+	49.00	151.08	2.16	250	! U90418 Human cell line THAI DCH
gb_pr2:SHSLABD14	+	49.00	151.08	2.16	250	! U90418 Human cell line THAI DCH
gb_pr2:SHSLABD15	+	49.00	151.08	2.16	250	! U90418 Human cell line THAI DCH
gb_pr2:SHSLABD16	+	49.00	151.08	2.16	250	! U90418 Human cell line THAI DCH
gb_pr2:SHSLABD17	+	49.00	151.08	2.16	250	! U90418 Human cell line THAI DCH
gb_pr2:SHSLABD18	+	49.00	151.08	2.16	250	! U90418 Human cell line THAI DCH
gb_pr2:SHSLABD19	+	49.00	151.08	2.16	250	! U90418 Human cell line THAI DCH
gb_pr2:SHSLABD20	+	49.00	151.08	2.16	250	! U90418 Human cell line THAI DCH
gb_pr2:SHSLABD21	+	49.00	151.08	2.16	250	! U90418 Human cell line THAI DCH
gb_pr2:SHSLABD22	+	49.00	151.08	2.16	250	! U90418 Human cell line THAI DCH
gb_pr2:SHSLABD23	+	49.00	151.08	2.16	250	! U90418 Human cell line THAI DCH
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US-08-653-294-26 x HSHLABHBA

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Align seg 1/1 to: HSHLABHBA from: 1 to: 250

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DEFINITION H.sapiens HLA-B gene, exon 2, HB(b) allele.
ACCESSION Y08693
VERSION Y08693.1 GI:1619288
KEYWORDS HLA-B gene; human leukocyte antigen.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
Primates; Catarrhini; Hominidae; Homo.
10-OCT-1996

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REFERENCE
AUTHORS Rojas-Munoz,A., Mendez,I. and Yunis,I.
TITLE Molecular evolution of HLA-B locus in a small population amerindian
community :The Nukak-Maku
JOURNAL Unpublished
REFERENCE
AUTHORS Rojas-Munoz,A.
TITLE Direct Submission
JOURNAL Submitted (07-OCT-1996) A. Rojas-Munoz, National Institute Of
Health, Immunogenetics, Avenida El Dorado, Carrera 50, Santafe De
Bogota / zona 6, COLOMBIA

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US-08-653-294-26 x HSHLABHBB

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Align seg 1/1 to: HSHLABHBB from: 1 to: 250

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ACCESSION Y08694
VERSION Y08694.1 GI:1619289
KEYWORDS HLA-B gene; human leukocyte antigen.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
Primates; Catarrhini; Hominidae; Homo.
10-OCT-1996

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REFERENCE
AUTHORS Rojas-Munoz,A., Mendez,I. and Yunis,I.
TITLE Molecular evolution of HLA-B locus in a small population amerindian
community :The Nukak-Maku
JOURNAL Unpublished
REFERENCE
AUTHORS Rojas-Munoz,A.
TITLE Direct Submission
JOURNAL Submitted (07-OCT-1996) A. Rojas-Munoz, National Institute Of
Health, Immunogenetics, Avenida El Dorado, Carrera 50, Santafe De
Bogota / Zona 6, COLOMBIA

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US-08-653-294-26 x HSHLABHBD

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Align seg 1/1 to: HSHLABHBD from: 1 to: 250

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/allele="HLA-B*51V; similar to exon 2 of B*5105"
/number=2
56 a 82 c 80 g 32 t

BASE COUNT
ORIGIN

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Quality: 49.00 Length: 10
Ratio: 4.900 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
US-08-653-294-26 x HSHLABF1
Align seg 1/1 to: HSHLABF1 from: 1 to: 250

11 ArgGluAsnLeuArgIleAlaLeuArgTyr 20
|||||
202 CGAGAGAACCTCGGATCGCTCGCTAC 231

seq_name: gb_pr2:HSHLABG1

seq_documentation_block: 250 bp DNA PRI 25-MAR-1997
LOCUS HSHLABG1
DEFINITION Human cell line THAI DCH011 MHC class I HLA-B gene (allele
HLA-B*51V), exon 2.
ACCESSION U90615
VERSION U90615.1 GI:1906037
KEYWORDS
SEGMENT
SOURCE
1 of 2
human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 250)
AUTHORS Chananayong, D., Sirikong, M., Longta, K., Srinak, D.,
Rungroung, E., Bejchandra, S., Blasczyk, R. and Grosse-Wilde, H.
B15 alleles (B*1513)
Unpublished
2 (bases 1 to 250)
AUTHORS Chananayong, D., Sirikong, M., Longta, K., Srinak, D.,
Rungroung, E., Bejchandra, S., Blasczyk, R. and Grosse-Wilde, H.
Direct Submission
Submitted (25-FEB-1997) Transfusion Medicine, Faculty of Medicine,
Siriraj Hospital, Mahidol University, Prannok Road, Bangkok 10700,
Thailand
FEATURES
Location/Qualifiers
source
1. .250
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="VI"
/map="6p21"
/cell_type="lymphoblastoid"
/cell_line="THAI DCH011"
1. .250
/gene="HLA-B"
/allele="Allele: HLA-B*1513"
/number=2
/product="MHC class I HLA-B"
BASE COUNT 55 a 83 c 80 g 32 t
ORIGIN

exon

alignment_scores:
Quality: 49.00 Length: 10
Ratio: 4.900 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
US-08-653-294-26 x HSHLABI1
Align seg 1/1 to: HSHLABI1 from: 1 to: 250

11 ArgGluAsnLeuArgIleAlaLeuArgTyr 20
|||||
202 CGAGAGAACCTCGGATCGCTCGCTAC 231

seq_name: gb_pr2:HSHLABJ1

seq_documentation_block: 250 bp DNA PRI 25-MAR-1997
LOCUS HSHLABJ1
DEFINITION Human cell line THAI DCH011 MHC class I HLA-B gene (allele
HLA-B*51V), exon 2.
ACCESSION U90615
VERSION U90615.1 GI:1906037
KEYWORDS
SEGMENT
SOURCE
1 of 2
human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 250)
AUTHORS Chananayong, D., Sirikong, M., Longta, K., Srinak, D.,
Rungroung, E., Bejchandra, S., Blasczyk, R. and Grosse-Wilde, H.
B*51V alleles
Unpublished
2 (bases 1 to 250)
AUTHORS Chananayong, D., Sirikong, M., Longta, K., Srinak, D.,
Siriboonrit, U., Rungroung, E. and Bejchandra, S.
Direct Submission
Submitted (25-FEB-1997) Transfusion Medicine, Faculty of Medicine,
Siriraj Hospital, Mahidol University, Prannok Road, Bangkok 10700,
Thailand
FEATURES
Location/Qualifiers
source
1. .250
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1. .250
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56 a 82 c 80 g 32 t

BASE COUNT
ORIGIN

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alignment_scores:
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Ratio: 4.900 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
US-08-653-294-26 x HSHLABG1
Align seg 1/1 to: HSHLABG1 from: 1 to: 250

11 ArgGluAsnLeuArgIleAlaLeuArgTyr 20
|||||
202 CGAGAGAACCTCGGATCGCTCGCTAC 231

seq_name: gb_pr2:HSHLABI1

seq_documentation_block: 250 bp DNA PRI 22-MAR-1997
LOCUS HSHLABI1
DEFINITION Human cell line THAI DCH011 MHC class I HLA-B gene (allele
HLA-B*1513), exon 2.
ACCESSION U90422
VERSION U90422.1 GI:1905834
KEYWORDS
SEGMENT
SOURCE
1 of 2
human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 250)
AUTHORS Chananayong, D., Sirikong, M., Longta, K., Srinak, D.,
Rungroung, E., Bejchandra, S., Blasczyk, R. and Grosse-Wilde, H.
B15 alleles (B*1513)
Unpublished
2 (bases 1 to 250)
AUTHORS Chananayong, D., Sirikong, M., Longta, K., Srinak, D.,
Rungroung, E., Bejchandra, S., Blasczyk, R. and Grosse-Wilde, H.
Direct Submission
Submitted (23-FEB-1997) Transfusion Medicine, Faculty of Medicine,
Siriraj Hospital, Mahidol University, Prannok Road, Bangkok 10700,
Thailand
FEATURES
Location/Qualifiers
source
1. .250
/organism="Homo sapiens"
/db_xref="taxon:9606"
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/map="6p21"
/cell_type="lymphoblastoid"
/cell_line="THAI DCH011"
1. .250
/gene="HLA-B"
/allele="Allele: HLA-B*1513"
/number=2
/product="MHC class I HLA-B"
BASE COUNT 55 a 83 c 80 g 32 t
ORIGIN

exon

alignment_scores:
Quality: 49.00 Length: 10
Ratio: 4.900 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
US-08-653-294-26 x HSHLABI1
Align seg 1/1 to: HSHLABI1 from: 1 to: 250

11 ArgGluAsnLeuArgIleAlaLeuArgTyr 20
|||||
202 CGAGAGAACCTCGGATCGCTCGCTAC 231

seq_name: gb_pr2:HSHLABJ1

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seq_documentation_block:
LOCUS      HSHLABJ1          250 bp      DNA          PRI          22-MAR-1997
DEFINITION Human cell line THAI DCH028 MHC class I HLA-B gene (allele
ACCESSION  U90424
VERSION     U90424.1  GI:1905838
KEYWORDS
SOURCE      human.
ORGANISM    Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 250)
AUTHORS     Chandanayingyong,D., Sirikong,M., Longta,K., Srinak,D.,
            Rungroung,E. and Bejchandra,S.
TITLE       B15 alleles (B*1513)
JOURNAL     Unpublished
AUTHORS     Chandanayingyong,D., Sirikong,M., Longta,K., Srinak,D.,
            Rungroung,E. and Bejchandra,S.
REFERENCE   2 (bases 1 to 250)
AUTHORS     Chandanayingyong,D., Sirikong,M., Longta,K., Srinak,D.,
            Rungroung,E. and Bejchandra,S.
TITLE       Direct Submission
JOURNAL     Submitted (23-FEB-1997) Transfusion Medicine, Faculty of Medicine,
            Siriraj Hospital, Mahidol University, Prannok Road, Bangkok 10700,
            Thailand
FEATURES    Location/Qualifiers
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               /chromosome="VI"
               /map="6p21"
               /cell_type="lymphoblastoid"
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               1..250
               /gene="HLA-B"
               /note="Allele: HLA-B*1513"
               /number=2
               /product="MHC class I HLA-B"
BASE COUNT  55 a 83 c 80 g 32 t
ORIGIN
11 ArgGluAsnLeuArgIleAlaLeuArgTyr 20
|||||
202 CGAGAGAACTCGGATCGCGTCCGCTAC 231

seq_name: gb_pr2:HSHLABJ1 from: 1 to: 250

alignment_scores:
Quality: 49.00 Length: 10
Ratio: 4.900 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
US-08-653-294-26 x HSHLABJ1
..
Align seg 1/1 to: HSHLABJ1 from: 1 to: 250
11 ArgGluAsnLeuArgIleAlaLeuArgTyr 20
|||||
202 CGAGAGAACTCGGATCGCGTCCGCTAC 231

seq_name: gb_pr2:HSHLABJ1

seq_documentation_block:
LOCUS      HSHLABJ1          250 bp      DNA          PRI          22-MAR-1997
DEFINITION Human cell line THAI DCH009 MHC class I HLA-B gene (allele
ACCESSION  U90418
VERSION     U90418.1  GI:1905826
KEYWORDS
SEGMENT     1 of 2
SOURCE      human.
ORGANISM    Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 250)
AUTHORS     Chandanayingyong,D., Sirikong,M., Longta,K., Srinak,D.,
            Rungroung,E., Bejchandra,S., Juji,T. and Tokunaga,K.
TITLE       B15 alleles (B*1513)
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JOURNAL     Unpublished
REFERENCE   2 (bases 1 to 250)
AUTHORS     Chandanayingyong,D., Sirikong,M., Longta,K., Srinak,D.,
            Rungroung,E., Bejchandra,S., Juji,T. and Tokunaga,K.
TITLE       Direct Submission
JOURNAL     Submitted (23-FEB-1997) Transfusion Medicine, Faculty of Medicine,
            Siriraj Hospital, Mahidol University, Prannok Road, Bangkok 10700,
            Thailand
FEATURES    Location/Qualifiers
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               1..250
               /gene="HLA-B"
               /note="Allele: HLA-B*1513"
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               /product="MHC class I HLA-B"
BASE COUNT  55 a 83 c 80 g 32 t
ORIGIN
11 ArgGluAsnLeuArgIleAlaLeuArgTyr 20
|||||
202 CGAGAGAACTCGGATCGCGTCCGCTAC 231

seq_name: gb_pr4:AF022159

seq_documentation_block:
LOCUS      AF022159          255 bp      DNA          PRI          05-JAN-1999
DEFINITION Homo sapiens isolate 026 MHC class I antigen HLA-H (HLA-H)
            pseudogene, partial sequence.
ACCESSION  AF022159
VERSION     AF022159.1  GI:2655062
KEYWORDS    human.
SOURCE      Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 255)
AUTHORS     Grimsley,C., Mather,K.A. and Ober,C.
TITLE       HLA-H: a pseudogene with increased variation due to balancing
            selection at neighboring loci
JOURNAL     Mol. Biol. Evol. 15 (12), 1581-1588 (1998)
MEDLINE     99083426
REFERENCE   2 (bases 1 to 255)
AUTHORS     Grimsley,C., Mather,K.A. and Ober,C.
TITLE       Direct Submission
JOURNAL     Submitted (03-SEP-1997) Fred Hutchinson Cancer Research Center,
            1100 Fairview Ave. N., M374, Seattle, WA 98109, USA
FEATURES    Location/Qualifiers
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               /organism="Homo sapiens"
               /isolate="026"
               /db_xref="taxon:9606"
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               /note="African-American individual"
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               /gene="HLA-H"
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  Ratio: 4.900       Gaps: 0
  Percent Similarity: 100.000  Percent Identity: 100.000
alignment_block:
US-08-653-294-26 x AF022159 ..
Align seg 1/1 to: AF022159 from: 1 to: 255
11 ArgGluAsnLeuArgIleAlaLeuArgTyr 20
|||||
223 CGAGAGAACCTGCGGATCGCGCTCGCTAC 252
seq_name: gb_pr4:AF022160
seq_documentation_block:
LOCUS      AF022160      259 bp      DNA
DEFINITION Homo sapiens isolate 034 MHC class I antigen HLA-H (HLA-H)
Pseudogene, partial sequence.
ACCESSION  AF022160
VERSION    AF022160.1 GI:2655063
KEYWORDS   human.
ORGANISM   Homo sapiens
Eukaryota; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1 (bases 1 to 259)
AUTHORS   Grimsley,C., Mather,K.A. and Ober,C.
TITLE     HLA-H: a pseudogene with increased variation due to balancing
          selection at neighboring loci
JOURNAL   Mol. Biol. Evol. 15 (12), 1581-1588 (1998)
MEDLINE   99083426
REFERENCE  2 (bases 1 to 259)
AUTHORS   Grimsley,C., Mather,K.A. and Ober,C.
TITLE     Direct Submission
JOURNAL   Submitted (03-SEP-1997) Fred Hutchinson Cancer Research Center,
          1100 Fairview Ave. N., M374, Seattle, WA 98109, USA
FEATURES   Location/Qualifiers
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                /note="African-American individual"
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                /note="MHC class I antigen HLA-H"
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BASE COUNT      52 a   83 c   85 g   37 t   2 others
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  Ratio: 4.900       Gaps: 0
  Percent Similarity: 100.000  Percent Identity: 100.000
alignment_block:
US-08-653-294-26 x AF022160 ..
Align seg 1/1 to: AF022160 from: 1 to: 259
11 ArgGluAsnLeuArgIleAlaLeuArgTyr 20
|||||
223 CGAGAGAACCTGCGGATCGCGCTCGCTAC 252
seq_name: gb_pat:114590
seq_documentation_block:
LOCUS      114590      270 bp      DNA
DEFINITION Sequence 67 from patent US 5451512.
ACCESSION  114590
VERSION    114590.1 GI:997073
KEYWORDS   .
SOURCE     Unknown.
ORGANISM   Unknown.
REFERENCE  1 (bases 1 to 270)
AUTHORS   Apple,R.J., Bugawan,T.L. and Erlich,H.A.
TITLE     Methods and reagents for HLA class I A locus DNA typing
JOURNAL   Patent: US 5451512-A 67 19-SEP-1995;
          Location/Qualifiers
FEATURES   Location/Qualifiers
            source
              1..270
                /organism="unknown"
            BASE COUNT      55 a   84 c   95 g   36 t
            ORIGIN
alignment_scores:
  Quality: 49.00      Length: 10
  Ratio: 4.900       Gaps: 0
  Percent Similarity: 100.000  Percent Identity: 100.000
alignment_block:
US-08-653-294-26 x 114590 ..
Align seg 1/1 to: 114590 from: 1 to: 270
11 ArgGluAsnLeuArgIleAlaLeuArgTyr 20
|||||
222 CGAGAGAACCTGCGGATCGCGCTCGCTAC 251
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OM of: US-08-653-294-26 to: N_Geneseq_36:* out_format : pfs
 Date: Feb 8, 2000 7:31 PM
 About: Results were produced by the GenCore software, version 4.5,
 Copyright (c) 1993-2000 Compugen Ltd.

Command line parameters:
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Search information block:

Query: US-08-653-294-26
 Query length: 20
 Database: N_Geneseq_36:*
 Database sequences: 311585
 Database length: 125096042
 Search time (sec): 873.190000

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Sequence	Strd Orig	ZScore	Escore	Len	Documentation
N_Geneseq_36:Q29167	+	49.00	0.5731	270	HLA-Bw 52 exon 2 alpha-1 domain
N_Geneseq_36:Q01834	+	49.00	3.28	1086	Sequence encoding HLA-B*51 anti
N_Geneseq_36:Q01822	+	49.00	3.28	1086	Sequence encoding HLA-B*52 anti
N_Geneseq_36:Q05693	+	49.00	3.29	1089	HLA-B*51 gene for production of
N_Geneseq_36:Q05701	+	49.00	3.29	1089	HLA-B*52 gene for production of
N_Geneseq_36:Q12114	+	49.00	3.29	1089	HLA-B*53 exon. HLA-B*53 gene,
N_Geneseq_36:Q42608	+	47.00	1.43	285	Synthetic gene, Lqhiv encoding
N_Geneseq_36:V55837	+	46.00	131.37	981	Methanococcus jannaschii FEN-1
N_Geneseq_36:V52209	-	46.00	187.51	10011	Streptococcus pneumoniae gene
N_Geneseq_36:Q28344	+	44.00	35.25	1344	pBULI core sequence from Lact
N_Geneseq_36:Q07447	+	43.00	10.39	362	B. subtilis aprE target DNA. De
N_Geneseq_36:Q08745	-	43.00	131.24	1220	Coding region of the aprA gene
N_Geneseq_36:Q06587	-	43.00	119.38	1220	apra gene encoding subtilin.
N_Geneseq_36:Q07890	-	43.00	119.38	1220	Thermotable Bacillus subtilis
N_Geneseq_36:Q03336	-	43.00	117.37	61.61	Subtilisin gene. Mutant prok
N_Geneseq_36:Q071241	-	43.00	117.36	1500	Subtilisin gene from Bacillus
N_Geneseq_36:Q07058	-	43.00	117.36	1500	Bacillus subtilis subtilisin g
N_Geneseq_36:Q09042	-	43.00	117.36	1500	B. subtilis subtilisin gene. Re
N_Geneseq_36:Q60475	-	43.00	117.20	1524	Sequence of the apr [bsu] gene
N_Geneseq_36:Q25097	+	43.00	132.34	2760	Bacillus subtilis metalloprote
N_Geneseq_36:Q25826	+	42.00	138.90	118	DNA upstream from the 9th codon
N_Geneseq_36:Q38732	+	42.00	138.90	118	DNA sequence upstream of 9th co
N_Geneseq_36:Q19105	-	42.00	115.14	1344	Tobacco myb1 cDNA. Tobacco myb
N_Geneseq_36:Q78777	+	42.00	112.40	1779	Aquifex glucosamine:fructose-6
N_Geneseq_36:Q74362	+	42.00	99.41	6730	Staphylococcus aureus contig 3
N_Geneseq_36:Q60544	+	41.50	126.78	345	(Pro23-Lys37del)An37-Ile-134) t
N_Geneseq_36:Q60544	+	41.50	124.93	417	MetGDNF degenerate DNA sequence
N_Geneseq_36:Q07008	+	41.00	137.33	99	Immunoglobulin gene from n-(ABCDE) he
N_Geneseq_36:Q08669	+	41.00	123.14	423	Type II topoisomerase database
N_Geneseq_36:Q20619	+	41.00	113.89	96.21	Polynucleotide sequence from t
N_Geneseq_36:Q52187	-	41.00	85.02	20986	Streptococcus pneumoniae gene
N_Geneseq_36:Q13117	-	41.00	81.05	31517	Enterococcus faecalis genome
N_Geneseq_36:Q20057	+	40.50	122.63	1119	Enterococcus faecalis EF030 ge
N_Geneseq_36:Q20056	+	40.50	110.98	1242	Enterococcus faecalis gene EF0
N_Geneseq_36:Q13168	+	40.50	102.40	2991	Enterococcus faecalis genome d
N_Geneseq_36:Q13257	+	40.00	119.67	431	23S rRNA gene (partial). Nucle
N_Geneseq_36:Q07462	+	40.00	119.32	447	DNA encoding the first domain.
N_Geneseq_36:Q12871	+	40.00	109.97	1164	Polyhedrin-soluble LAG-3 fusio
N_Geneseq_36:Q75169	+	40.00	109.87	1176	Staphylococcus aureus contig 9
N_Geneseq_36:Q06756	+	40.00	107.70	1468	Human lymphocyte activation ge
N_Geneseq_36:Q63006	-	40.00	107.49	1500	Caenorhabditis elegans SEL-12

N_Geneseq_36:Q06755 + 40.00 106.69 242.35 1629 ! Human lymphocyte activation
 N_Geneseq_36:Q12869 + 40.00 105.33 288.25 1871 ! Lymphocyte Activation Gene-
 N_Geneseq_36:Q06754 + 40.00 103.41 369.04 2279 ! Human lymphocyte activation
 N_Geneseq_36:Q46543 - 40.00 102.97 390.46 2384 ! Drosophila SSRP composite s

seq_name: N_Geneseq_36:Q29167

seq_documentation_block:

ID Q29167 standard; DNA; 270 BP.
 AC Q29167;
 DT 03-MAR-1993 (first entry)
 DE HLA-Bw 52 exon 2 alpha-1 domain.
 KW Human leukocyte antigen; transgenic; germ cells; somatic cells;
 KW expression; ss.
 PN J04091731-A.
 PD 25-MAR-1992.
 PF 03-AUG-1990; 207329.
 PR 03-AUG-1990; JP-207329.
 PA (OLYU) OLYMPUS OPTICAL CO.
 DR WPI: 92-342893/42.
 PT Transgenic non-human mammalian HLA-Bw 52 gene - useful for
 PT analysis of expression of gene structure, and prodn. of
 PT mouse model of human disease
 PS Disclosure; Fig 1; 8pp; Japanese.
 CC The sequence shows the exon 2 alpha-1-domain of the human leukocyte
 CC antigen-Bw 52 gene. The complete gene may be introduced into non-
 CC human mammals, pref. rat or mouse, or their ancestors at the primary
 CC developmental biological step via transplantation into the zygote or
 CC embryo to generate transgenic non-human mammals incorporating the
 CC HLA-Bw 52 gene in both their germ cells and somatic cells. Transgenic
 CC non-human mammals contg. HLA-Bw 52 are useful for the analysis of
 CC expression of the gene, its structure, and prodn. of mouse models of
 CC human disease. See also Q29166-72.
 SQ Sequence 270 BP; 59 A; 88 C; 86 G; 37 T;

alignment_scores:

Quality: 49.00 Length: 10
 Ratio: 4.900 Gaps: 0
 Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:

US-08-653-294-26 x Q29167 ..

Align seg 1/1 to: Q29167 from: 1 to: 270

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 222 CGAGAGACCTGCGGATGCGCTCGCTAC 251

seq_name: N_Geneseq_36:Q01834

seq_documentation_block:

ID Q01834 standard; DNA; 1086 BP.
 AC Q01834;
 DT 19-MAR-1991 (first entry)
 DE Sequence encoding HLA-B*51 antigen.
 KW Probe: HLA class I DNA; immunogen; ss.
 OS Homo sapiens.
 PN EP35480-A.
 PD 14-FEB-1990.
 PF 10-AUG-1989.
 PR 11-AUG-1988; JP-200758.
 PA (OLYU) Olympus Optical Co., Ltd.
 PI Kano K, Takiguchi;
 DR WPI: 90-046289/07.
 DT New DNA for class 1 human leucocyte antigens and derived probes and
 PT transformed cells, useful for DNA typing, as immunogens etc.
 PS Claim 1: Page 11; 23pp; English.
 CC The HLA class I DNA can be used as a source of probes for use in DNA
 CC typing. Transformed cells, which are useful as immunogens, can be
 CC obtained by introducing these DNAs into eucaryotic cells.
 SQ Sequence 1086 BP; 224 A; 334 C; 356 G; 172 T;

alignment_scores:
 Quality: 49.00 Length: 10
 Ratio: 4.900 Gaps: 0
 Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:

US-08-653-294-26 x Q01834 ..

Align seg 1/1 to: Q01834 from: 1 to: 1086

11 ArgGluAsnLeuArgIleAlaLeuArgTyr 20

|||||
 294 CGAGAGAACCTGCGGATCGCGCTCGCTAC 323

seq_name: N_Geneseq_36:Q01822

seq_documentation_block:

ID Q01822 standard; DNA; 1086 BP.

AC Q01822;

DT 19-MAY-1991 (first entry)

DE Sequence encoding HLA-Bw52 antigen.

KW Probe: HLA class I DNA; immunogen; ss.

OS Homo sapiens.

FH Key Location/Qualifiers

FT cds 1..1086

FT /*tag= a

PN EP-354580-A.

PD 14-FEB-1990.

PF 10-AUG-1989.

PR 11-AUG-1988; JP-200758.

PA (OLYU) Olympos Optical Co., Ltd.

PI Kano K, Takiguchi;

DR WPI; 90-046289/07.

DR P-PSDB; R03142.

PT New DNA for class I human leucocyte antigens and derived probes and

PT transformed cells, useful for DNA typing, as immunogens etc.

PS Claim 2; pp11-12; 23pp; English.

CC The HLA class I DNA can be used as a source of probes for use in DNA

CC typing. Transformed cells, which are useful as immunogens, can be

CC obtained by introducing these DNAs into eucaryotic cells.

SQ Sequence 1086 BP; 223 A; 335 C; 358 G; 170 T;

alignment_scores:
 Quality: 49.00 Length: 10
 Ratio: 4.900 Gaps: 0
 Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:

US-08-653-294-26 x Q01822 ..

Align seg 1/1 to: Q01822 from: 1 to: 1086

11 ArgGluAsnLeuArgIleAlaLeuArgTyr 20

|||||
 294 CGAGAGAACCTGCGGATCGCGCTCGCTAC 323

seq_name: N_Geneseq_36:Q05693

seq_documentation_block:

ID Q05693 standard; DNA; 1089 BP.

AC Q05693;

DT 03-JAN-1991 (first entry)

DE HLA-B51 gene for production of monoclonal antibodies.

KW Allotype specific monoclonal anti-HLA antibodies; hybridomas;

KW transgenic animals; HLA-B51 gene; ss.

FH Key Location/Qualifiers

FT exon 1..73

FT /*tag= a

FT /number=1

FT 74..343

FT /*tag= b

FT /number=2

FT /*tag= b
 FT /number=2
 FT /note="alpha 1-domain"
 FT 344..619
 FT /*tag= c
 FT /number=3
 FT /note="alpha 2-domain"
 FT 620..895
 FT /*tag= d
 FT /number=4
 FT /note="alpha 3-domain"
 FT 896..1012
 FT /*tag= e
 FT /number=5
 FT 1013..1042
 FT /*tag= f
 FT /number=6
 FT 1043..1089
 FT /*tag= g
 FT /number=7

EP-383183-A.

22-AUG-1990.

07-FEB-1990; 102424.

08-FEB-1989; JP-029313.

(OLYU) OLYMPUS OPTICAL KK.

Takiguchi M;

WPI; 90-255479/34.

Allotype specific monoclonal anti- HLA antibodies prodn. - using

hybridomas derived from transgenic animals carrying HLA gene and

immunised with HLA antigen of different allotype

Disclosure; Fig 1 A-G; 20pp; English.

The human HLA-B51 gene was injected into fertilised mouse eggs and

then these introduced into the uterus of a pseudo pregnant mouse.

The young were tested to ensure incorporation of the gene into the

chromosome, and one of them mated 3 times with a normal male to

produce 16 young, seven of which carried the HLA-B51 gene.

The transgenic offspring were immunised with HLA antigen.

The spleen lymphocytes were fused with myeloma cells. Hybridomas

producing antibodies were selected.

See also Q05701.

Sequence 1089 BP; 224 A; 335 C; 357 G; 173 T;

alignment_scores:

Quality: 49.00 Length: 10

Ratio: 4.900 Gaps: 0

Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:

US-08-653-294-26 x Q05693 ..

Align seg 1/1 to: Q05693 from: 1 to: 1089

11 ArgGluAsnLeuArgIleAlaLeuArgTyr 20

|||||
 295 CGAGAGAACCTGCGGATCGCGCTCGCTAC 324

seq_name: N_Geneseq_36:Q05701

seq_documentation_block:

ID Q05701 standard; DNA; 1089 BP.

AC Q05701;

DT 03-JAN-1991 (first entry)

DE HLA-Bw52 gene for production of monoclonal antibodies.

KW Allotype specific monoclonal anti-HLA antibodies; hybridomas;

KW transgenic animals; HLA-Bw52 gene; ss.

FH Key Location/Qualifiers

FT exon 1..73

FT /*tag= a

FT /number=1

FT 74..343

FT /*tag= b

FT /number=2

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FT      exon      /note="alpha 1-domain"
FT      344..619
FT      /tag= c
FT      /number=3
FT      /note="alpha 2-domain"
FT      620..895
FT      /tag= d
FT      /number=4
FT      /note="alpha 3-domain"
FT      896..1012
FT      /tag= e
FT      /number=5
FT      1013..1042
FT      /tag= f
FT      /number=6
FT      1043..1089
FT      /tag= g
FT      /number=7
PN      EP-383183-A.
PD      22-AUG-1990.
PF      07-FEB-1990. 102424.
PR      08-FEB-1989. JP-029313.
PA      (OLYU ) OLYMPUS OPTICAL KK.
PI      Takiguchi M;
DR      WPI; 90-255479/34.
PT      Allotype specific monoclonal anti- HLA antibodies prodn. - using
PT      hybridomas derived from transgenic animals carrying HLA gene and
PT      immunised with HLA antigen of different allotype
PS      Disclosure: Fig 1 A-G; 20pp; English.
CC      The human HLA-Bw52 gene was introduced into mouse L cells and
CC      then these cells used to immunise one of the transgenic mice
CC      (See Q05693).
CC      The spleen lymphocytes were fused with myeloma cells (P3x63-Ag8.653).
CC      Hybridomas producing antibodies were selected.
SQ      Sequence 1089 BP; 223 A; 336 C; 359 G; 171 T;

alignment_scores:
  Quality: 49.00      Length: 10
  Ratio: 4.900      Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
US-08-653-294-26 x Q05701 ..
  Align seg 1/1 to: Q05701 from: 1 to: 1089

  11 ArgGluAsnLeuArgIleAlaLeuArgTyr 20
  |||||
  295 CGAGAGAACTGCGGATCGGCTCGCTAC 324

seq_name: N_Geneseq_36:Q12114

seq_documentation_block:
ID Q12114 standard; DNA: 1089 BP.
AC Q12114;
DT 29-AUG-1991 (first entry)
DE HLA-Bw53 exon.
KW Human leukocyte antigen; probe; major histocompatibility complex;
KW MHC; class I; ss.
OS Homo sapiens.
FH Key Location/Qualifiers
FT cds 1..1089 /tag= a
FT J03112487-A.
PN 14-MAY-1991.
PD 22-SEP-1989; 247697.
PF 22-SEP-1989; JP-247697.
PA (OLYU ) OLYMPUS OPTICAL KK.
DR WPI; 91-182991/25.
DR P-PSDB; R12463.
PT HLA-Bw53 gene, DNA probe and transformant cells - used for
PT immunisation, identifying specificity of antiserum etc.

```

```

PS Claim 1; Page 1; lpp; Japanese.
CC Probes comprising part of the sequence can be used to identify
CC Class I genes. The DNA can be expressed for immunisation of
CC animals and prodn. of monoclonal antibodies specific for the
CC HLA-Bw53 antigen. See also J03112485 and J03112486. 174 T;
SQ Sequence 1089 BP; 222 A; 337 C; 356 G; 174 T;

alignment_scores:
  Quality: 49.00      Length: 10
  Ratio: 4.900      Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
US-08-653-294-26 x Q12114 ..
  Align seg 1/1 to: Q12114 from: 1 to: 1089

  11 ArgGluAsnLeuArgIleAlaLeuArgTyr 20
  |||||
  295 CGAGAGAACTGCGGATCGGCTCGCTAC 324

seq_name: N_Geneseq_36:T42608

seq_documentation_block:
ID T42608 standard; DNA: 285 BP.
AC T42608;
DT 07-AUG-1997 (first entry)
DE Synthetic gene, lqhiv encoding scorpion neurotoxin.
KW neurotoxin; pest control; insect; acarid; nematode; lqhiv; lqhvi;
KW venom; Leirus quinquistriatus hebraeus; scorpion; lepidptera;
KW baculovirus; arthropod; ds.
OS Synthetic.
FH Key Location/Qualifiers
FT cds 70..287 /tag= a
FT /note= "no start codon given"
FT WO9636221-A2.
PN 21-NOV-1996.
PD 30-APR-1996; U06076.
PR 08-MAY-1995; US-435040.
PA (REGC ) UNIV CALIFORNIA.
PI Hammock BD, Herrmann R, Moskowitz H;
DR WPI; 97-011744/01.
DR P-PSDB; W06339.
PT Control of insects, acarids and nematodes - using novel scorpion
PT toxins or a combination of 2 or more insect toxins
PS Claim 1; Fig 1; 35pp; English.
CC A novel method for controlling pests selected from insects, acarids, and
CC nematodes, comprises treating the pests or their loci with at least two
CC different insect toxins, the source of the toxins being at least one
CC recombinant microbe, the toxins having non-overlapping binding sites at
CC an insect cellular membrane channel. The present sequence is a synthetic
CC gene for lqhiv toxin, derived from the venom of leirus quinquistriatus
CC hebraeus (Scorpion). lqhiv is the most potent lepidpteros toxin
CC isolated from scorpion venom to date, whilst lqhvi (W06340) has weak
CC mammal toxicity. In particular the insect toxin genes are expressed
CC by baculovirus vectors, as the baculoviruses infect only arthropods,
CC therefore pose little or no risk to humans, plants or the environment.
SQ Sequence 285 BP; 67 A; 92 C; 70 G; 56 T;

alignment_scores:
  Quality: 47.00      Length: 19
  Ratio: 2.938      Gaps: 0
Percent Similarity: 84.211 Percent Identity: 52.632

alignment_block:
US-08-653-294-26 x T42608 ..
  Align seg 1/1 to: T42608 from: 1 to: 285

  1 TyrArgLeuAlaIleArgLeuAsnGluArgGluAsnLeuArgIleAl 17

```


PA (MEIP) MEIJI MILK PROD CO LTD.
 PI Ito Y, Sasaki T, Sasaki Y;
 DR WPI: 92-316178/38.
 PT Plasmid pBULI derived from Lactobacillus delbrueckii strain - is
 PT lactic acid bacteria culture promotion vector and lactic acid
 PT bacteria-Escherichia coli shuttle vector
 PS Claim 4; Page 3; 34pp; Japanese.
 CC The sequence is a 1344 bp SmaI cleavage fragment of pBULI isolated
 CC from Lactobacillus delbrueckii subsp. bulgaricus M-878 (FERM
 CC BP-3758), a new strain of lactobacillus. The plasmid of its derivs.
 CC is a vector for promoting culture of microorganisms such as lactic
 CC bacteria, e.g. in the prodn. of yoghurt. It may also be used as a
 CC lactic acid bacteria/E. coli shuttle vector.
 SQ Sequence 1344 BP; 392 A; 295 C; 356 G; 301 T;

alignment_scores:
 Quality: 44.00 Length: 14
 Ratio: 3.385 Gaps: 0
 Percent Similarity: 92.857 Percent Identity: 57.143

alignment_block:
 US-08-653-294-26 x Q28344 ..

Align seg 1/1 to: Q28344 from: 1 to: 1344

2 ArgLeuAlaIleArgLeuAsnGluArgGluAsnLeuArg 15
 ||||| :|||:||||:||||:||||:||||:||||:||||:
 148 GCCTTAGAATACGATTGACGACAGGAAAGAGAAATTCCTG 189

seq_name: N_Geneseq_36:T07447

seq_documentation_block:
 ID T07447 standard; DNA; 362 BP.
 AC T07447;
 DT 27-APR-1996 (first entry)
 DE B. subtilis aprE target DNA.
 KW DNA; nucleic acid; analyte; lateral flow detection; PCR;
 KW polymerase chain reaction; capture probe; hybridisation; aprE gene;
 KW ss.
 OS Bacillus subtilis.
 PN W09527081-AI.
 PD 12-OCT-1995.
 PF 30-MAR-1995; U03773.
 PR 31-MAR-1994; US-221769.
 PA (DUPO) DU PONT DE NEMOURS & CO E I.
 PI Ebersole RC, Fitzpatrick-McElligott S, Hendrickson ER;
 PI Majarian WR, Payne MS, Rafalski JA;
 DR WPI: 95-358650/46.
 PT Detecting the presence of a nucleic acid analyte - by contact with a
 PT test strip having immobilised capture moieties.
 PS Example 1; Page 43; 82pp; English.
 CC A specific segment (T07447) of the B. subtilis aprE gene was amplified
 CC by PCR using primers 3 (T07448) and 4 (T07449) in the presence of
 CC biotin-14-dATP and digoxigenin-11-dUTP. Detection of the PCR product
 CC was performed using a lateral flow nucleic acid detection system in
 CC which anti-digoxigenin coupled to alkaline phosphatase was
 CC deposited on the 'application zone' of a nitrocellulose membrane,
 CC and avidin on the 'capture zone'. Amplified aprE target DNA was
 CC applied to the application zone and allowed to wick to the capture
 CC zone, where it was detected by colorimetry. In another method,
 CC target aprE DNA amplified in the presence of biotin-labeled dNTP
 CC was hybridised in solution with aprE DNA amplified in the presence
 CC of digoxigenin-labeled dNTP to demonstrate lateral flow detection of a
 CC bifunctional nucleic acid hybrid.
 SQ Sequence 362 BP; 99 A; 89 C; 82 G; 92 T;

alignment_scores:
 Quality: 43.00 Length: 17
 Ratio: 2.867 Gaps: 0
 Percent Similarity: 88.235 Percent Identity: 52.941

alignment_block:
 US-08-653-294-26 x T07447/rev ..

Align seg 1/1 to reverse of: T07447 from: 1 to: 362

3 LeuAlaIleArgLeuAsnGluArgGluAsnLeuArgGluAlaLeuArg 19
 :|||:||||:||||:||||:||||:||||:||||:||||:
 111 GTAGCTTGAGAGTGAAGACGGCGCTTATTATTGAGAAATGCCATAAG 62
 19 g 19
 61 G 61

seq_name: N_Geneseq_36:N80745

seq_documentation_block:

ID N80745 standard; DNA; 1220 BP.
 AC N80745;
 DT 14-SEP-1990 (first entry)
 DE Coding region of the aprA gene encoding subtilisin in Bacillus subtilis
 DE Bacillus subtilis strain Q8127 (trpC2 leuA8 sacU200); subtilisin;
 KW thermal stability; pH stability; specific activity;
 KW substrate specificity; detergent; ss.
 OS Bacillus subtilis strain Q8127 (trpC2 leuA8 sacU200).
 FH Key
 FT mat_peptide 1..1143
 FT Location/Qualifiers
 FT /*tag= a
 PN W08808033-A.
 PD 20-OCT-1988.
 PF 28-MAR-1988; U01038.
 PR 10-APR-1988; US-036872.
 PA (AMGE-) Amgen Inc.
 PI Zurovski MM, Stabinsky Y, Levitt M;
 DR WPI: 88-307568/43.
 DR P-PSDB: P80744.
 PT New subtilisin analogues -
 PT have aminoacid(s) present in calcium binding site replaced by
 PT negatively charged aminoacid(s)
 PS Example 2; Table 1, Pages 22-24; 60pp; English.
 CC Genomic DNA was isolated from cells of B. subtilis strain Q8127 (trpC2
 CC leuA8 sacU200). The coding region of the aprA gene was sequenced and
 CC the results of the sequence are given in n80745. The specific identity
 CC of the initial 5 codons of the leader region is attributable to the
 CC report of Stahl, et al., J. Bacteriol., 158, 411-418, (1984) and Wong,
 CC et al P.N.A.S., 81, 1184-1188 (1984). There exist codon sequence
 CC differences from Stahl, et al., at amino acid positions 84 and 85.
 CC Specifically, Stahl, et al., reports a codon GTT (coding for valine) at
 CC amino acid position 84 while the codon GTA (also coding for valine)
 CC appears in n80745. Stahl, et al., also reports a codon AGC (coding for
 CC serine) at amino acid position 85 as opposed to the codon GCG (coding for
 CC alanine) in n80745. The patent concerns a novel subtilisin analogue
 CC which has an amino acid sequence of a naturally occurring Bacillus
 CC subtilisin which has been modified by having: one or more of the amino
 CC acids present in a calcium binding site of the naturally occurring
 CC Bacillus subtilisin replaced by a negatively charged amino acid, and
 CC one or more of any Asn-Gly sequence of the naturally occurring Bacillus
 CC subtilisin deleted or replaced by a different amino acid. Pref. it is
 CC an analogue of subtilisin Carlsberg, subtilisin DY, subtilisin BPN', an
 CC aprA subtilisin of B. subtilis or subtilisin from B. mesentericus. The
 CC subtilisin analogues exhibit improved thermal and pH stability,
 CC increased specific activity and broad substrate specificity thereby
 CC increasing the detergent of detergent formulations contg. such
 CC analogues.
 SQ Sequence 1220 BP; 355 A; 281 C; 283 G; 301 T;

alignment_scores:
 Quality: 43.00 Length: 17
 Ratio: 2.867 Gaps: 0
 Percent Similarity: 88.235 Percent Identity: 52.941

alignment_block:
 US-08-653-294-26 x N80745/rev ..

Align seg 1/1 to reverse of: N80745 from: 1 to: 1220

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3 LeuAlaIleArgLeuAnGluArgGluAsnLeuArgIleAlaLeuAr 19
:::|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
381 GTAGCCTTGAGAGTGAAGCGCGCTTTAATTGAGAAATGCCATAAG 332
19 g 19
331 G 331

```

seq_name: N_Geneseq_36:Q06587

```

seq_documentation_block:
ID Q06587 standard; DNA; 1220 BP.
AC Q06587;
DT 18-FEB-1991 (first entry)
DE aprA gene encoding subtilisin.
KW Detergents; depilatory tanning; serology; ds.
OS Bacillus subtilis.
FH Key Location/Qualifiers
FT conflict 568..573
FT /label= a
FT /note= "Stahl et al. J.Bacteriol., 158, 411-418 (1984)"
FT cds 1..1143
FT /tag= b
FT mat_peptide 319..1143
FT /tag= c
PN EP-398539-A.
PD 22-NOV-1990.
PF 01-MAY-1990; 304715.
PR 17-MAY-1989; US-353124.
PA (AMGE-) AMGEN INC.
PI Zukowski MM, Narhi LO, Levitt M;
DR WPI: 90-350298/47.
DR P-PSDB; R07970.
PT Bacillus subtilin analogues - with improved pH thermal and oxidn.
PS Claim 20; Table 1; 39pp; English.
CC Modified analogues of subtilisin are useful in cleaning fabrics, and
CC have an improved resistance to oxidation, heat and pH extremes.
CC Analogues have one or more negative AAs present in the calcium
CC binding site (CBS) and may also be used in manufacture of protein
CC hydrolysates, and detection of incomplete Abs in serology.
SQ Sequence 1220 BP; 355 A; 283 C; 283 G; 301 T;

```

alignment_scores:
Quality: 43.00 Length: 17
Ratio: 2.867 Gaps: 0
Percent Similarity: 88.235 Percent Identity: 52.941

alignment_block:
US-08-653-294-26 x Q06587/rev ..

Align seg 1/1 to reverse of: Q06587 from: 1 to: 1220

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3 LeuAlaIleArgLeuAnGluArgGluAsnLeuArgIleAlaLeuAr 19
:::|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
381 GTAGCCTTGAGAGTGAAGCGCGCTTTAATTGAGAAATGCCATAAG 332
19 g 19
331 G 331

```

seq_name: N_Geneseq_36:N70890

```

seq_documentation_block:
ID N70890 standard; DNA; 1220 BP.
AC N70890;
DT 26-FEB-1991 (first entry)
DE Thermostable Bacillus subtilisin encoded by aprA gene.

```

```

KW aprA gene; subtilisin; thermostable enzyme; protease; surfactant; ds.
OS Bacillus subtilis.
FH Key Location/Qualifiers
FT cds 1..1143
FT /tag= a
FT mat_peptide 319..1143
FT /tag= b
FT /label= aprA gene
PN W08704461-A.
PD 30-JUL-1987.
PF 07-JAN-1987; U00027.
PR 15-JAN-1986; US-819241.
PA (AMGE-) AMGEN.
PI Stabinsky Y, Zukowski M;
DR WPI: 87-221262/31.
DR P-PSDB; P70555.
PT Thermally stable and pH stable subtilisin analogues - produced by
PT deleting or replacing at least one of the asparagine-glycine
PT sequences.
PS Disclosure: Table 1; 56pp; English.
CC Modified subtilisin may be used in detergent compositions, it has
CC an improved pH and heat stability. See also P70556.
SQ Sequence 1220 BP; 355 A; 283 C; 281 G; 301 T;

```

alignment_scores:
Quality: 43.00 Length: 17
Ratio: 2.867 Gaps: 0
Percent Similarity: 88.235 Percent Identity: 52.941

alignment_block:
US-08-653-294-26 x N70890/rev ..

Align seg 1/1 to reverse of: N70890 from: 1 to: 1220

```

3 LeuAlaIleArgLeuAnGluArgGluAsnLeuArgIleAlaLeuAr 19
:::|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
381 GTAGCCTTGAGAGTGAAGCGCGCTTTAATTGAGAAATGCCATAAG 332
19 g 19
331 G 331

```

seq_name: N_Geneseq_36:Q03536

```

seq_documentation_block:
ID Q03536 standard; DNA; 1499 BP.
AC Q03536;
DT 16-AUG-1990 (first entry)
DE Subtilisin gene.
KW Carboxyl hydrolase; subtilisin; neutral protease; ds.
OS Bacillus subtilis.
FH Key Location/Qualifiers
FT cds 137..1280
FT /tag= a
PN EP-357157-A.
PD 7-MAR-1990.
PF 22-JUN-1984; 202584.
PR 24-JUN-1983; US-507419.
PR 29-MAY-1984; US-614612.
PR 29-MAY-1984; US-614615.
PR 29-MAY-1984; US-614491.
PR 29-MAY-1984; US-614616.
PR 29-MAY-1984; US-614617.
PA (GETH) Genentech Inc.
PI Bott RR, Estell DA, Ferrari E, Henner DJ, Wells JA;
DR WPI: 90-068909/10.
DR P-PSDB; R03737.

```

```

PT Mutant prokaryotic carboxyl hydrolase enzymes -
PT obtd. by site-directed oligo-nucleotide mutagenesis, used in
PT food processing and cleaning industries.
PS Claim 16; Fig 7; 39pp; English.
CC Probe derived from subtilisin gene was used to isolate carboxyl

```

```

alignment_block:
US-08-653-294-26 x Q03536/rev ..

Align seg 1/1 to reverse of: Q03536 from: 1 to: 1499

3 LeuAlaIleArgLeuAsnGluArgGluAsnLeuArgIleAlaLeuAr 19
:::|||||:|||||:|||||:|||||:|||||:|||||:|||||:
517 GTAGCGTTGAGAGTGARGAGCCGCGCTTTAATTGAAATGCCATAAG 468

19 g 19
      |
467 G 467

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Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.

REFERENCE 1 (bases 1 to 360)
 AUTHORS Kohara,Y., Mitsuki,H., Nishigaki,A., Motohashi,T., Sugimoto,A. and Tabara,H.
 TITLE Toward an expression map of the C.elegans genome
 JOURNAL Unpublished (1994)
 COMMENT Contact: Yuji Kohara
 Gene Library Lab
 National Institute of Genetics
 Yata 1111, Mishima, Shizuoka 411, Japan
 Tel: 81-559-81-6854
 Fax: 81-559-81-6855
 Email: ykohara@lab.nig.ac.jp.

FEATURES
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 1..360
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 /strain="CB1489 him-8(e1489)"
 /db_xref="taxon:6239"
 /clone="yk196"
 /clone_lib="Yuji Kohara unpublished cDNA"
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 /tissue_type="whole animal"
 /dev_stage="varied"
 BASE COUNT 116 a 85 c 79 g 80 t
 ORIGIN

alignment_scores
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 Ratio: 3.667 Gaps: 0
 Percent Similarity: 88.235 Percent Identity: 70.588

alignment_block:
 US-08-653-294-26 x D35321 ..
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 2 ArgLeuAlaIleArgLeuAsnGluArgGluAsnLeuArgIleAlaLe 18
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 79 AGATCCCGGTTAAGTTGACGGAAGAAGATCCCAATCTGAGGATTATCT 128

18 u 18
 129 G 129

seq_name: gb_est1:D35579

seq_documentation_block:
 LOCUS D35579 360 bp mRNA EST 08-AUG-1994
 DEFINITION CELK022G9F Yuji Kohara unpublished cDNA Caenorhabditis elegans CDNA
 clone yk22g9 5', mRNA sequence.

ACCESSION D35579
 VERSION D35579.1 GI:527030
 KEYWORDS EST.
 SOURCE Caenorhabditis elegans.
 ORGANISM Caenorhabditis elegans.

Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditidae;
 Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
 REFERENCE 1 (bases 1 to 360)
 AUTHORS Kohara,Y., Mitsuki,H., Nishigaki,A., Motohashi,T., Sugimoto,A. and Tabara,H.

Toward an expression map of the C.elegans genome
 JOURNAL Unpublished (1994)
 COMMENT Contact: Yuji Kohara
 Gene Library Lab
 National Institute of Genetics
 Yata 1111, Mishima, Shizuoka 411, Japan
 Tel: 81-559-81-6854
 Fax: 81-559-81-6855
 Email: ykohara@lab.nig.ac.jp.

FEATURES
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 /organism="Caenorhabditis elegans"

/strain="CB1489 him-8(e1489)"
 /db_xref="taxon:6239"
 /clone="yk22g9"
 /clone_lib="Yuji Kohara unpublished cDNA"
 /sex="hermaphrodite, male"
 /tissue_type="whole animal"
 /dev_stage="varied"
 BASE COUNT 106 a 84 c 87 g 77 t 6 others
 ORIGIN

alignment_scores
 Quality: 55.00 Length: 17
 Ratio: 3.667 Gaps: 0
 Percent Similarity: 88.235 Percent Identity: 70.588

alignment_block:
 US-08-653-294-26 x D35579 ..
 Align seg 1/1 to: D35579 from: 1 to: 360
 2 ArgLeuAlaIleArgLeuAsnGluArgGluAsnLeuArgIleAlaLe 18
 ||| |||:::|||||:::|||||:::|||||:::|||||:::|||||::: ||
 24 AGATCCCGGTTAAGTTGACGGAAGAAGATCCCAATCTGAGGATTATCT 73

18 u 18
 74 G 74

seq_name: gb_est17:C69731

seq_documentation_block:
 LOCUS C69731 360 bp mRNA EST 23-SEP-1997
 DEFINITION C69731 Yuji Kohara unpublished cDNA Caenorhabditis elegans CDNA
 clone yk368h10 5', mRNA sequence.

ACCESSION C69731
 VERSION C69731.1 GI:2431087
 KEYWORDS EST.
 SOURCE Caenorhabditis elegans.
 ORGANISM Caenorhabditis elegans.

Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditidae;
 Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
 REFERENCE 1 (bases 1 to 360)
 AUTHORS Kohara,Y., Motohashi,T., Tabara,H., Watanabe,H., Sugimoto,A., Sano,M., Miyata,A. and Nishigaki,A.

Expression map of the C.elegans genome
 JOURNAL Unpublished (1996)
 COMMENT On Sep 12, 1996 this sequence version replaced gi:1316439.
 Contact: Yuji Kohara
 Gene Library Lab
 National Institute of Genetics
 Yata 1111, Mishima, Shizuoka 411, Japan
 Tel: 81-559-81-6854
 Fax: 81-559-81-6855
 Email: ykohara@lab.nig.ac.jp.

FEATURES
 source
 1..360
 /organism="Caenorhabditis elegans"
 /strain="CB1489 him-8(e1489)"
 /db_xref="taxon:6239"
 /clone="yk368h10"
 /clone_lib="Yuji Kohara unpublished cDNA"
 /sex="hermaphrodite, male"
 /tissue_type="whole animal"
 /dev_stage="varied"

BASE COUNT 109 a 90 c 85 g 76 t
 ORIGIN

alignment_scores
 Quality: 55.00 Length: 17
 Ratio: 3.667 Gaps: 0
 Percent Similarity: 88.235 Percent Identity: 70.588


```

/clone_lib="C:\IOWAG\DNA1"
/lab_host="E.coli XL2 Blue MRF"
/note="Vector: pBluescript II (SK-); Site:1: EcoRV; C.
parvum (IOWA isolate) genomic DNA was hydrodynamically
sheared to produce fragments having a tight size
distribution between 2-4 kb by Dr. Yvonne Thorstenson of
the Stanford DNA Sequencing and Technology Center
(http://sequence.
www.stanford.edu/group/techdev/shear.htm). The randomly
sheared gDNA was chromatographed on Sephacryl S-400 to
remove any small fragments and DNA eluting in the void
volume was subcloned into an EcoR V-digested, alkaline
phosphatase-treated pBluescript II (SK-) vector and
transformed into E. coli strain XL2 Blue MRF".
Recombinant clones from the first plating of the library
were selected for sequence analysis using T3 and T7
primers."
BASE COUNT      252 a 130 c 108 g 300 t 1 others
ORIGIN

alignment_scores:
    Quality: 51.00      Length: 20
    Ratio: 3.400      Gaps: 0
    Percent Similarity: 75.000      Percent Identity: 55.000

alignment_block:
US-08-653-294-26 x AQ855602/rev ..

Align seg 1/1 to reverse of: AQ855602 from: 1 to: 791

1 TyArgLeuAlaIleArgLeuAsnGluArgArgGluAsnLeuArgIleAl 17
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
674 TATAGGAATTCATCAGGGAARACCGAGGTCGATAATATGAGGATTCA 625

17 aLeuArgTyr 20
|||||:::
624 ACTCAGATT 615

seq_name: gb_est8:C03945

seq_documentation_block:
LOCUS C03945 232 bp mRNA EST 30-JUL-1996
DEFINITION C03945 Human heart cDNA (Ynakamura) Homo sapiens cDNA clone
3NHC2454, mRNA sequence.
ACCESSION C03945
VERSION C03945.1 GI:1467196
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS Tanaka,T., Ogiwara,A., Uchiyama,I., Takagi,T., Yazaki,Y. and
Nakamura,Y.
TITLE Construction of a normalized directionally cloned cDNA library fr
adult heart and analysis of 3040 clones by partial sequencing
JOURNAL Genomics 35 (1), 231-235 (1996)
MEDLINE 96299762
COMMENT On Oct 24, 1995 this sequence version replaced gi:1040105.
Contact: Yusuke Nakamura
Institute of Medical Science
University of Tokyo
4-6-1, Shirokanedai, Minato-ku, Tokyo 108, Japan
Tel: 81-3-5449-5372
Fax: 81-3-5449-5433
Email: yusuke@ims.u-tokyo.ac.jp.
Location/Qualifiers
1..232
/organism="Homo sapiens"
/db_xref="caxon:9606"
/clone="3NHC2454"
/clone_lib="Human heart cDNA (Ynakamura)"

FEATURES
Source

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/dev_stage="adult"
/Note="Organ: heart; normalized directionally cloned cDNA
from adult heart"

```

```

BASE COUNT      55 a      77 c      68 g      32 t
ORIGIN

```

```

alignment_scores:
  Quality:      49.00      Length:      10
  Ratio:        4.900      Gaps:        0
Percent Similarity: 100.000 Percent Identity: 100.000

```

```

alignment_block:

```

```

US-08-653-294-26 x C03945 ..

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```

Align seg 1/1 to: C03945 from: 1 to: 232

```

```

11 ArgGluAsnLeuArgIleAlaLeuArgTyr 20
|||||
40 CGAGAGAACCTGCGGATCGGCTCCGCTAC 69

```

```

seq_name: gb_est10:AA151891

```

```

seq_documentation_block:
LOCUS      AA151891      255 bp      mRNA      EST      10-DEC-1996
DEFINITION zool105.r1 Stratagene colon (#937204) Homo sapiens cDNA clone
IMAGE:566435 5' similar to gb:M15497.cds1 HLA CLASS I
HISTOCOMPATIBILITY ANTIGEN, A-24(A-9) A*2401 (HUMAN);, mRNA
sequence.

```

```

ACCESSION      AA151891
VERSION        AA151891.1 GI:1720754
KEYWORDS       EST.
SOURCE         human.
ORGANISM       Homo sapiens

```

```

REFERENCE      1 (bases 1 to 255)
AUTHORS        Hillier,L., Lennon,G., Becker,M., Bonaldo,M.F., Chiapelli,B.,
                Chissoe,S., Dietrich,N., Dubuque,T., Favellio,A., Gish,W.,
                Hawkins,M., Hultman,M., Kucaba,T., Lacy,M., Le,M., Le.N.,
                Mardis,E., Moore,B., Morris,M., Parsons,J., Prange,C., Rifkin,L.,
                Rohlfing,T., Schellenberg,K., Soares,M.B., Tan,F., Thierry-Mieg,J.,
                Trevisan,E., Underwood,K., Wohlmann,P., Waterston,R., Wilson,R.
                and Marra.M.

```

```

ORGANISM       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
                Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE      1 (bases 1 to 255)
AUTHORS        Hillier,L., Lennon,G., Becker,M., Bonaldo,M.F., Chiapelli,B.,
                Chissoe,S., Dietrich,N., Dubuque,T., Favellio,A., Gish,W.,
                Hawkins,M., Hultman,M., Kucaba,T., Lacy,M., Le,M., Le.N.,
                Mardis,E., Moore,B., Morris,M., Parsons,J., Prange,C., Rifkin,L.,
                Rohlfing,T., Schellenberg,K., Soares,M.B., Tan,F., Thierry-Mieg,J.,
                Trevisan,E., Underwood,K., Wohlmann,P., Waterston,R., Wilson,R.
                and Marra.M.

```

```

TITLE          Generation and analysis of 280,000 human expressed sequence tags
JOURNAL        Genome Res. 6 (9), 807-828 (1996)
MEDLINE        9704478
COMMENT        On May 8, 1995 this sequence version replaced gi:800234.
                Contact: Wilson RK
                Washington University School of Medicine
                4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
                Tel: 314 286 1800
                Fax: 314 286 1810

```

```

Email: est@watson.wustl.edu
This clone is available royalty-free through LNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Trace considered overall poor quality
Seq primer: -28M13 rev2 from Amersham
High quality sequence stop: 1.
Location/Qualifiers
1..255
/organism="Homo sapiens"
/db_xref="GDB:4590888"
/db_xref="taxon:9606"
/clone="IMAGE:566435"
/clone_lib="Stratagene colon (#937204)"
/lab_host="SOLR cells (kanamycin resistant)"
/Note="Organ: colon; Vector: pBluescript SK-; Site:1:
EcoRI; Site:2: XhoI; cloned unidirectionally. primer:
Oligo dt. T-84 colonic epithelial cell line. Average
insert size: 1.0 kb; Uni-ZAP XR Vector; -5' adaptor
sequence: 5' GAATTCGGCAGAG 3' -3' adaptor sequence: 5'
CTCGAGTATTTTTTTTTTTT 3'"

```

```

FEATURES
source

```

```

BASE COUNT      57 a      70 c      75 g      44 t      9 others
ORIGIN

```

```

alignment_scores:
  Quality:      49.00      Length:      10
  Ratio:        4.900      Gaps:        0
Percent Similarity: 100.000 Percent Identity: 100.000

```

```

alignment_block:

```

```

US-08-653-294-26 x AA151891 ..

```

```

Align seg 1/1 to: AA151891 from: 1 to: 255

```

```

11 ArgGluAsnLeuArgIleAlaLeuArgTyr 20
|||||
77 CGAGAGAACCTGCGGATCGGCTCCGCTAC 106

```

```

seq_name: gb_est11:AA263158

```

```

seq_documentation_block:
LOCUS      AA263158      283 bp      mRNA      EST      02-JUL-1998
DEFINITION PHY0534 KGI-a Lambda zap Express cDNA library Homo sapiens CDNA 5',
mRNA sequence.

```

```

ACCESSION      AA263158
VERSION        AA263158.1 GI:1898964
KEYWORDS       EST.
SOURCE         human.
ORGANISM       Homo sapiens
                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
                Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE      1 (bases 1 to 283)
AUTHORS        Claudio,J.O., Liew,C.C., Dempsey,A.A., Cukerman,E., Stewart,A.K.,
                Na.E., Atkins,H.I., Iscoe,N.N. and Hawley,R.G.

```

```

TITLE          Identification of sequence-tagged transcripts differentially
                expressed within the human hematopoietic hierarchy
JOURNAL        Genomics 50 (1), 44-52 (1998)
MEDLINE        98292493
COMMENT        On May 5, 1995 this sequence version replaced gi:797810.
                Contact: Hawley RG
                Oncology Research Laboratories
                The Toronto Hospital
                CRCS-424, 67 College St., Toronto, Ontario M5G 2M1, Canada
                Tel: 416 3403834
                Fax: 416 3403453
                Email: r.hawley@utoronto.ca
                Similar to M58636 MHC class I HLA-Bw gene. Clone was randomly
                picked from KGIa primary library.
                Seq primer: 5' GAAATTAACCTCCTCAAGGG 3'
                High quality sequence stop: 283.
                Location/Qualifiers
                1..283
                /organism="Homo sapiens"
                /db_xref="taxon:9606"
                /clone_lib="KGI-a Lambda Zap Express cDNA library"
                /cell_type="promyeloblast"
                /cell_line="KGI-a"
                /note="Vector: Lambda Zap Express (Stratagene); Site:1:
                EcoRI; Site:2: XhoI; Unidirectional cloning sites:
                EcoRI-XhoI. mRNA was purified from KGI-a cell line, cDNA
                was synthesized using an XhoI-Oligodt linker primer. EcoRI
                adaptors were ligated, followed by digestion with XhoI for
                directional cloning into predigested Lambda Zap Express"

```

```

FEATURES
source

```

```

BASE COUNT      64 a      91 c      88 g      40 t
ORIGIN

```

```

alignment_scores:
  Quality:      49.00      Length:      10
  Ratio:        4.900      Gaps:        0
Percent Similarity: 100.000 Percent Identity: 100.000

```

```

alignment_block:

```

```

US-08-653-294-26 x AA263158
Align seg 1/1 to: AA263158 from: 1 to: 283

11 ArgGluAsnLeuArgIleAlaLeuArgTyr 20
|||||
120 CGAGAGAACCTGCGGATCGCGCTCGCTAC 149

seq_name: gb_est6:D82221

seq_documentation_block:
LOCUS D82221 375 bp mRNA EST 09-FEB-1996
DEFINITION HUMHBC4626 Human pancreatic islet Homo sapiens cDNA similar to
HLA-B mRNA sequence.
ACCESSION D82221
VERSION D82221.1 GI:1183739
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 375)
AUTHORS Takeda, J.
JOURNAL Human pancreatic islet ESTs
COMMENT On Apr 14, 1993 this sequence version replaced gi:785255.
Contact: Jun Takeda
Institute for Molecular and Cellular Regulation, Gunma University
3-39-15 Showa-machi, Maebashi Gunma 371, Japan
Tel: 272-20-8856
Fax: 272-20-8896
Email: jtakeda@sb.gunma-u.ac.jp.
Location/Qualifiers
1. 375
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="Human pancreatic islet"
/notes="Vector: Lambda ZAPII; Site.1: Eco RI; Site.2: Xho
I; mRNA was prepared from normal adult human islets. cDNA
was directionally synthesized from the Xho I in the vector
to the EcoRI site. cDNA was size fractionated to remove
sequences <1000 bp in size."
BASE COUNT 75 a 124 c 118 g 55 t 3 others
ORIGIN

alignment_scores:
Quality: 49.00 Length: 10
Ratio: 4.900 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
US-08-653-294-26 x D82221
Align seg 1/1 to: D82221 from: 1 to: 375

11 ArgGluAsnLeuArgIleAlaLeuArgTyr 20
|||||
306 CGAGAGAACCTGCGGATCGCGCTCGCTAC 335

seq_name: gb_est26:AI359260

seq_documentation_block:
LOCUS AI359260 618 bp mRNA EST 15-FEB-1999
DEFINITION qy27b07.x1 NCI_CGAP_Brn23 Homo sapiens cDNA clone IMAGE:2013205 3'
similar to gb:D32129 HLA CLASS I HISTOCOMPATIBILITY ANTIGEN,
AW-66(A-10) A*6601 ALPHA (HUMAN);, mRNA sequence.
ACCESSION AI359260
VERSION AI359260.1 GI:4110881
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;

US-08-653-294-26 x AA263158
Align seg 1/1 to: AA263158 from: 1 to: 283

11 ArgGluAsnLeuArgIleAlaLeuArgTyr 20
|||||
120 CGAGAGAACCTGCGGATCGCGCTCGCTAC 149

seq_name: gb_est6:D82221

seq_documentation_block:
LOCUS D82221 375 bp mRNA EST 09-FEB-1996
DEFINITION HUMHBC4626 Human pancreatic islet Homo sapiens cDNA similar to
HLA-B mRNA sequence.
ACCESSION D82221
VERSION D82221.1 GI:1183739
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 375)
AUTHORS Takeda, J.
JOURNAL Human pancreatic islet ESTs
COMMENT On Apr 14, 1993 this sequence version replaced gi:785255.
Contact: Jun Takeda
Institute for Molecular and Cellular Regulation, Gunma University
3-39-15 Showa-machi, Maebashi Gunma 371, Japan
Tel: 272-20-8856
Fax: 272-20-8896
Email: jtakeda@sb.gunma-u.ac.jp.
Location/Qualifiers
1. 375
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="Human pancreatic islet"
/notes="Vector: Lambda ZAPII; Site.1: Eco RI; Site.2: Xho
I; mRNA was prepared from normal adult human islets. cDNA
was directionally synthesized from the Xho I in the vector
to the EcoRI site. cDNA was size fractionated to remove
sequences <1000 bp in size."
BASE COUNT 75 a 124 c 118 g 55 t 3 others
ORIGIN

alignment_scores:
Quality: 49.00 Length: 10
Ratio: 4.900 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
US-08-653-294-26 x D82221
Align seg 1/1 to: D82221 from: 1 to: 375

11 ArgGluAsnLeuArgIleAlaLeuArgTyr 20
|||||
306 CGAGAGAACCTGCGGATCGCGCTCGCTAC 335

seq_name: gb_est26:AI359260

seq_documentation_block:
LOCUS AI359260 618 bp mRNA EST 15-FEB-1999
DEFINITION qy27b07.x1 NCI_CGAP_Brn23 Homo sapiens cDNA clone IMAGE:2013205 3'
similar to gb:D32129 HLA CLASS I HISTOCOMPATIBILITY ANTIGEN,
AW-66(A-10) A*6601 ALPHA (HUMAN);, mRNA sequence.
ACCESSION AI359260
VERSION AI359260.1 GI:4110881
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;

Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute / National Institute of Neurological
Disorders and Stroke, Brain Tumor Genome Anatomy Project
(CGAP/BTGP), Tumor Gene Index
Unpublished (1998)
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D.,
Ph.D.
cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
Bonaldo, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www.bio.llnl.gov/bbrp/image/image.html

Insert Length: 691 Std Error: 0.00
Seq primer: -40UP from Gbco
High quality sequence stop: 458.
Location/Qualifiers
1. 618
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_image="IMAGE:2013205"
/clone_lib="NCI_CGAP_Brn23"
/tissue_type="glioblastoma (pooled)"
/lab_host="DH10B"
/notes="Organ: brain; Vector: pT7T3D-Pac (Pharmacia) with a
modified polylinker; Site.1: Not I; Site.2: Eco RI; 1st
strand cDNA was primed with a Not I - oligo(dt) primer [5',
TGTTCACATCTGAATGGAGCGGCGCATATCTTTTTTTTTTTTTTTTTTTT
T 3']; double-stranded cDNA was ligated to Eco RI
adaptors (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of the modified pT7T3 vector.
Library is normalized, and was constructed by Bento
Soares and M.Fatima Bonaldo."
BASE COUNT 128 a 171 c 182 g 137 t
ORIGIN

alignment_scores:
Quality: 49.00 Length: 10
Ratio: 4.900 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
US-08-653-294-26 x AI359260/rev
Align seg 1/1 to reverse of: AI359260 from: 1 to: 618

11 ArgGluAsnLeuArgIleAlaLeuArgTyr 20
|||||
319 CGAGAGAACCTGCGGATCGCGCTCGCTAC 290

seq_name: gb_gss15:AQ649574

seq_documentation_block:
LOCUS AQ649574 698 bp DNA GSS 22-JUN-1999
DEFINITION Sheared DNA-28D9.TF Sheared DNA Trypanosoma brucei genomic clone
Sheared DNA-28D9, genomic survey sequence.
ACCESSION AQ649574
VERSION AQ649574.1 GI:5142760
KEYWORDS GSS.
SOURCE Trypanosoma brucei.
ORGANISM Trypanosoma brucei.
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;

REFERENCE 1 (bases 1 to 698)
AUTHORS El-Sayed, N., Zhao, S., Zhao, H., Gill, S., Suh, E., Malek, J., Fujii, C.,

```


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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: February 8, 2000, 04:05:43 ; Search time 133.56 seconds
(without alignments)
3.547 Million cell updates/sec

Title: US-08-653-294-27

Perfect score: 102

Sequence: 1 YGRNRLSERRESLRLRGY 20

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 188963 seqs, 23686106 residues

Total number of hits satisfying chosen parameters: 188963

Minimum DB seq length: 0

Maximum DB seq length: 1000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : A_Geneseq_36.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	102	100.0	20	1 R92913	HLA-B*7 CTL modul
2	102	100.0	20	1 R95415	HLA-B*7.84-75-84 Pa
3	102	100.0	20	1 W33790	Peptide B*7.84-75/7
4	102	100.0	20	1 W33797	Peptide B*7.84-75/7
5	51	50.0	10	1 R41209	Peptide fragment o
6	51	50.0	10	1 R83061	HLA-B*7 CTL modul
7	51	50.0	10	1 W07515	T-cell modulating
8	51	50.0	10	1 W33786	Peptide B*7.75-84 t
9	51	50.0	10	1 W33796	Peptide B*7.75-84 t
10	51	50.0	25	1 R41207	Peptide fragment o
11	51	50.0	25	1 R83073	HLA-Bw62 CTL modul
12	51	50.0	25	1 R95431	HLA-B*7.60-84. Comp
13	51	50.0	25	1 R95419	HLA-Bw62.60-84. Co
14	51	50.0	362	1 R12484	HLA-B35 antigen. H
15	47.5	46.6	605	1 W62838	Glycine max antiimi
16	46	45.1	509	1 W26792	Mouse TIE-2 recept
17	44	43.1	20	1 R92910	HLA-B*2702 CTL modu
18	44	43.1	20	1 W33793	Peptide B*2702.84-7
19	44	43.1	25	1 R41206	Peptide fragment o
20	44	43.1	25	1 R83072	HLA-Bw46 CTL modul
21	44	43.1	25	1 R95418	HLA-Bw46.60-84. Co
22	44	43.1	366	1 R12465	HLA-C exon Cb-1. H
23	44	43.1	366	1 R12466	HLA-C exon Cb-2. H
24	44	43.1	366	1 Y07033	Breast cancer asso
25	43	42.2	430	1 R20642	Glyphosate oxidore
26	43	42.2	431	1 R22262	Glyphosate oxidore
27	42	41.2	20	1 R92909	HLA-B*2702 CTL modu
28	42	41.2	20	1 R92908	HLA-B*2702 CTL modu
29	42	41.2	20	1 W33791	Peptide B*2702.84-7
30	42	41.2	20	1 W33792	Peptide B*2702.84-7
31	42	41.2	2233	1 W48711	HP1V-3 JS isolate
32	42	41.2	2233	1 W48712	HP1V-3 FRh1 cp45 v
33	42	41.2	2233	1 W48713	HP1V-3 vero cp45 v
34	41	40.2	217	1 W46424	Human macrophage s

35	41	40.2	219	1 W98326	H. pylori GHPO 144
36	41	40.2	274	1 P80911	Consensus sequence
37	41	40.2	705	1 R66597	Human L5/3 tumour
38	41	40.2	705	1 R66598	Human L5/3 tumour
39	41	40.2	705	1 W14266	Human L5/3 partial
40	41	40.2	705	1 W14267	Human L5/3 partial
41	41	40.2	710	1 W07691	Macrophage stimula
42	41	40.2	711	1 R66602	Human L5/3 tumour
43	41	40.2	711	1 W07692	Macrophage stimula
44	41	40.2	711	1 W14270	Human growth facto
45	41	40.2	711	1 W82789	Human MSP protein.

ALIGNMENTS

RESULT 1

R92913
ID R92913 standard; peptide; 20 AA.
AC R92913;
DT 16-MAY-1996 (first entry)
DE HLA-B*7 CTL modulating peptide (B*7.84-75/75-84)
KW Cytotoxic T lymphocyte; CTL; major histocompatibility complex; MHC;
KW immunosuppressant; graft versus host disorder; transplantation; therapy;
KW class I MHC; HLA-B*7.
OS Synthetic.
PN W09526979-A1.
PD 12-OCT-1995.
PF 05-APR-1995; U04349.
PR 05-APR-1994; US-222851.
PA (STRD) UNIV LELAND STANFORD JUNIOR.
PI Clayberger C, Krensky AM, Parham P;
DR WPI: 95-358582/46.
PT Extension of acceptance period of transplants from MHC unmatched
PT donor hosts - using Class I B*75-84 MHC antigen of the recipient
PT host
PS Example 15; Page 36; 80pp; English.
CC R83061-R83085, R83090-R83096 and R92907-R92913 represent fragments of
CC class I major histocompatibility complex (MHC) antigens. This sequence
CC is an inverted dimer of residues 75-84 of the alpha-1 domain of the class
CC I MHC HLA-B*7. These sequences can be used to extend the period of
CC acceptance by a recipient of a transplant from an MHC unmatched donor.
CC The peptides are administered to a patient in conjunction with a
CC subtherapeutic amount of an immunosuppressant. This is administered to
CC the patient for a limited period of time (compared to the lifetime
CC administration for current treatments). The peptides particularly
CC modulate (or inhibit) the activity of the cytotoxic T lymphocytes (CTLs)
CC of the patient.
SQ Sequence 20 AA;

Query Match 100.0%; Score 102; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. NO. 1.3e-09;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YGRNRLSERRESLRLRGY 20
|||||
DB 1 YGRNRLSERRESLRLRGY 20

RESULT 2

R95415
ID R95415 standard; peptide; 20 AA.
AC R95415;
DT 12-NOV-1996 (first entry)
DE HLA-B*7.84-75-84 Palindrome.
KW HLA; p74; alpha1-helix; human-leucocyte-associated antigen; inhibitor;
KW T-cell lysate; membrane protein; mammal; heat shock protein; Hsc70; APC;
KW B cell; calcium influx; cytotoxic T lymphocyte; CTL; differentiation;
KW cytolysis; antigen presenting cell.
OS Synthetic.
PN W09513288-A1.
PD 18-MAY-1995.

PF 10-NOV-1994; U12985.
 PR 10-NOV-1993; US-150493.
 PA (STRD) UNIV LELAND STANFORD JUNIOR.
 PI Clayberger C, Krensky AM;
 DR WPI: 95-194027/25.
 PT Compens. comprising lymphoid surface membrane proteins - which may
 PT inhibit cytolytic activity and differentiation of CTLs.
 PS Example; Page 18; 29pp; English.
 CC R95413, and R95415-R95431 represent palindromes and fragments of
 CC human-leucocyte-associated antigens. This sequence represents the
 CC HLA-B*78-75/75-84 palindrome. These sequences can be used to isolate
 CC the protein p74 from a T-cell lysate. p74 is a T-cell surface membrane
 CC protein associated with T-cell activation in mammalian T-cells, and is
 CC also immunologically cross reactive with the heat shock protein Hsc70.
 CC p74 is found in a limited number of cell types, but is particularly
 CC expressed on B and T cells. p74 can be isolated by lysis of a suitable
 CC cell with an amphoteric detergent, and then passed through an affinity
 CC column containing a covalently bound HLA-B2702 palindromic peptide.
 CC Compositions comprising the extracellular fragment of p74 combined with
 CC HLA-B2702.60-84 (see R95416), induces calcium influx, and inhibits
 CC cytotoxic T lymphocyte (CTL) differentiation or cytotoxicity. Candidate
 CC compounds can be screened for their effect on the cytolytic activity of
 CC T-cells, by combining them with the extracellular portion of p74 and
 CC determining the amount of binding between the candidate compound and p74.
 CC Modulation of CTL activity can be inhibited in a cellular composition
 CC containing T-cells and antigen presenting cells (APCs), by adding to the
 CC mix the extracellular portion of p74, in an amount sufficient to compete
 CC with p74 for the binding of the p74 ligand.
 CC Sequence 20 AA;

Query Match 100.0%; Score 102; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.3e-09;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YGRNLRSERRESRLNRYG 20
 DB 1 YGRNLRSERRESRLNRYG 20
 |||||

RESULT 3

ID W33790 standard; peptide; 20 AA.
 AC W33790;
 DT 19-JUN-1998 (first entry)
 DE Peptide B7.84-75/75-84 tested for immunomodulating activity.
 KW Immunomodulating dimer; immunosuppressant drug; CTL activation;
 KW transplantation; autoimmune disease; Class I HLA-B alpha-1 domain;
 KW rejection.
 OS Synthetic.
 OS Homo sapiens.
 PN WO9744351-A1.
 PD 27-NOV-1997.
 PF 22-MAY-1997; U08689.
 PR 24-MAY-1996; US-653294.
 PA (STRD) UNIV LELAND STANFORD JUNIOR.
 PI Beulow R, Clayberger C, Krensky AM;
 DR WPI: 98-086530/08.
 PT New immunomodulating dimer peptide(s) - based on a Class I HLA-B
 PT alpha-1 domain, used for preventing rejection of transplants or
 PT treating autoimmune diseases
 PS Example 1; Page 19; 41pp; English.
 CC Peptides W33784-98 and W33778-9 were assayed for their immunomodulating
 CC activity. A peptide-type compound or variant is claimed which has
 CC immunomodulating activity, including the N-terminal acylated and/or
 CC C-terminal amidated or esterified forms of up to 60 amino acids, where
 CC the peptide-type compound comprises the formula: A-B, where A, B =
 CC (R aa76-77L) (aa79-84) or (aa84-79) (Laa77-76R); aa76 = E or V; aa77 =
 CC D, S or N; aa79 = R or G; aa80 = I or N; aa81, aa84 = a hydrophobic or
 CC small amino acid; aa82 = R or L; aa83 = G or R; and aa represents amino
 CC acid. The sequence in the brackets may optionally be absent or truncated
 CC at any peptide type bond within the brackets. The compounds comprise
 CC amino acid sequences related to a Class I HLA-B alpha-1 domain (positions
 CC 79-84). They can be used to inhibit cytotoxic T-lymphocytes (CTL) from
 CC undesirably attacking cells in a host or in vitro. They can also be
 CC used in combination with antigenic peptides or proteins of interest to
 CC activate CTLs. They can also inhibit the proliferation of T cells in
 CC response to anti-CD3. The peptide can be used for preventing rejection
 CC of transplants or for treating autoimmune diseases, e.g. diabetes,
 CC rheumatoid arthritis and lupus erythematosus. The products can also be
 CC used for detection and diagnosis.

CC 79-84). They can be used to inhibit cytotoxic T-lymphocytes (CTL) from
 CC undesirably attacking cells in a host or in vitro. They can also be
 CC used in combination with antigenic peptides or proteins of interest to
 CC activate CTLs. They can also inhibit the proliferation of T cells in
 CC response to anti-CD3. The peptide can be used for preventing rejection
 CC of transplants or for treating autoimmune diseases, e.g. diabetes,
 CC rheumatoid arthritis and lupus erythematosus. The products can also be
 CC used for detection and diagnosis.

SQ Sequence 20 AA;

Query Match 100.0%; Score 102; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.3e-09;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YGRNLRSERRESRLNRYG 20
 DB 1 YGRNLRSERRESRLNRYG 20
 |||||

RESULT 4

ID W33797 standard; peptide; 20 AA.
 AC W33797;
 DT 19-JUN-1998 (first entry)
 DE Peptide B7.84-75/75-84 tested for immunomodulating activity.
 KW Immunomodulating dimer; immunosuppressant drug; CTL activation;
 KW transplantation; autoimmune disease; Class I HLA-B alpha-1 domain;
 KW rejection.
 OS Synthetic.
 OS Homo sapiens.
 PN WO9744351-A1.
 PD 27-NOV-1997.
 PF 22-MAY-1997; U08689.
 PR 24-MAY-1996; US-653294.
 PA (STRD) UNIV LELAND STANFORD JUNIOR.
 PI Beulow R, Clayberger C, Krensky AM;
 DR WPI: 98-086530/08.
 PT New immunomodulating dimer peptide(s) - based on a Class I HLA-B
 PT alpha-1 domain, used for preventing rejection of transplants or
 PT treating autoimmune diseases
 PS Example 1; Page 19; 41pp; English.
 CC Peptides W33784-98 and W33778-9 were assayed for their immunomodulating
 CC activity. A peptide-type compound or variant is claimed which has
 CC immunomodulating activity, including the N-terminal acylated and/or
 CC C-terminal amidated or esterified forms of up to 60 amino acids, where
 CC the peptide-type compound comprises the formula: A-B, where A, B =
 CC (R aa76-77L) (aa79-84) or (aa84-79) (Laa77-76R); aa76 = E or V; aa77 =
 CC D, S or N; aa79 = R or G; aa80 = I or N; aa81, aa84 = a hydrophobic or
 CC small amino acid; aa82 = R or L; aa83 = G or R; and aa represents amino
 CC acid. The sequence in the brackets may optionally be absent or truncated
 CC at any peptide type bond within the brackets. The compounds comprise
 CC amino acid sequences related to a Class I HLA-B alpha-1 domain (positions
 CC 79-84). They can be used to inhibit cytotoxic T-lymphocytes (CTL) from
 CC undesirably attacking cells in a host or in vitro. They can also be
 CC used in combination with antigenic peptides or proteins of interest to
 CC activate CTLs. They can also inhibit the proliferation of T cells in
 CC response to anti-CD3. The peptide can be used for preventing rejection
 CC of transplants or for treating autoimmune diseases, e.g. diabetes,
 CC rheumatoid arthritis and lupus erythematosus. The products can also be
 CC used for detection and diagnosis.

SQ Sequence 20 AA;

Query Match 100.0%; Score 102; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.3e-09;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YGRNLRSERRESRLNRYG 20
 DB 1 YGRNLRSERRESRLNRYG 20
 |||||

RESULT 5
R41209
ID R41209 standard; peptide; 10 AA.
AC R41209, 1994 (first entry)
DE Peptide fragment of Class I HLA peptide.
KW Human leukocyte antigen; HLA; peptide; transplantation; neoplasia;
KW parasitic disease; cytotoxic T lymphocyte; modulation.
OS Synthetic.
PN W09317699-A.
PD 16-SEP-1993.
PF 25-FEB-1993; U01758.
PR 02-MAR-1992; US-844716.
PA (STRD) UNIV LELAND STANFORD JUNIOR.
PI Clayberger CA, Krensky AM;
DR WPI; 93-303134/38.
PT New peptides(s) based on Class I HLA antigen domains - used for
PT modulating cytotoxic T-lymphocyte activity towards targets
PS Claim 11; Page 54; 61pp; English.
CC The peptide is used to modulate cytotoxic T-lymphocyte (CTL)
CC activity, either by inhibition of stimulation. It can be used
CC for inhibiting CTL toxicity in transplantations, for inducing CTL
CC activity in parasitic diseases and neoplasia and in studies on viral
CC infection. The peptide can also be used for identifying CTLs which
CC bind to it and removing subsets of CTLs from a T-cell composition.
CC This peptide sequence is more commonly found within larger peptide
CC compounds of not more than 30 amino acids in length.
SQ Sequence 10 AA;

Query Match 50.0%; Score 51; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.043;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 RESLNRLRGY 20
DB 1 RESLNRLRGY 10
|||||

RESULT 7
W07515
ID W07515 standard; peptide; 10 AA.
AC W07515;
DE 04-AUG-1997 (first entry)
DE T-cell modulating peptide #4.
KW T-cell modulator; autoimmune disease; tissue destruction; alpha-domain;
KW mammal; major histocompatibility complex; MHC class I; antigen; perforin;
KW insulin-dependent diabetes mellitus; multiple sclerosis; inflammation;
KW rheumatoid arthritis; psoriasis; pemphigus vulgaris; Sjogren's disease;
KW thyroid disease; Hashimoto's thyroiditis; myasthenia gravis; granzyme;
KW autologous target cell; cytokine release; T cell activation; therapy.
OS Synthetic.
PN W09635443-A1.
PD 14-NOV-1996.
PF 05-APR-1996; U04710.
PR 12-MAY-1995; US-440504.
PA (SANG-) SANGSTAT MEDICAL CORP.
PI Buelow R;
DR WPI; 96-518410/51.
PT Treatment of auto-immune disease by admin. of peptide(s) corresp. to
PT major histocompatibility complex antigens - esp. for delaying onset
PT of clinical symptoms of insulin dependent diabetes by modulating T
PT cell mediated attack on target cells
PS Claim 7; Page 20; 24pp; English.
CC W07512-W07518 represent T-cell modulating peptides that can be used in
CC the method of the invention. These sequences are based on a portion of
CC the generic peptide corresponding to residues 70-91 of the alpha-domain
CC of the major histocompatibility complex (MHC) class I antigen (see
CC W07510). The method is for affecting the course of an autoimmune disease
CC involving T-cell mediated destruction of tissue in mammals. These
CC peptides are used especially to treat insulin-dependent diabetes
CC mellitus, preferably being administered during the pre-clinical stage to
CC delay onset of the disease. Other diseases that can be treated are
CC multiple sclerosis, rheumatoid arthritis, psoriasis, pemphigus vulgaris,
CC Sjogren's disease, thyroid disease, Hashimoto's thyroiditis, myasthenia
CC gravis, etc. The peptides modulate T-cell mediated attack on autologous
CC target cells, and may also reduce inflammation, swelling, and release of
CC cytokines, perforins, granzymes etc. associated with T cell activation.
SQ Sequence 10 AA;

Query Match 50.0%; Score 51; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.043;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 RESLNRLRGY 20
DB 1 RESLNRLRGY 10
|||||

RESULT 6
R83061
ID R83061 standard; peptide; 10 AA.
AC R83061;
DE 15-MAY-1996 (first entry)
DE HLA-B7 CTL modulating peptide (B7.75-84).
KW Cytotoxic T lymphocyte; CTL; major histocompatibility complex; MHC;
KW immunosuppressant; graft versus host disorder; transplantation; therapy;
OS Synthetic.
PN W09526979-A1.
PD 12-OCT-1995.
PF 05-APR-1995; U04349.
PR 03-APR-1994; US-222851.
PA (STRD) UNIV LELAND STANFORD JUNIOR.
PI Clayberger C, Krensky AM, Parham P;
DR WPI; 95-358582/46.
PT Extension of acceptance period of transplants from MHC unmatched
PT donor hosts - using Class I B75-84 MHC antigen of the recipient
PT host
PS Claim 13; Page 66; 80pp; English.
CC This sequence represents a fragment of a class I major histocompatibility
CC complex (MHC) antigen. This sequence corresponds to residues 75-84 of
CC the alpha-1 domain of the class I MHC HLA-B7. This sequence, and the
CC peptide fragments represented by R83062-R83085, R83090-R83096 and
CC R92907-R92913 can be used to extend the period of acceptance by a
CC recipient of a transplant from an MHC unmatched donor. The peptides are
CC administered to a patient in conjunction with a subtherapeutic amount of
CC an immunosuppressant. This is administered to the patient for a limited
CC period of time (compared to the lifetime administration for current
CC treatments). The peptides particularly modulate (or inhibit) the
CC activity of the cytotoxic T lymphocytes (CTLs) of the patient.
SQ Sequence 10 AA;

Query Match 50.0%; Score 51; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.043;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 RESLNRLRGY 20
DB 1 RESLNRLRGY 10
|||||

RESULT 8
W33786
ID W33786 standard; peptide; 10 AA.
AC W33786;
DE 19-JUN-1998 (first entry)
DE Peptide B7.75-84 tested for immunomodulating activity.
KW Immunomodulating dimer; immunosuppressant drug; CTL activation;
KW transplantation; autoimmune disease; Class I HLA-B alpha-1 domain;
KW rejection.
OS Synthetic.
PN W09744351-A1.

PD 27-NOV-1997.
 PF 22-MAY-1997; U08689.
 PR 24-MAY-1996; US-653294.
 PI (STRD) UNIV LELAND STANFORD JUNIOR.
 PI Beulow R, Clayberger C, Krensky AM;
 DR WPI: 98-086530/08.
 PT New immunomodulating dimer peptide(s) - based on a Class I HLA-B
 PT alpha-1 domain, used for preventing rejection of transplants or
 PT treating autoimmune diseases
 PS Example 1: Page 19; 41pp; English.
 CC Peptides W33784-98 and W33778-9 were assayed for their immunomodulating
 CC activity. A peptide-type compound or variant is claimed which has
 CC immunomodulating activity, including the N-terminal acylated and/or
 CC C-terminal amidated or esterified forms of up to 60 amino acids, where
 CC the peptide-type compound comprises the formula: A-B, where A, B =
 CC (R aa76-77L) (aa79-84) or (aa84-79) (Laa77-76R); aa76 = E or V; aa77 =
 CC D, S or N; aa79 = R or G; aa80 = I or N; aa81, aa84 = a hydrophobic or
 CC small amino acid; aa82 = R or L; aa83 = G or R; and aa represents amino
 CC acid. The sequence in the brackets may optionally be absent or truncated
 CC at any peptide type bond within the brackets. The compounds comprise
 CC amino acid sequences related to a Class I HLA-B alpha domain (positions
 CC 79-84). They can be used to inhibit cytotoxic T-lymphocytes (CTL) from
 CC undesirably attacking cells in a host or in vitro. They can also be
 CC used in combination with antigenic peptides or proteins of interest to
 CC activate CTLs. They can also inhibit the proliferation of T cells in
 CC response to anti-CD3. The peptide can be used for preventing rejection
 CC of transplants or for treating autoimmune diseases, e.g. diabetes,
 CC rheumatoid arthritis and lupus erythematosus. The products can also be
 CC used for detection and diagnosis.
 SQ Sequence 10 AA;
 CC amino acid sequences related to a Class I HLA-B alpha domain (positions
 CC 79-84). They can be used to inhibit cytotoxic T-lymphocytes (CTL) from
 CC undesirably attacking cells in a host or in vitro. They can also be
 CC used in combination with antigenic peptides or proteins of interest to
 CC activate CTLs. They can also inhibit the proliferation of T cells in
 CC response to anti-CD3. The peptide can be used for preventing rejection
 CC of transplants or for treating autoimmune diseases, e.g. diabetes,
 CC rheumatoid arthritis and lupus erythematosus. The products can also be
 CC used for detection and diagnosis.
 SQ Sequence 10 AA;
 Query Match 50.0%; Score 51; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.043;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 11 RESLNRLGY 20
 Db 1 RESLNRLGY 10
 RESULT 10
 R41207
 ID R41207 standard; peptide; 25 AA.
 AC R41207;
 DT 15-MAR-1994 (first entry)
 DE Peptide fragment of Class I HLA peptide.
 KW Human leukocyte antigen; HLA; peptide; transplantation; neoplasia;
 KW parasitic disease; cytotoxic T lymphocyte; modulation.
 OS Synthetic.
 PN WO9317699-A.
 PD 16-SEP-1993.
 PF 25-FEB-1993; U01758
 PR 02-MAR-1992; US-844716.
 PA (STRD) UNIV LELAND STANFORD JUNIOR.
 PI Clayberger CA, Krensky AM;
 DR WPI: 93-303134/38.
 PT New peptide(s) based on Class I HLA antigen domains - used for
 PT modulating cytotoxic T-lymphocyte activity towards targets
 PS Claim 10; Page 54; 61pp; English.
 CC The peptide (or a fragment of at least 10 amino acids, joined at at
 CC least one terminus to a sequence other than that of wild type HLA
 CC antigen) is used to modulate cytotoxic T-lymphocyte (CTL) activity,
 CC either by inhibition or stimulation. It can be used for
 CC inhibiting CTL toxicity in transplantations, for inducing CTL
 CC activity in parasitic diseases and neoplasia and in studies on viral
 CC infection. The peptide can also be used for identifying CTLs which
 CC bind to it and removing subsets of CTLs from a T-cell composition.
 SQ Sequence 25 AA;
 Query Match 50.0%; Score 51; DB 1; Length 25;
 Best Local Similarity 100.0%; Pred. No. 0.11;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 11 RESLNRLGY 20
 Db 16 RESLNRLGY 25
 RESULT 11
 R83073
 ID R83073 standard; peptide; 25 AA.
 AC R83073;
 DT 16-MAR-1996 (first entry)
 DE HLA-Bw62 CTL modulating peptide (Bw62.60-84).
 KW Cytotoxic T lymphocyte; CTL; major histocompatibility complex; MHC;
 KW immunosuppressant; graft versus host disorder; transplantation; therapy;
 KW class I MHC; HLA-Bw62.
 OS Synthetic.
 PN WO9528979-A1.
 PD 12-OCT-1995.
 PF 05-APR-1995; U04349.

PD 27-NOV-1997.
 PF 22-MAY-1997; U08689.
 PR 24-MAY-1996; US-653294.
 PI (STRD) UNIV LELAND STANFORD JUNIOR.
 PI Beulow R, Clayberger C, Krensky AM;
 DR WPI: 98-086530/08.
 PT New immunomodulating dimer peptide(s) - based on a Class I HLA-B
 PT alpha-1 domain, used for preventing rejection of transplants or
 PT treating autoimmune diseases
 PS Example 1: Page 19; 41pp; English.
 CC Peptides W33784-98 and W33778-9 were assayed for their immunomodulating
 CC activity. A peptide-type compound or variant is claimed which has
 CC immunomodulating activity, including the N-terminal acylated and/or
 CC C-terminal amidated or esterified forms of up to 60 amino acids, where
 CC the peptide-type compound comprises the formula: A-B, where A, B =
 CC (R aa76-77L) (aa79-84) or (aa84-79) (Laa77-76R); aa76 = E or V; aa77 =
 CC D, S or N; aa79 = R or G; aa80 = I or N; aa81, aa84 = a hydrophobic or
 CC small amino acid; aa82 = R or L; aa83 = G or R; and aa represents amino
 CC acid. The sequence in the brackets may optionally be absent or truncated
 CC at any peptide type bond within the brackets. The compounds comprise
 CC amino acid sequences related to a Class I HLA-B alpha domain (positions
 CC 79-84). They can be used to inhibit cytotoxic T-lymphocytes (CTL) from
 CC undesirably attacking cells in a host or in vitro. They can also be
 CC used in combination with antigenic peptides or proteins of interest to
 CC activate CTLs. They can also inhibit the proliferation of T cells in
 CC response to anti-CD3. The peptide can be used for preventing rejection
 CC of transplants or for treating autoimmune diseases, e.g. diabetes,
 CC rheumatoid arthritis and lupus erythematosus. The products can also be
 CC used for detection and diagnosis.
 SQ Sequence 10 AA;
 Query Match 50.0%; Score 51; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.043;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 11 RESLNRLGY 20
 Db 1 RESLNRLGY 10
 RESULT 9
 W33796
 ID W33796 standard; peptide; 10 AA.
 AC W33796;
 DT 19-JUN-1998 (first entry)
 DE Peptide B7.75-84 tested for immunomodulating activity.
 KW Immunomodulating dimer; immunosuppressant drug; CTL activation;
 KW transplantation; autoimmune disease; Class I HLA-B alpha-1 domain;
 KW rejection.
 OS Synthetic.
 PN Homo sapiens.
 PN WO9744351-A1.
 PD 27-NOV-1997.
 PF 22-MAY-1997; U08689.
 PR 24-MAY-1996; US-653294.
 PA (STRD) UNIV LELAND STANFORD JUNIOR.
 PI Beulow R, Clayberger C, Krensky AM;
 DR WPI: 98-086530/08.
 PT New immunomodulating dimer peptide(s) - based on a Class I HLA-B
 PT alpha-1 domain, used for preventing rejection of transplants or
 PT treating autoimmune diseases
 PS Example 1: Page 19; 41pp; English.
 CC Peptides W33784-98 and W33778-9 were assayed for their immunomodulating
 CC activity. A peptide-type compound or variant is claimed which has
 CC immunomodulating activity, including the N-terminal acylated and/or
 CC C-terminal amidated or esterified forms of up to 60 amino acids, where
 CC the peptide-type compound comprises the formula: A-B, where A, B =
 CC (R aa76-77L) (aa79-84) or (aa84-79) (Laa77-76R); aa76 = E or V; aa77 =
 CC D, S or N; aa79 = R or G; aa80 = I or N; aa81, aa84 = a hydrophobic or
 CC small amino acid; aa82 = R or L; aa83 = G or R; and aa represents amino
 CC acid. The sequence in the brackets may optionally be absent or truncated
 CC at any peptide type bond within the brackets. The compounds comprise

PR 05-APR-1994; US-222851.
 PA (STRD) UNIV LELAND STANFORD JUNIOR.
 PI Clayberger C, Krensky AM, Parham P;
 DT WPI: 95-358582/46.
 PT Extension of acceptance period of transplants from MHC unmatched
 PT donor hosts - using Class I B7-1 MHC antigen of the recipient
 PT host
 PS Example 13; Page 32; 80pp; English.
 CC R83061-R83085, R83090-R83096 and R92907-R92913 represent fragments of
 CC class I major histocompatibility complex (MHC) antigens. This sequence
 CC corresponds to residues 60-84 of the alpha-1 domain of the class I MHC
 CC HLA-B*62. These sequences can be used to extend the period of acceptance
 CC by a recipient of a transplant from an MHC unmatched donor. The peptides
 CC are administered to a patient in conjunction with a subtherapeutic amount
 CC of an immunosuppressant. This is administered to the patient for a
 CC limited period of time (compared to the lifetime administration for
 CC current treatments). The peptides particularly modulate (or inhibit) the
 CC activity of the cytotoxic T lymphocytes (CTLs) of the patient.
 SQ Sequence 25 AA;

Query Match 50.0%; Score 51; DB 1; Length 25;
 Best Local Similarity 100.0%; Pred. No. 0.11;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 RESLRNLRGY 20
 DB 16 RESLRNLRGY 25
 |||||

RESULT 12
 ID R95431 standard; peptide; 25 AA.
 AC R95431;
 DT 12-NOV-1996 (first entry)
 DE HLA-B*7.60-84.
 KW HLA; p74; alpha-helix; human-leucocyte-associated antigen; inhibitor;
 KW T-cell lysate; membrane protein; mammal; heat shock protein; Hsc70; APC;
 KW B cell; calcium influx; cytotoxic T lymphocyte; CTL; differentiation;
 KW cytolysis; antigen presenting cell.
 OS Synthetic.
 PN W09513288-A1.
 PD 18-MAY-1995.
 PF 10-NOV-1994; U12985.
 PR 10-NOV-1993; US-150493.
 PA (STRD) UNIV LELAND STANFORD JUNIOR.
 PI Clayberger C, Krensky AM;
 DT WPI: 95-194027/25.
 PT Compens. comprising lymphoid surface membrane proteins - which may
 PT inhibit cytolytic activity and differentiation of CTLs.
 PS Example; Page 12; 29pp; English.
 CC R95431, and R95415-R95431 represent palindromes and fragments of
 CC human-leucocyte-associated antigens. This sequence represents the
 CC HLA-B*62.60-84. These sequences can be used to isolate the protein p74
 CC from a T-cell lysate. p74 is a T-cell surface membrane protein
 CC associated with T-cell activation in mammalian T-cells, and is also
 CC immunologically cross reactive with the heat shock protein Hsc70. p74 is
 CC found in a limited number of cell types, but is particularly expressed on
 CC B and T cells. p74 can be isolated by lysis of a suitable cell with an
 CC amphoteric detergent, and then passed through an affinity column
 CC containing a covalently bound HLA-B2702 palindromic peptide.
 CC Compositions comprising the extracellular fragment of p74 combined with
 CC HLA-B2702.60-84 (see R95416), induces calcium influx, and inhibits
 CC cytotoxic T lymphocyte (CTL) differentiation or cytolysis. Candidate
 CC compounds can be screened for their effect on the cytolytic activity of
 CC T-cells, by combining them with the extracellular portion of p74 and
 CC determining the amount of binding between the candidate compound and p74.
 CC Modulation of CTL activity can be inhibited in a cellular composition
 CC containing T-cells and antigen presenting cells (APCs), by adding to the
 CC mix the extracellular portion of p74, in an amount sufficient to compete
 CC with p74 for the binding of the p74 ligand.
 SQ Sequence 25 AA;

Query Match 50.0%; Score 51; DB 1; Length 25;
 Best Local Similarity 100.0%; Pred. No. 0.11;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 RESLRNLRGY 20
 DB 16 RESLRNLRGY 25
 |||||

RESULT 14
 ID R12464 standard; Protein; 362 AA.
 AC R12464;
 DT 29-AUG-1991 (first entry)
 DE HLA-B*35 antigen.
 KW Human leukocyte antigen; probe; major histocompatibility complex;
 KW MHC; class I.
 OS Homo sapiens.
 PN J03112486-A.

Query Match 50.0%; Score 51; DB 1; Length 25;
 Best Local Similarity 100.0%; Pred. No. 0.11;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 RESLRNLRGY 20
 DB 16 RESLRNLRGY 25
 |||||

RESULT 13
 ID R95419 standard; peptide; 25 AA.
 AC R95419;
 DT 12-NOV-1996 (first entry)
 DE HLA-B*62.60-84.
 KW HLA; p74; alpha-helix; human-leucocyte-associated antigen; inhibitor;
 KW T-cell lysate; membrane protein; mammal; heat shock protein; Hsc70; APC;
 KW B cell; calcium influx; cytotoxic T lymphocyte; CTL; differentiation;
 KW cytolysis; antigen presenting cell.
 OS Synthetic.
 PN W09513288-A1.
 PD 18-MAY-1995.
 PF 10-NOV-1994; U12985.
 PR 10-NOV-1993; US-150493.
 PA (STRD) UNIV LELAND STANFORD JUNIOR.
 PI Clayberger C, Krensky AM;
 DT WPI: 95-194027/25.
 PT Compens. comprising lymphoid surface membrane proteins - which may
 PT inhibit cytolytic activity and differentiation of CTLs.
 PS Example; Page 9; 29pp; English.
 CC R95413, and R95415-R95431 represent palindromes and fragments of
 CC human-leucocyte-associated antigens. This sequence represents the
 CC HLA-B*62.60-84. These sequences can be used to isolate the protein p74
 CC from a T-cell lysate. p74 is a T-cell surface membrane protein
 CC associated with T-cell activation in mammalian T-cells, and is also
 CC immunologically cross reactive with the heat shock protein Hsc70. p74 is
 CC found in a limited number of cell types, but is particularly expressed on
 CC B and T cells. p74 can be isolated by lysis of a suitable cell with an
 CC amphoteric detergent, and then passed through an affinity column
 CC containing a covalently bound HLA-B2702 palindromic peptide.
 CC Compositions comprising the extracellular fragment of p74 combined with
 CC HLA-B2702.60-84 (see R95416), induces calcium influx, and inhibits
 CC cytotoxic T lymphocyte (CTL) differentiation or cytolysis. Candidate
 CC compounds can be screened for their effect on the cytolytic activity of
 CC T-cells, by combining them with the extracellular portion of p74 and
 CC determining the amount of binding between the candidate compound and p74.
 CC Modulation of CTL activity can be inhibited in a cellular composition
 CC containing T-cells and antigen presenting cells (APCs), by adding to the
 CC mix the extracellular portion of p74, in an amount sufficient to compete
 CC with p74 for the binding of the p74 ligand.
 SQ Sequence 25 AA;

Query Match 50.0%; Score 51; DB 1; Length 25;
 Best Local Similarity 100.0%; Pred. No. 0.11;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 RESLRNLRGY 20
 DB 16 RESLRNLRGY 25
 |||||

RESULT 14
 ID R12464 standard; Protein; 362 AA.
 AC R12464;
 DT 29-AUG-1991 (first entry)
 DE HLA-B*35 antigen.
 KW Human leukocyte antigen; probe; major histocompatibility complex;
 KW MHC; class I.
 OS Homo sapiens.
 PN J03112486-A.

PD 14-MAY-1991.
 PF 22-SEP-1989; 247697.
 PR 22-SEP-1989; JP-247697.
 PA (OLYU) OLYMPUS OPTICAL KK.
 DR WPI; 91-182991/25.
 DR N-PSDB; Q12115.
 PT HLA-B35 gene - used in DNA probe and transformant cells for
 PT immunising animals, for developing monoclonal antibody.
 PS Claim 1; Page 1; lpp; Japanese.
 CC Probes comprising part of the sequence encoding this sequence can
 CC be used to identify Class I genes. The DNA can be expressed for
 CC immunisation of animals and prodn. of monoclonal antibodies
 CC specific for the HLA-B35 antigen. See also J03112485 and J03112487.
 SQ Sequence 362 AA;

Query Match 50.0%; Score 51; DB 1; Length 362;
 Best Local Similarity 100.0%; Pred. No. 1.8;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 RESLRNLRCY 20
 DB 99 RESLRNLRCY 108

RESULT 15

W62838
 ID W62838 standard; Protein; 605 AA.
 AC W62838;
 DT 27-OCT-1998 (first entry)
 DE Glycine max antimicrobial protein.
 KW antimicrobial protein; infestation; control.
 OS Glycine max.
 PN W09827805-A1.
 PD 02-JUL-1998.
 PF 22-DEC-1997; AU0874.
 PR 20-DEC-1996; AU-004275.
 PA (RETR-) COOP RES CENT TROPICAL PLANT PATHOLOGY.
 PI Bower NI, Goulter KC, Green JL, Manners JM, Marcus JP;
 DR WPI; 98-37729/32.
 PT Novel anti-microbial protein from e.g. Macadamia integrifolia -
 PT useful for controlling microbial infestations of plants or mammals
 PS Claim 1; Page 63-65; 96pp; English.
 CC The sequence is that of an antimicrobial protein which can
 CC be used to control microbial infestations in plants and mammalian
 CC animals.
 SQ Sequence 605 AA;

Query Match 46.6%; Score 47.5; DB 1; Length 605;
 Best Local Similarity 47.8%; Pred. No. 11;
 Matches 11; Conservative 3; Mismatches 6; Indels 3; Gaps 1;

QY 1 YGR---LNRLSERRESLRNLRCY 20
 DB 211 YGRIRVLRQFNQSPQLQNLRDY 233

Search completed: February 8, 2000, 04:05:43
 Job time: 9360 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: February 7, 2000, 18:04:38 ; Search time 111.22 Seconds
(without alignments)
8.482 Million cell updates/sec

Title: US-08-653-294-27

Perfect score: 102

Sequence: 1 YGRNLRSLRSLRLRGY 20

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 142080 seqs, 47169319 residues

Total number of hits satisfying chosen parameters: 142080

Minimum DB seq length: 0

Maximum DB seq length: 1000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : PIR62.*

1: pir1.*

2: pir2.*

3: pir3.*

4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	51	50.0	137	2	I38875 MHC class I antige
2	51	50.0	137	2	I38876 MHC class I antige
3	51	50.0	137	2	I38860 MHC class I antige
4	51	50.0	137	2	I38874 MHC class I antige
5	51	50.0	181	2	I39188 MHC cell surface g
6	51	50.0	270	1	HLHU40 MHC class I histoc
7	51	50.0	274	2	I68774 MHC HLA-B39 chain
8	51	50.0	274	2	S24439 class I histocompa
9	51	50.0	300	2	I68701 cell surface antig
10	51	50.0	308	2	I36956 MHC class I lympho
11	51	50.0	350	2	I68747 MHC class I antige
12	51	50.0	350	2	I34308 MHC HLA B71 - huma
13	51	50.0	354	2	S24436 class I histocompa
14	51	50.0	354	2	S24437 class I histocompa
15	51	50.0	354	2	S24438 class I histocompa
16	51	50.0	354	2	S24440 class I histocompa
17	51	50.0	354	2	S24433 class I histocompa
18	51	50.0	358	2	S03538 MHC class I histoc
19	51	50.0	361	2	I54418 MHC class I histoc
20	51	50.0	362	1	HLHUB7 MHC class I histoc
21	51	50.0	362	2	S77966 MHC class I histoc
22	51	50.0	362	2	G01230 MHC class I histoc
23	51	50.0	362	2	S16789 MHC class I histoc
24	51	50.0	362	2	A45880 MHC class I histoc
25	51	50.0	362	2	I37519 MHC class I histoc
26	51	50.0	362	2	I37520 MHC class I histoc
27	51	50.0	362	2	I37522 MHC class I histoc
28	51	50.0	362	2	I84431 MHC HLA-B8 chain -
29	51	50.0	362	2	I72755 HLA-B*5602 - human
30	51	50.0	362	2	I84488 lymphocyte antigen

31 51 50.0 362 2 I72752 HLA-B*5501 - human
32 51 50.0 362 2 I72753 HLA-B*5502 - human
33 51 50.0 362 2 I72754 HLA-B*5601 - human
34 51 50.0 362 2 I38437 MHC class I histoc
35 51 50.0 362 2 I37492 HLA-B alpha-chain
36 51 50.0 362 2 I34505 lymphocyte antigen
37 51 50.0 362 2 I56130 HLA-B*5401 - human
38 51 50.0 362 2 I36962 MHC class I protei
39 51 50.0 362 2 I37475 HLA-B35 variant -
40 51 50.0 362 2 I56149 lymphocyte antigen
41 51 50.0 362 2 I59655 lymphocyte antigen
42 51 50.0 362 2 I59651 lymphocyte antigen
43 51 50.0 362 2 I61865 MHC HLA-Bw42, HLA-
44 51 50.0 362 2 I61859 MHC HLA-B14 chain
45 51 50.0 362 2 I61860 MHC HLA-B18 chain

ALIGNMENTS

RESULT 1

I38875 MHC class I antigen - human (fragment)

C:Species: Homo sapiens (man)

C>Date: 07-Jun-1996 #sequence_revision 07-Jun-1996 #text_change 23-Jul-1999

C:Accession: I38875

R:Garber, T.L.; Butler, L.M.; Trachtenberg, E.A.; Erlich, H.A.; Rickards, O.; De Stef

Immunogenetics 42, 19-27, 1995

A:Title: HLA-B alleles of the Cayapa of Ecuador: new B39 and B15 alleles.

A:Reference number: I38860; MUID:95317819

A:Accession: I38875

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-137 <RES>

A:Cross-references: EMBL:U15639; NID:G930332; PIDN:AAA74046.1; PID:G930333

C:Superfamily: class I histocompatibility antigen; immunoglobulin homology

Query Match 50.0%; Score 51; DB 2; Length 137;
Best Local Similarity 100.0%; Pred. No. 0.91;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 RESLRNLRGY 20

Db 40 RESLRNLRGY 49

RESULT 2

I38876 MHC class I antigen - human (fragment)

C:Species: Homo sapiens (man)

C>Date: 07-Jun-1996 #sequence_revision 07-Jun-1996 #text_change 23-Jul-1999

C:Accession: I38876

R:Garber, T.L.; Butler, L.M.; Trachtenberg, E.A.; Erlich, H.A.; Rickards, O.; De Stef

Immunogenetics 42, 19-27, 1995

A:Title: HLA-B alleles of the Cayapa of Ecuador: new B39 and B15 alleles.

A:Reference number: I38860; MUID:95317819

A:Accession: I38876

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-137 <RES>

A:Cross-references: EMBL:U15640; NID:G930334; PIDN:AAA74047.1; PID:G930335

C:Superfamily: class I histocompatibility antigen; immunoglobulin homology

Query Match 50.0%; Score 51; DB 2; Length 137;
Best Local Similarity 100.0%; Pred. No. 0.91;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 RESLRNLRGY 20

Db 40 RESLRNLRGY 49

```

RESULT 3
I38860
MHC class I antigen - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 07-Jun-1996 #sequence_revision 07-Jun-1996 #text_change 23-Jul-1999
C:Accession: I38860
R:Garber, T.L.; Butler, L.M.; Trachtenberg, E.A.; Erlich, H.A.; Rickards, O.; De Stefani
Immunogenetics 42, 19-27, 1995
A:Title: HLA-B alleles of the Cayapa of Ecuador: new B39 and B15 alleles.
A:Reference number: I38860; MUID:95317819
A:Accession: I38860
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-137 <RES>
A:Cross-references: EMBL:U14756; NID:g930328; PIDN:AA50171.1; PID:g930329
C:Superfamily: class I histocompatibility antigen; immunoglobulin homology

Query Match 50.0%; Score 51; DB 2; Length 137;
Best Local Similarity 100.0%; Pred. No. 0.91; Mismatches 0; Indels 0; Gaps 0;
Matches 10; Conservative 0;

Qy 11 RESLNRLRGY 20
Db 40 RESLNRLRGY 49

RESULT 4
I38874
MHC class I antigen - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 07-Jun-1996 #sequence_revision 07-Jun-1996 #text_change 23-Jul-1999
C:Accession: I38874
R:Garber, T.L.; Butler, L.M.; Trachtenberg, E.A.; Erlich, H.A.; Rickards, O.; De Stefani
Immunogenetics 42, 19-27, 1995
A:Title: HLA-B alleles of the Cayapa of Ecuador: new B39 and B15 alleles.
A:Reference number: I38860; MUID:95317819
A:Accession: I38874
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-137 <RES>
A:Cross-references: EMBL:U15638; NID:g930330; PIDN:AAA74045.1; PID:g930331
C:Superfamily: class I histocompatibility antigen; immunoglobulin homology

Query Match 50.0%; Score 51; DB 2; Length 137;
Best Local Similarity 100.0%; Pred. No. 0.91; Mismatches 0; Indels 0; Gaps 0;
Matches 10; Conservative 0;

Qy 11 RESLNRLRGY 20
Db 40 RESLNRLRGY 49

RESULT 5
I59188
MHC cell surface glycoprotein - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 23-Jul-1999
C:Accession: I59188
R:Bronson, S.K.; Pei, J.; Taillon-Miller, P.; Chorney, M.J.; Geraghty, D.E.; Chaplin, D.;
Proc. Natl. Acad. Sci. U.S.A. 88, 1676-1680, 1991
A:Title: Isolation and characterization of yeast artificial chromosome clones linking th
A:Reference number: I59188; MUID:91156671
A:Accession: I59188
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-181 <RES>
A:Cross-references: GB:M59841; NID:g187697; PIDN:AAA59623.1; PID:g187698
C:Genetics:
A:Gene: GDB:HLA-B
A:Cross-references: GDB:120048; OMIM:142830

Query Match 50.0%; Score 51; DB 2; Length 274;
Best Local Similarity 100.0%; Pred. No. 1.8; Mismatches 0; Indels 0; Gaps 0;
Matches 10; Conservative 0;

```

```

A:Map position: 6p21.3-6p21.3
A:Introns: 90/1
C:Superfamily: class I histocompatibility antigen; immunoglobulin homology
C:Keywords: glycoprotein

Query Match 50.0%; Score 51; DB 2; Length 181;
Best Local Similarity 100.0%; Pred. No. 1.2; Mismatches 0; Indels 0; Gaps 0;
Matches 10; Conservative 0;

Qy 11 RESLNRLRGY 20
Db 74 RESLNRLRGY 83

RESULT 6
HLH040
MHC class I histocompatibility antigen HLA-B40 alpha chain - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 28-Aug-1985 #sequence_revision 28-Aug-1985 #text_change 02-Sep-1997
C:Accession: A02186
R:Lopez de Castro, J.A.; Bragado, R.; Strong, D.M.; Strominger, J.L.
Biochemistry 22, 3961-3969, 1983
A:Title: Primary structure of papain-solubilized human histocompatibility antigen HLA
A:Reference number: A02186; MUID:84000412
A:Accession: A02186
A:Molecule type: protein
A:Residues: 1-270 <LOP>
C:Comment: Comparison of a number of class I allelic sequences (-B40 vs. -B7 and -A2
y restricted to the alpha-1 and alpha-2 domains. The most conspicuous clustering of v
ossible alloantigenic determinants of these antigens.
C:Genetics:
A:Gene: GDB:HLA-B
A:Cross-references: GDB:120048; OMIM:142830
A:Map position: 6p21.3-6p21.3
C:Superfamily: class I histocompatibility antigen; immunoglobulin homology
C:Keywords: duplication; glycoprotein; heterodimer; membrane protein; transplantation
F:1-90/Domain: alpha-1 <EX1>
F:91-181/Domain: alpha-2 <EX2>
F:195-260/Domain: immunoglobulin homology <IMM>
F:86/Binding site: carbohydrate (Asn) (covalent) #status experimental
F:101-163,202-258/Disulfide bonds: #status predicted

Query Match 50.0%; Score 51; DB 1; Length 270;
Best Local Similarity 100.0%; Pred. No. 1.8; Mismatches 0; Indels 0; Gaps 0;
Matches 10; Conservative 0;

Qy 11 RESLNRLRGY 20
Db 75 RESLNRLRGY 84

RESULT 7
I68774
MHC HLA-B39 chain - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 07-Jun-1996 #sequence_revision 07-Jun-1996 #text_change 23-Jul-1999
C:Accession: I68774
R:Mueller, C.A.; Engler-Blum, G.; Gekeler, V.; Steiert, I.; Weiss, E.; Schmidt, H.
Immunogenetics 30, 200-207, 1989
A:Title: Genetic and serological heterogeneity of the supertypic HLA-B locus specific
A:Reference number: I54463; MUID:89379286
A:Accession: I68774
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-274 <RES>
A:Cross-references: GB:M29865; NID:g187676; PIDN:AAA36223.1; PID:g187677
C:Superfamily: class I histocompatibility antigen; immunoglobulin homology

Query Match 50.0%; Score 51; DB 2; Length 274;
Best Local Similarity 100.0%; Pred. No. 1.8;

```

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 RESLNRLGY 20

Db 75 RESLNRLGY 84

RESULT 8

S24439

Class I histocompatibility antigen HLA-B-3901 - human (fragment)

C:Species: Homo sapiens (man)

C:Date: 22-Nov-1993 #sequence_revision 01-Nov-1996 #text_change 07-Nov-1997

C:Accession: S24439

R:Watkins, D.I.; McAdam, S.N.; Liu, X.; Strang, C.R.; Milford, E.L.; Levine, C.G.; Garbe

Nature 357, 329-333, 1992

A:Title: New recombinant HLA-B alleles in a tribe of South American Amerindians indicate

A:Reference number: S24027; MUID:92269956

A:Accession: S24439

A:Molecule type: mRNA

A:Residues: 1-274 <WAT>

C:Genetics:

A:Gene: HLA-B-3901

C:Superfamily: class I histocompatibility antigen; immunoglobulin homology

C:Keywords: glycoprotein

F:1-274/Product: class I histocompatibility antigen HLA-B-3901 #status predicted <MAT>

F:1-90/Domain: alpha-1 #status predicted <EX1>

F:91-182/Domain: alpha-2 #status predicted <EX2>

F:196-261/Domain: immunoglobulin homology <IMM>

F:86/Binding site: carbohydrate (Asn) (covalent) #status predicted

F:101-184,203-259/Disulfide bonds: #status predicted

Query Match

Best Local Similarity 50.0%; Score 51; DB 2; Length 274;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 RESLNRLGY 20

Db 75 RESLNRLGY 84

RESULT 9

I68701

cell surface antigen - human (fragment)

C:Species: Homo sapiens (man)

C:Date: 07-Jun-1996 #sequence_revision 07-Jun-1996 #text_change 23-Jul-1999

C:Accession: I68701

R:Arnot, D.; Lillie, J.W.; Auffray, C.; Kappes, D.; Strominger, J.L.

Immunogenetics 20, 237-252, 1984

A:Title: Inter-locus and intra-allelic polymorphisms of HLA class I antigen gene mRNA.

A:Reference number: I54412; MUID:84287690

A:Accession: I68701

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-300 <RES>

A:Cross-references: GB:M27540; NID:g187733; PIDN:AAA59638.1; PID:g386890

C:Superfamily: class I histocompatibility antigen; immunoglobulin homology

C:Keywords: surface antigen

Query Match

Best Local Similarity 50.0%; Score 51; DB 2; Length 300;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 RESLNRLGY 20

Db 37 RESLNRLGY 46

RESULT 10

I36956

MHC class II chain - chimpanzee (fragment)

C:Species: Pan troglodytes (chimpanzee)

C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 23-Jul-1999

C:Accession: I36956

R:Parham, P.; Lawlor, D.A.; Lomen, C.E.; Ennis, P.D.

J. Immunol. 142, 3937-3950, 1989

A:Title: Diversity and diversification of HLA-A,B,C alleles.

A:Reference number: I36956; MUID:892335215

A:Accession: I36956

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-308 <RES>

A:Cross-references: GB:M24044; NID:g176812; PIDN:AAA53423.1; PID:g176813

C:Superfamily: class I histocompatibility antigen; immunoglobulin homology

Query Match

Best Local Similarity 50.0%; Score 51; DB 2; Length 308;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 RESLNRLGY 20

Db 45 RESLNRLGY 54

RESULT 11

I68747

MHC class I lymphocyte antigen - human (fragment)

C:Species: Homo sapiens (man)

C:Date: 07-Jun-1996 #sequence_revision 07-Jun-1996 #text_change 23-Jul-1999

C:Accession: I68747

R:Pohl, H.; Kuon, W.; Tabaczewski, P.; Doerner, C.; Weiss, E.H.

Immunogenetics 29, 297-307, 1989

A:Title: Allelic variation in HLA-B and HLA-C sequences and the evolution of the HLA-

A:Reference number: I54457; MUID:89233295

A:Accession: I68747

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-350 <RES>

A:Cross-references: GB:M28204; NID:g576472; PIDN:AAA53257.1; PID:g576473

C:Superfamily: class I histocompatibility antigen; immunoglobulin homology

Query Match

Best Local Similarity 50.0%; Score 51; DB 2; Length 350;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 RESLNRLGY 20

Db 87 RESLNRLGY 96

RESULT 12

I54308

MHC HLA B71 - human (fragment)

C:Species: Homo sapiens (man)

C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 23-Jul-1999

C:Accession: I54308

R:Rodriguez, S.G.; Johnson, A.H.; Hurley, C.K.

Hum. Immunol. 37, 192-194, 1993

A:Title: Molecular characterization of HLA-B71 from an African American individual.

A:Reference number: I54308; MUID:94064392

A:Accession: I54308

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-350 <RES>

A:Cross-references: GB:L07950; NID:g307236; PIDN:AAA59683.1; PID:g307237

C:Genetics:

A:Gene: GDB:HLA-B

A:Cross-references: GDB:I20048; OMIM:142830

A:Map position: 6p21.3-6p21.3

C:Superfamily: class I histocompatibility antigen; immunoglobulin homology

Query Match

Best Local Similarity 50.0%; Score 51; DB 2; Length 350;

Best Local Similarity 100.0%; Pred. No. 2.3;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 RESLRNLGY 20
| | | | | | | | | |
DB 99 RESLRNLGY 108

RESULT 13
S24436
class I histocompatibility antigen HLA-B-3504 precursor - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 22-Nov-1993 #sequence_revision 18-Jul-1997 #text_change 07-Nov-1997
C:Accession: S24436
R:Watkins, D.I.; McAdam, S.N.; Liu, X.; Strang, C.R.; Milford, E.L.; Levine, C.G.; Garber
Nature 357, 329-333, 1992
A:Title: New recombinant HLA-B alleles in a tribe of South American Amerindians indicate
A:Reference number: S24027; MUID:92269956
A:Accession: S24436
A:Molecule type: mRNA
A:Residues: 1-354 <WAT>
C:Genetics:
A:Gene: HLA-B-3504
C:Superfamily: class I histocompatibility antigen; immunoglobulin homology
C:Keywords: glycoprotein; transmembrane protein
F:1-17/Domain: signal sequence #status predicted <SIG>
F:17-354/Product: class I histocompatibility antigen HLA-B-3504 #status predicted <WAT>
F:17-299/Domain: extracellular #status predicted <EXT>
F:107-198/Domain: alpha-2 #status predicted <EX2>
F:212-277/Domain: immunoglobulin homology <IMM>
F:300-323/Domain: transmembrane #status predicted <TM>
F:324-354/Domain: intracellular #status predicted <INT>
F:102/Binding site: carbohydrate (Asn) (covalent) #status predicted
F:117-180,219-275/Disulfide bonds: #status predicted

Query Match 50.0%; Score 51; DB 2; Length 354;
Best Local Similarity 100.0%; Pred. No. 2.4;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 RESLRNLGY 20
| | | | | | | | | |
DB 91 RESLRNLGY 100

RESULT 14
S24437
class I histocompatibility antigen HLA-B-4802 precursor - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 22-Nov-1993 #sequence_revision 18-Jul-1997 #text_change 07-Nov-1997
C:Accession: S24437
R:Watkins, D.I.; McAdam, S.N.; Liu, X.; Strang, C.R.; Milford, E.L.; Levine, C.G.; Garber
Nature 357, 329-333, 1992
A:Title: New recombinant HLA-B alleles in a tribe of South American Amerindians indicate
A:Reference number: S24027; MUID:92269956
A:Accession: S24437
A:Molecule type: mRNA
A:Residues: 1-354 <WAT>
C:Genetics:
A:Gene: HLA-B-4802
C:Superfamily: class I histocompatibility antigen; immunoglobulin homology
C:Keywords: glycoprotein; transmembrane protein
F:1-17/Domain: signal sequence #status predicted <SIG>
F:17-354/Product: class I histocompatibility antigen HLA-B-4802 #status predicted <WAT>
F:17-299/Domain: extracellular #status predicted <EXT>
F:107-198/Domain: alpha-2 #status predicted <EX2>
F:212-277/Domain: immunoglobulin homology <IMM>
F:300-323/Domain: transmembrane #status predicted <TM>
F:324-354/Domain: intracellular #status predicted <INT>
F:102/Binding site: carbohydrate (Asn) (covalent) #status predicted
F:117-180,219-275/Disulfide bonds: #status predicted

Query Match 50.0%; Score 51; DB 2; Length 354;
Best Local Similarity 100.0%; Pred. No. 2.4;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 RESLRNLGY 20
| | | | | | | | | |
DB 91 RESLRNLGY 100

RESULT 15
S24438
class I histocompatibility antigen HLA-B-4801 precursor - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 22-Nov-1993 #sequence_revision 18-Jul-1997 #text_change 07-Nov-1997
C:Accession: S24438
R:Watkins, D.I.; McAdam, S.N.; Liu, X.; Strang, C.R.; Milford, E.L.; Levine, C.G.; Ga
Nature 357, 329-333, 1992
A:Title: New recombinant HLA-B alleles in a tribe of South American Amerindians indic
A:Reference number: S24027; MUID:92269956
A:Accession: S24438
A:Molecule type: mRNA
A:Residues: 1-354 <WAT>
C:Genetics:
A:Gene: HLA-B-4801
C:Superfamily: class I histocompatibility antigen; immunoglobulin homology
C:Keywords: glycoprotein; transmembrane protein
F:1-17/Domain: signal sequence #status predicted <SIG>
F:17-354/Product: class I histocompatibility antigen HLA-B-4801 #status predicted <W
F:17-299/Domain: extracellular #status predicted <EXT>
F:107-198/Domain: alpha-2 #status predicted <EX2>
F:212-277/Domain: immunoglobulin homology <IMM>
F:300-323/Domain: transmembrane #status predicted <TM>
F:324-354/Domain: intracellular #status predicted <INT>
F:102/Binding site: carbohydrate (Asn) (covalent) #status predicted
F:117-180,219-275/Disulfide bonds: #status predicted

Query Match 50.0%; Score 51; DB 2; Length 354;
Best Local Similarity 100.0%; Pred. No. 2.4;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 RESLRNLGY 20
| | | | | | | | | |
DB 91 RESLRNLGY 100

Search completed: February 7, 2000, 18:04:38
Job time: 22204 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: February 8, 2000, 01:25:59 ; Search time 68.63 Seconds
(without alignments)

8.703 Million cell updates/sec

Title: US-08-653-294-27

Perfect score: 102

Sequence: 1 YGRNLSRSLRLRGY 20

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 82229 seqs, 29864866 residues

Total number of hits satisfying chosen parameters: 82229

Minimum DB seq length: 0

Maximum DB seq length: 1000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : SwissProt_38.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	51	50.0	270	1	1B33_HUMAN
2	51	50.0	354	1	1B24_HUMAN
3	51	50.0	362	1	1A02_PANTR
4	51	50.0	362	1	1B02_HUMAN
5	51	50.0	362	1	1B02_PANTR
6	51	50.0	362	1	1B04_HUMAN
7	51	50.0	362	1	1B07_HUMAN
8	51	50.0	362	1	1B08_HUMAN
9	51	50.0	362	1	1B10_HUMAN
10	51	50.0	362	1	1B11_HUMAN
11	51	50.0	362	1	1B12_HUMAN
12	51	50.0	362	1	1B13_HUMAN
13	51	50.0	362	1	1B21_HUMAN
14	51	50.0	362	1	1B22_HUMAN
15	51	50.0	362	1	1B23_HUMAN
16	51	50.0	362	1	1B25_HUMAN
17	51	50.0	362	1	1B26_HUMAN
18	51	50.0	362	1	1B27_HUMAN
19	51	50.0	362	1	1B28_HUMAN
20	51	50.0	362	1	1B31_HUMAN
21	51	50.0	362	1	1B32_HUMAN
22	51	50.0	362	1	1B34_HUMAN
23	51	50.0	362	1	1B35_HUMAN
24	51	50.0	362	1	1B36_HUMAN
25	51	50.0	362	1	1B38_HUMAN
26	51	50.0	362	1	1B39_HUMAN
27	51	50.0	362	1	1B43_HUMAN
28	51	50.0	362	1	1B46_HUMAN
29	51	50.0	362	1	1B48_HUMAN
30	51	50.0	362	1	1B55_HUMAN
31	51	50.0	362	1	1B56_HUMAN
32	51	50.0	362	1	1B57_HUMAN
33	51	50.0	362	1	1B58_HUMAN
34	51	50.0	362	1	1B59_HUMAN

35 51 50.0 362 1 1B63_HUMAN P30498 homo sapien
36 47.5 46.6 605 1 GLCA_SOYBN P33916 glycine max
37 46 45.1 346 1 HRPJ_PSESY Q05395 pseudomonas
38 45.5 44.6 366 1 1C01_HUMAN P30499 homo sapien
39 44.5 43.6 639 1 GLCX_SOYBN P11827 glycine max
40 44 43.1 342 1 1CXX_HUMAN P10321 homo sapien
41 44 43.1 362 1 1B44_HUMAN P30484 homo sapien
42 44 43.1 366 1 1C01_PANTR P30686 pan troglod
43 44 43.1 366 1 1C02_HUMAN P30500 homo sapien
44 44 43.1 366 1 1C05_HUMAN P04222 homo sapien
45 44 43.1 366 1 1C06_HUMAN P30503 homo sapien

ALIGNMENTS

RESULT 1
ID 1B33_HUMAN STANDARD; PRT; 270 AA.
AC P01890;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 01-APR-1993 (Rel. 25, Last annotation update)
DE HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, BW-60(B-40) B*4001 ALPHA CHAIN
DE (FRAGMENT).
GN HLA-B OR HLAB.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Primates; Catarrhini; Hominidae; Homo.
RN [1]
RP SEQUENCE.
RX MEDLINE; 84000412.
RA LOPEZ DE CASTRO J.A., BRAGADO R., STRONG D.M., STROMINGER J.L.;
RT "Primary structure of papain-solubilized human histocompatibility
RT antigen HLA-B*40 (-Bw60), an outline of alloantigenic determinants";
RL Biochemistry 22:3961-3969(1983).
CC -!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
CC THE IMMUNE SYSTEM.
CC -!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
CC MICROGLOBULIN).
DR PIR; A02186; HLU40.
DR HSP; P30460; IAGB.
DR MIM; 142830; .
DR PROSITE; PS00290; IG_MHC; 1.
DR PFAM; PF00047; Ig; 1.
DR PFAM; PF00129; MHC_I; 1.
KW MHC I; Glycoprotein.
FT DOMAIN 1 90 EXTRACELLULAR ALPHA-1.
FT DOMAIN 91 181 EXTRACELLULAR ALPHA-2.
FT DOMAIN 182 >270 EXTRACELLULAR ALPHA-3.
FT CARBOHYD 86 86
FT DISULFID 101 163
FT DISULFID 202 258
FT NON_TER 270 270
SQ SEQUENCE 270 AA; BFE44EFF CRC32;

Query Match 50.08; Score 51; DB 1; Length 270;
Best Local Similarity 100.0%; Pred. No. 0.59; 0; Indels 0; Gaps 0;
Matches 10; Conservative 0; Mismatches 0;
Qy 11 RESLRNLRGY 20
Db 75 RESLRNLRGY 84

RESULT 2
ID 1B24_HUMAN STANDARD; PRT; 354 AA.
AC P30470;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)

DE HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-35 B*3504 ALPHA CHAIN
DE PRECURSOR (FRAGMENT).

GN HLA-B OR HLAB.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;

OC Eutheria; Primates; Catarrhini; Hominidae; Homo.

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE; 92269556.

RA WATKINS D.I., MCADAM S.N., LIU X., STANG C.R., MILFORD E.L.,

RA LEVINE C.G., GARBER T.L., DOGAN A.L., LORD C.I., GHIM S.H.,

RA TROUP G.M., HUGHES A.B., LETVIN N.L.;

RT "New recombinant HLA-B alleles in a tribe of South American

RT Amerindians indicate rapid evolution of MHC class I loci.;

RL Nature 357:329-333(1992).

CC -!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO

CC THE IMMUNE SYSTEM.

CC -!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-

CC MICROGLOBULIN).

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CC -----

CC EMBL; M86403; ; NOT_ANNOTATED_CDS.

DR HSSP; P30685; 1AIN.

DR MIM; 142830; .

DR PROSITE; PS00290; IG_MHC; 1.

DR PFAM; PF00047; ig; 1.

DR PFAM; PF00129; MHC_I; 1.

KW MHC I; Transmembrane; Glycoprotein; Signal.

FT NON_TER 1 1

FT SIGNAL <1 16

FT CHAIN 17 354

FT HLA CLASS I HISTOCOMPATIBILITY ANTIGEN,

FT B-35 B*3504 ALPHA CHAIN.

FT EXTRACELLULAR ALPHA-1.

FT EXTRACELLULAR ALPHA-2.

FT EXTRACELLULAR ALPHA-3.

FT CONNECTING PEPTIDE.

FT CYTOPLASMIC TAIL.

FT BY SIMILARITY.

FT BY SIMILARITY.

FT BY SIMILARITY.

FT CARBOHYD 102 102

FT DISULFID 117 180

FT SEQUENCE 354 AA; 39617 MW; 6564795A CRC32;

SQ

Query Match 50.0%; Score 51; DB 1; Length 354;
Best Local Similarity 100.0%; Pred. No. 0.8;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 RESLRNLRCY 20

|||||

Db 91 RESLRNLRCY 100

|||||

RESULT 3

1A02_PANTR

STANDARD; PRT; 362 AA.

AC P16210;

DT 01-APR-1990 (Rel. 14, Created)

DT 01-APR-1990 (Rel. 14, Last sequence update)

DT 01-APR-1993 (Rel. 25, Last annotation update)

DE CHLA CLASS I HISTOCOMPATIBILITY ANTIGEN, A-5 ALPHA CHAIN PRECURSOR.

OS Pan troglodytes (Chimpanzee).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;

OC Eutheria; Primates; Catarrhini; Hominidae; Pan.

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE; 90201944.
RA LAWOR D.A., WARREN E., WARD F.E., PARHAM P.;
RT "Comparison of class I MHC alleles in humans and apes.";
RL Immunol. Rev. 113:147-185(1990).
CC -!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
CC THE IMMUNE SYSTEM.
CC -!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
CC MICROGLOBULIN).

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CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).

CC -----

CC EMBL; M30679; AAA87971.1; .

DR HSSP; P30685; 1AIN.

DR PROSITE; PS00290; IG_MHC; 1.

DR PFAM; PF00047; ig; 1.

DR PFAM; PF00129; MHC_I; 1.

KW MHC I; Transmembrane; Glycoprotein; Signal.

FT SIGNAL 1 24

FT CHAIN 25 362

FT CHLA CLASS I HISTOCOMPATIBILITY ANTIGEN,

FT A-5 ALPHA CHAIN.

FT EXTRACELLULAR ALPHA-1.

FT EXTRACELLULAR ALPHA-2.

FT EXTRACELLULAR ALPHA-3.

FT CONNECTING PEPTIDE.

FT CYTOPLASMIC TAIL.

FT BY SIMILARITY.

FT BY SIMILARITY.

FT BY SIMILARITY.

FT CARBOHYD 110 110

FT SEQUENCE 362 AA; 40487 MW; 97E6CE8A CRC32;

SQ

Query Match 50.0%; Score 51; DB 1; Length 362;
Best Local Similarity 100.0%; Pred. No. 0.8;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 RESLRNLRCY 20

|||||

Db 99 RESLRNLRCY 108

|||||

RESULT 4

1B02_HUMAN

STANDARD; PRT; 362 AA.

AC P01889;

DT 21-JUL-1986 (Rel. 01, Created)

DT 01-FEB-1991 (Rel. 17, Last sequence update)

DT 01-OCT-1996 (Rel. 34, Last annotation update)

DE HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-7 B*0702 ALPHA CHAIN

DE PRECURSOR (B7.2).

GN HLA-B OR HLAB.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;

OC Eutheria; Primates; Catarrhini; Hominidae; Homo.

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE; 90207291.

RA ENNIS P.D., ZEMMOUR J., SALTER R.D., PARHAM P.;

RT "Rapid cloning of HLA-A,B CDNA by using the polymerase chain

RT reaction: frequency and nature of errors produced in amplification.";

RL Proc. Natl. Acad. Sci. U.S.A. 87:2833-2837(1990).

RN [2]

RP SEQUENCE FROM N.A.

RX MEDLINE; 90315860.

RA PARHAM P., BENJAMIN R.J., CHEN B.P., CLAYBERGER C., ENNIS P.D.,

RA KRENSKY A.M., LAWOR D.A., LITTMAN D.R., NORRMENT A.M., ORR H.T.,

RA SALTER R.D., ZEMMOUR J.;

RT "Diversity of class I HLA molecules: functional and evolutionary
 interactions with T cells.";
 RL Cold Spring Harb. Symp. Quant. Biol. 54:529-543(1989).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 85287366.
 RA SOOD A.K., PAN J., BIRO P.A., PEREIRA D., SRIVASTAVA R., REDDY V.B.,
 DUCEMAN B.W., WEISSMAN S.M.;
 RT "Structure and polymorphism of class I MHC antigen mRNA.";
 RL Immunogenetics 22:101-121(1985).
 RN [4]
 RP SEQUENCE FROM N.A.
 RA ELLEXSON M.E., ZHANG L., HILDEBRAND W.H.;
 RL Submitted (JUN-1995) to the EMBL/GenBank/DBJ databases.
 RN [5]
 RP SEQUENCE OF 25-295.
 RX MEDLINE; 80088278.
 RA ORR H.T., LOPEZ DE CASTRO J.A., LANCET D., STROMINGER J.L.;
 RT "Complete amino acid sequence of a papain-solubilized human
 histocompatibility antigen, HLA-B*7.2. Sequence determination and
 search for homologies.";
 RL Biochemistry 18:5711-5720(1979).
 CC -!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
 THE IMMUNE SYSTEM.
 CC -!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
 MICROGLOBULIN).
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 or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; M32317; AAA36230.1; -;
 DR EMBL; M16102; AAA59622.1; ALT_SEQ.
 DR EMBL; U29057; AAA91229.1; -;
 DR PIR; A02185; HLHUB7.
 DR PIR; B35997; B35997.
 DR HSSP; P30460; 1AGB.
 DR MIM; 142830; -;
 DR PROSITE; PS00290; IG_MHC; 1.
 DR PFAM; PF00047; ig; 1.
 DR PFAM; PF00129; MHC I; 1.
 DR MHC I; Transmembrane; Glycoprotein; Signal.
 KW MHC I; Transmembrane; Glycoprotein; Signal.
 FT SIGNAL 1 24
 FT CHAIN 25 362 HLA CLASS I HISTOCOMPATIBILITY ANTIGEN,
 FT B-7 B*0702 ALPHA CHAIN.
 FT DOMAIN 25 114
 FT DOMAIN 115 206 EXTRACELLULAR ALPHA-1.
 FT DOMAIN 207 298 EXTRACELLULAR ALPHA-2.
 FT DOMAIN 299 309 EXTRACELLULAR ALPHA-3.
 FT DOMAIN 310 333 CONNECTING PEPTIDE.
 FT TRANSMEM 334 362 CYTOPLASMIC TAIL.
 FT CARBOHYD 110 110
 FT DISULFID 125 188
 FT DISULFID 227 283
 FT CONFLICT 15 18
 FT CONFLICT 266 266 Q -> E (IN REF. 3).
 FT CONFLICT 268 268 W -> S (IN REF. 5).
 FT CONFLICT 297 297 R -> G (IN REF. 3).
 FT CONFLICT 314 315 GL -> RP (IN REF. 3).
 FT CONFLICT 344 345
 FT SEQUENCE 362 AA; 40460 MW; 87B2ED84 CRC32;
 AAIA -> GPW (IN REF. 3).
 Q -> E (IN REF. 5).
 W -> S (IN REF. 3).
 R -> G (IN REF. 3).
 GL -> RP (IN REF. 3).
 Query Match 50.0%; Score 51; DB 1; Length 362;
 Best Local Similarity 100.0%; Pred. No. 0.82;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 11 RESRLNLRGY 20
 DB 99 RESRLNLRGY 108
 RESULT 6
 ID 1B04_HUMAN STANDARD; PRT; 362 AA.
 AC P30460;

RESULT 5
 ID 1B02_PANTR STANDARD; PRT; 362 AA.
 AC P13751;
 DT 01-JAN-1990 (Rel. 13, Created)
 DT 01-JAN-1990 (Rel. 13, Last sequence update)
 DT 01-APR-1993 (Rel. 25, Last annotation update)
 DE CHLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-2 ALPHA CHAIN PRECURSOR.
 OS Pan troglodytes (Chimpanzee).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 RN Eutheria; Primates; Catarrhini; Hominidae; Pan.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 89030641.
 RA MAYER W.E., JONKER M., KLEIN D., IVANYI P., VAN SEVENTER G.,
 KLEIN J.;
 RT "Nucleotide sequences of chimpanzee MHC class I alleles: evidence for
 trans-species mode of evolution.";
 RL EMBO J. 7:2765-2774(1988).
 RN [2]
 RP REVISIONS.
 RA MAYER W.;
 RL Submitted (FEB-1989) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
 THE IMMUNE SYSTEM.
 CC -!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
 MICROGLOBULIN).
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 or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; X13116; CAA31508.1; -;
 DR PIR; S03538; S03538.
 DR HSSP; P30685; 1AIN.
 DR PROSITE; PS00290; IG_MHC; 1.
 DR PFAM; PF00047; ig; 1.
 DR PFAM; PF00129; MHC I; 1.
 DR MHC I; Transmembrane; Glycoprotein; Signal.
 KW MHC I; Transmembrane; Glycoprotein; Signal.
 FT SIGNAL 1 24
 FT CHAIN 25 362 HLA CLASS I HISTOCOMPATIBILITY ANTIGEN,
 FT B-2 ALPHA CHAIN.
 FT DOMAIN 25 114
 FT DOMAIN 115 206 EXTRACELLULAR ALPHA-1.
 FT DOMAIN 207 298 EXTRACELLULAR ALPHA-2.
 FT DOMAIN 299 308 EXTRACELLULAR ALPHA-3.
 FT TRANSMEM 309 332 CONNECTING PEPTIDE.
 FT DOMAIN 333 362 CYTOPLASMIC TAIL.
 FT DISULFID 125 188 BY SIMILARITY.
 FT DISULFID 227 283 BY SIMILARITY.
 FT CARBOHYD 110 110 BY SIMILARITY.
 FT SEQUENCE 362 AA; 40488 MW; 4BF65A6C CRC32;
 Query Match 50.0%; Score 51; DB 1; Length 362;
 Best Local Similarity 100.0%; Pred. No. 0.82;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 11 RESRLNLRGY 20
 DB 99 RESRLNLRGY 108
 RESULT 6
 ID 1B04_HUMAN STANDARD; PRT; 362 AA.
 AC P30460;

DT 01-APR-1993 (Rel. 25, Created)
 DT 01-APR-1993 (Rel. 25, Last sequence update)
 DE 15-JUL-1998 (Rel. 36, Last annotation update)
 DE HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-8 B*0801 ALPHA CHAIN
 DE PRECURSOR.
 GN HLA-B OR HLAB.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Eutheria; Primates; Catarrhini; Hominidae; Homo.
 RN [1]
 RX MEDLINE: 89235215.
 RA PARHAM P., LAWLER D.A., LOMEN C.E., ENNIS P.D.;
 RT "Diversity and diversification of HLA-A,B,C alleles."
 RL J. Immunol. 142:3937-3950(1989).
 RN [2]
 RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS) OF 25-300.
 RX MEDLINE: 97130420.
 RA REID S.W., MCADAM S., SMITH K.J., KLENERMAN P., O'CALLAGHAN C.A.,
 RA HARLOS K., JAKOBSEN B.K., MCMICHAEL A.J., BELL J.I., STUART D.I.,
 RA JONES E.Y.;
 RT "Antagonist HIV-1 Gag peptides induce structural changes in HLA B8."
 RL J. Exp. Med. 184:2279-2286(1996).
 CC -!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
 CC THE IMMUNE SYSTEM.
 CC -!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
 CC MICROGLOBULIN).
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 CC -----
 DR EMBL: M24036; AAA52662.1; -;
 DR PDB: 1AGB; 16-JUN-97.
 DR PDB: 1AGC; 16-JUN-97.
 DR PDB: 1AGD; 16-JUN-97.
 DR PDB: 1AGE; 16-JUN-97.
 DR PDB: 1AGF; 16-JUN-97.
 DR MIM: 142830; -;
 DR PROSITE: PS00290; IG_MHC; 1.
 DR PFAM: PF00047; ig; 1.
 DR MHC I; Transmembrane; Glycoprotein; Signal;
 KW MHC I; Transmembrane; Glycoprotein; Signal;
 FT SIGNAL 1 24
 FT CHAIN 25 362
 FT DOMAIN 25 114
 FT DOMAIN 115 206
 FT DOMAIN 207 298
 FT DOMAIN 299 309
 FT TRANSMEM 310 333
 FT DOMAIN 334 362
 FT CARBOHYD 110 110
 FT DISULFID 125 188
 FT DISULFID 227 283
 SQ SEQUENCE 362 AA; 40331 MW; 1467B9EB CRC32;
 Query Match 50.0%; Score 51; DB 1; Length 362;
 Best Local Similarity 100.0%; Pred. No. 0.82;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 11 RESLNRLRGY 20
 Db 99 RESLNRLRGY 108
 RESULT 7
 1B07_HUMAN

1B07_HUMAN STANDARD; PRT; 362 AA.
 P30462;
 DT 01-APR-1993 (Rel. 25, Created)
 DT 01-APR-1993 (Rel. 25, Last sequence update)
 DE 01-APR-1993 (Rel. 25, Last annotation update)
 DE HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-14 B*1401 ALPHA CHAIN
 DE PRECURSOR.
 GN HLA-B OR HLAB.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Eutheria; Primates; Catarrhini; Hominidae; Homo.
 RN [1]
 RX MEDLINE: 89235215.
 RA PARHAM P., LAWLER D.A., LOMEN C.E., ENNIS P.D.;
 RT "Diversity and diversification of HLA-A,B,C alleles."
 RL J. Immunol. 142:3937-3950(1989).
 CC -!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
 CC THE IMMUNE SYSTEM.
 CC -!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
 CC MICROGLOBULIN).
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: M24040; AAA59661.1; -;
 DR HSSP: P30460; 1AGB.
 DR MIM: 142830; -;
 DR PROSITE: PS00290; IG_MHC; 1.
 DR PFAM: PF00047; ig; 1.
 DR MHC I; Transmembrane; Glycoprotein; Signal.
 KW MHC I; Transmembrane; Glycoprotein; Signal.
 FT SIGNAL 1 24
 FT CHAIN 25 362
 FT DOMAIN 25 114
 FT DOMAIN 115 206
 FT DOMAIN 207 298
 FT DOMAIN 299 309
 FT TRANSMEM 310 333
 FT DOMAIN 334 362
 FT CARBOHYD 110 110
 FT DISULFID 125 188
 FT DISULFID 227 283
 SQ SEQUENCE 362 AA; 40358 MW; 9BED8199 CRC32;
 Query Match 50.0%; Score 51; DB 1; Length 362;
 Best Local Similarity 100.0%; Pred. No. 0.82;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 11 RESLNRLRGY 20
 Db 99 RESLNRLRGY 108
 RESULT 8
 1B08_HUMAN STANDARD; PRT; 362 AA.
 P30463;
 DT 01-APR-1993 (Rel. 25, Created)
 DT 01-APR-1993 (Rel. 25, Last sequence update)
 DE 01-APR-1993 (Rel. 25, Last annotation update)
 DE HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, BW-65(B-14) B*1402 ALPHA CHAIN
 DE PRECURSOR.
 GN HLA-B OR HLAB.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;

OC Eutheria; Primates; Catarrhini; Homiidae; Homo.
 RN [1]
 RX SEQUENCE FROM N.A.
 RP MEDLINE; 89235215.
 RA PARRAM P., LAWOR D.A., LOMEN C.E., ENNIS P.D.;
 RT "Diversity and diversification of HLA-A,B,C alleles."
 RL J. Immunol. 142:3937-3950(1989).
 CC -!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
 CC THE IMMUNE SYSTEM.
 CC -!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
 CC MICROGLOBULIN).
 CC -----
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 CC -----
 CC EMBL; M24032; AAA59664.1; -
 DR HSSP; P30450; LAGB.
 DR MIM; 142830; -
 DR PROSITE; PS00290; IG_MHC; 1.
 DR PFAM; PF00047; ig; 1.
 DR PFAM; PF00129; MHC_I; 1.
 KW MHC I; Transmembrane; Glycoprotein; Signal.
 FT SIGNAL 1 24
 FT CHAIN 25 362
 FT HLA CLASS I HISTOCOMPATIBILITY ANTIGEN,
 FT BW-65(B-14) B*1402 ALPHA CHAIN.
 FT DOMAIN 25 114
 FT DOMAIN 115 206
 FT DOMAIN 207 298
 FT DOMAIN 299 309
 FT DOMAIN 310 333
 FT TRANSMEM 334 362
 FT DOMAIN 334 362
 FT CARBOHYD 110 110
 FT DISULFID 125 188
 FT DISULFID 227 283
 FT SEQUENCE 362 AA; 40342 MW; BE68AC9E CRC32;

Query Match 50.0%; Score 51; DB 1; Length 362;
 Best Local Similarity 100.0%; Pred. No. 0.82;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 RESLRLRGY 20
 |||||
 DB 99 RESLRLRGY 108

RESULT 9
 ID 1B10_HUMAN STANDARD; PRT; 362 AA.
 AC P30464;
 DT 01-APR-1993 (Rel. 25, Created)
 DT 01-APR-1993 (Rel. 25, Last sequence update)
 DT 15-JUL-1998 (Rel. 36, Last annotation update)
 DE HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, BW-75(B-15) B*1502 ALPHA CHAIN
 DE PRECURSOR.
 GN HLA-B OR HLAB.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Eutheria; Primates; Catarrhini; Homiidae; Homo.
 RN [1]
 RX MEDLINE; 92196792.
 RA LITTLE A.-M., PARRAM P.;
 RT "The HLA-B*75 subtype of B15: molecular characterization and
 RT comparison with crossreacting antigens."
 RL Tissue Antigens 38:186-190(1991).
 RN [2]
 RP SEQUENCE FROM N.A.

TISSUE-BLOOD;
 RX MEDLINE; 96369309.
 RA LIN L., TOKUNAGA K., TANAKA H., NAKAJIMA F., IMANISHI T.,
 RA KASHIWASE K., BANNAI M., MIZUNO S., AKAZA T., TADOKORO K.,
 RA SHIBATA Y., JUJI T.;
 RT "Further molecular diversity in the HLA-B15 group."
 RL Tissue Antigens 47:265-274(1996).
 CC -!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
 CC THE IMMUNE SYSTEM.
 CC -!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
 CC MICROGLOBULIN).
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; M75138; AAA59630.1; -
 DR EMBL; D50293; BAA08824.1; -
 DR HSSP; P30685; IAIN.
 DR MIM; 142830; -
 DR PROSITE; PS00290; IG_MHC; 1.
 DR PFAM; PF00047; ig; 1.
 DR PFAM; PF00129; MHC_I; 1.
 KW MHC I; Transmembrane; Glycoprotein; Signal.
 FT SIGNAL 1 24
 FT CHAIN 25 362
 FT HLA CLASS I HISTOCOMPATIBILITY ANTIGEN,
 FT BW-75(B-15) B*1502 ALPHA CHAIN.
 FT DOMAIN 25 114
 FT DOMAIN 115 206
 FT DOMAIN 207 298
 FT DOMAIN 299 309
 FT TRANSMEM 310 333
 FT DOMAIN 334 362
 FT CARBOHYD 110 110
 FT DISULFID 125 188
 FT DISULFID 227 283
 FT SEQUENCE 362 AA; 40338 MW; 8CF9BCD0 CRC32;

Query Match 50.0%; Score 51; DB 1; Length 362;
 Best Local Similarity 100.0%; Pred. No. 0.82;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 RESLRLRGY 20
 |||||
 DB 99 RESLRLRGY 108

RESULT 10
 ID 1B11_HUMAN STANDARD; PRT; 362 AA.
 AC P30465;
 DT 01-APR-1993 (Rel. 25, Created)
 DT 01-APR-1993 (Rel. 25, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, BW-72(BW-70) B*1503 ALPHA
 DE CHAIN PRECURSOR.
 GN HLA-B OR HLAB.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Eutheria; Primates; Catarrhini; Homiidae; Homo.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 93056508.
 RA MADRIGAL J.A., BELICH M.P., HILDEBRAND W.H., BENJAMIN R.J.,
 RA LITTLE A.-M., ZEMMOUR J., ENNIS P.D., WARD F.E., PETZL-ERLER M.L.,
 RA MARTELL R.W., DU TOIT E.D., PARRAM P.;
 RT "Distinctive HLA-A,B antigens of black populations formed by
 RT interallelic conversion.";

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RL J. Immunol. 149:3411-3415(1992).
CC -1- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
CC THE IMMUNE SYSTEM.
CC -1- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
CC MICROGLOBULIN).
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; X61709; CAA43878.1; -
DR PIR; S16789; S16789.
DR HSP; P30685; 1A1N.
DR MIM; 142830; -
DR PROSITE; PS00290; IG_MHC; 1.
DR PFAM; PF00047; Ig; 1.
DR PFAM; PF00129; MHC_I; 1.
KW MHC I; Transmembrane; Glycoprotein; Signal.
FT SIGNAL 1 24
FT CHAIN 25 362 HLA CLASS I HISTOCOMPATIBILITY ANTIGEN,
FT BW-72(BW-70) B*1503 ALPHA CHAIN.
FT DOMAIN 25 114 EXTRACELLULAR ALPHA-1.
FT DOMAIN 115 206 EXTRACELLULAR ALPHA-2.
FT DOMAIN 207 298 EXTRACELLULAR ALPHA-3.
FT DOMAIN 299 309 CONNECTING PEPTIDE.
FT TRANSMEM 310 333
FT DOMAIN 334 362 CYTOPLASMIC TAIL.
FT CARBOHYD 110 110 BY SIMILARITY.
FT DISULFID 125 188 BY SIMILARITY.
FT DISULFID 227 283 BY SIMILARITY.
FT SEQUENCE 362 AA; 40387 MW; 99D70546 CRC32;
SQ

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Query Match 50.0%; Score 51; DB 1; Length 362;
Best Local Similarity 100.0%; Pred. No. 0.82;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 11 RESLRNLRGY 20
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DB 99 RESLRNLRGY 108

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RESULT 11
1B12_HUMAN
ID 1B12_HUMAN STANDARD; PRT; 362 AA.
AC P30513;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-62 B*1504 ALPHA CHAIN
DE PRECURSOR.
DE HLA-B OR HLAB.
GN Homo sapiens (Human).
OS Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia;
OC Eutheria; Primates; Catarrhini; Hominoidea; Homo.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 92269956.
RA WATKINS D.I., MCADAM S.N., LIU X., STANG C.R., MILFORD E.L.,
RA LEVINE C.G., GABER T.L., DOGON A.L., LORD C.I., GHIM S.H.,
RA TROUP G.M., HUGHES A.L., LETVIN N.L.;
RT "New recombinant HLA-B alleles in a tribe of South American
RT Amerindians indicate rapid evolution of MHC class I loci."
RN Nature 357:329-333(1992).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE-BLOOD:
RA RAWOS M., BARBER D.F., LAYRISSE Z., DE CASTRO J.A.;
RA Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.

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CC -1- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
CC THE IMMUNE SYSTEM.
CC -1- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
CC MICROGLOBULIN).
CC -----
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CC -----
DR EMBL; M84382; AAA59632.1; -
DR EMBL; U70528; AAB16918.1; -
DR PIR; S24433; S24433.
DR HSP; P30685; 1A1N.
DR MIM; 142830; -
DR PROSITE; PS00290; IG_MHC; 1.
DR PFAM; PF00047; Ig; 1.
DR PFAM; PF00129; MHC_I; 1.
KW MHC I; Transmembrane; Glycoprotein; Signal.
FT SIGNAL 1 24
FT CHAIN 25 362 HLA CLASS I HISTOCOMPATIBILITY ANTIGEN,
FT B-62 B*1504 ALPHA CHAIN.
FT DOMAIN 25 114 EXTRACELLULAR ALPHA-1.
FT DOMAIN 115 206 EXTRACELLULAR ALPHA-2.
FT DOMAIN 207 298 EXTRACELLULAR ALPHA-3.
FT DOMAIN 299 309 CONNECTING PEPTIDE.
FT TRANSMEM 310 333
FT DOMAIN 334 362 CYTOPLASMIC TAIL.
FT CARBOHYD 110 110 BY SIMILARITY.
FT DISULFID 125 188 BY SIMILARITY.
FT DISULFID 227 283 BY SIMILARITY.
FT SEQUENCE 362 AA; 40406 MW; E80FC24C CRC32;
SQ

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Query Match 50.0%; Score 51; DB 1; Length 362;
Best Local Similarity 100.0%; Pred. No. 0.82;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 11 RESLRNLRGY 20
| | | | | | | |
DB 99 RESLRNLRGY 108

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```

RESULT 12
1B13_HUMAN
ID 1B13_HUMAN STANDARD; PRT; 362 AA.
AC P30466;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-18 B*1801 ALPHA CHAIN
DE PRECURSOR.
DE HLA-B OR HLAB.
GN Homo sapiens (Human).
OS Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia;
OC Eutheria; Primates; Catarrhini; Hominoidea; Homo.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 89235215.
RA PARHAM P., LAWLOR D.A., LOMEN C.E., ENNIS P.D.;
RT "Diversity and diversification of HLA-A,B,C alleles."
RL J. Immunol. 142:3937-3950(1989).
CC -1- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
CC THE IMMUNE SYSTEM.
CC -1- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
CC MICROGLOBULIN).
CC -----
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CC -----
 CC EMBL; M24039; AAA59662.1; -
 CC HSSP; P30460; IAGB.
 CC DR MIM; 142830; -
 CC DR PROSITE; PS00290; IG_MHC; 1.
 CC DR PFAM; PF00047; Ig; 1.
 CC DR PFAM; PF00129; MHC_I; 1.
 CC KW MHC I; Transmembrane; Glycoprotein; Signal.
 CC FT SIGNAL 1 24
 CC FT CHAIN 25 362

CC HLA CLASS I HISTOCOMPATIBILITY ANTIGEN,
 CC B-18 B*1801 ALPHA CHAIN.
 CC FT DOMAIN 25 114
 CC FT DOMAIN 115 206
 CC FT DOMAIN 207 298
 CC FT DOMAIN 299 309
 CC FT TRANSMEM 310 333
 CC FT DOMAIN 334 362
 CC FT CARBOHYD 110 110
 CC FT DISULFID 125 188
 CC FT DISULFID 227 283

CC CYTOPLASMIC TAIL.
 CC BY SIMILARITY.
 CC BY SIMILARITY.
 CC BY SIMILARITY.
 CC BY SIMILARITY.
 CC SEQUENCE 362 AA; 40275 MW; 038EC3FC CRC32;

Query Match 50.0%; Score 51; DB 1; Length 362;
 Best Local Similarity 100.0%; Pred. No. 0.82;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 RESLNRLRGY 20
 |||||
 Db 99 RESLNRLRGY 108

RESULT 13
 1B21_HUMAN

ID 1B21_HUMAN STANDARD; PRT; 362 AA.
 AC P30685;
 DT 01-APR-1993 (Rel. 25, Created)
 DT 01-APR-1993 (Rel. 25, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-35 B*3501 ALPHA CHAIN
 DE PRECURSOR.
 GN HLA-B OR HLAB.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia;
 OC Eutheria; Primates; Catarrhini; Hominidae; Homo.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 89339610.
 RA COBA T., HAYASHI H., KARAKI S., TANABE M., KANO K., TAKIGUCHI M.;
 RT "The structure of HLA-B*35 suggests that it is derived from HLA-B*58
 RT by two genetic mechanisms."
 RL Immunogenetics 30:76-80(1989).
 RN [2]
 RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF 25-300.
 RX MEDLINE; 96209671.
 RA SMITH K.J., REID S.W., STUART D.I., MCMICHAEL A.J., JONES E.Y.,
 RA BELL J.I.;
 RT "An altered position of the alpha 2 helix of MHC class I is revealed
 RT by the crystal structure of HLA-B*3501."
 RL Immunity 4:203-214(1996).
 RN [3]

CC X-RAY CRYSTALLOGRAPHY (3.2 ANGSTROMS).
 CC RA MENSSON R., ORTH P., ZIEGLER A., SAENGER W.;
 CC Submitted (APR-1998) to the PDB data bank.
 CC RL -1- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
 CC THE IMMUNE SYSTEM.
 CC -1- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
 CC MICROGLOBULIN).

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CC -----
 CC EMBL; M28115; AAA59617.1; -
 CC DR MIM; 142830; -
 CC DR PROSITE; PS00290; IG_MHC; 1.
 CC DR PFAM; PF00047; Ig; 1.
 CC DR PFAM; PF00129; MHC_I; 1.
 CC KW MHC I; Transmembrane; Glycoprotein; Signal; 3D-structure.
 CC FT SIGNAL 1 24
 CC FT CHAIN 25 362

CC HLA CLASS I HISTOCOMPATIBILITY ANTIGEN,
 CC B-35 B*3501 ALPHA CHAIN.
 CC FT DOMAIN 25 114
 CC FT DOMAIN 115 206
 CC FT DOMAIN 207 298
 CC FT DOMAIN 299 308
 CC FT TRANSMEM 309 332
 CC FT DOMAIN 333 362
 CC FT CARBOHYD 110 110
 CC FT DISULFID 125 188
 CC FT DISULFID 227 283

CC CYTOPLASMIC TAIL.
 CC BY SIMILARITY.
 CC BY SIMILARITY.
 CC BY SIMILARITY.
 CC SEQUENCE 362 AA; 40455 MW; AECIC675 CRC32;

Query Match 50.0%; Score 51; DB 1; Length 362;
 Best Local Similarity 100.0%; Pred. No. 0.82;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 RESLNRLRGY 20
 |||||
 Db 99 RESLNRLRGY 108

RESULT 14
 1B22_HUMAN

ID 1B22_HUMAN STANDARD; PRT; 362 AA.
 AC P30468;
 DT 01-APR-1993 (Rel. 25, Created)
 DT 01-APR-1993 (Rel. 25, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-35 B*3502 ALPHA CHAIN
 DE PRECURSOR.
 GN HLA-B OR HLAB.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia;
 OC Eutheria; Primates; Catarrhini; Hominidae; Homo.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 91365651.
 RA CHERTKOFF L.P., HERRERA M., FAIBOIM L., SATZ M.L.;
 RT "Completed nucleotide sequence of a genomic clone encoding HLA-B*35
 RT isolated from a Caucasian individual of Hispanic origin.
 RT Identification of a new variant of HLA-B*35."
 RL Hum. Immunol. 31:153-158(1991)
 CC -1- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
 CC THE IMMUNE SYSTEM.
 CC -1- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
 CC MICROGLOBULIN).

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OM protein - protein search, using sw model

Run on: February 8, 2000, 19:16:13 ; Search time 176.54 Seconds
(without alignments)
7.855 Million cell updates/sec

Title: US-08-653-294-27

Perfect score: 102

Sequence: 1 YGRNLSRRESLNLRG 20

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 225878 seqs, 69334122 residues

Total number of hits satisfying chosen parameters: 225878

Minimum DB seq length: 0

Maximum DB seq length: 1000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

SPREMBL12.*
1: sp_archaea.*
2: sp_bacteria.*
3: sp_fungi.*
4: sp_human.*
5: sp_invertebrate.*
6: sp_mammal.*
7: sp_mhc.*
8: sp_organelle.*
9: sp_phase.*
10: sp_plant.*
11: sp_rudent.*
12: sp_virus.*
13: sp_vertebrate.*
14: sp_unclassified.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	51	50.0	81	7 O19523	O19523 homo sapien
2	51	50.0	81	7 O19525	O19525 homo sapien
3	51	50.0	81	7 O19527	O19527 homo sapien
4	51	50.0	81	7 O19529	O19529 homo sapien
5	51	50.0	81	7 O19531	O19531 homo sapien
6	51	50.0	81	7 O19533	O19533 homo sapien
7	51	50.0	81	7 O19535	O19535 homo sapien
8	51	50.0	81	7 O19537	O19537 homo sapien
9	51	50.0	83	7 O19539	O19539 homo sapien
10	51	50.0	83	7 O19541	O19541 homo sapien
11	51	50.0	83	7 O19543	O19543 homo sapien
12	51	50.0	89	4 Q9F452	Q9F452 homo sapien
13	51	50.0	89	7 P79615	P79615 homo sapien
14	51	50.0	89	7 P79620	P79620 homo sapien
15	51	50.0	89	7 O19548	O19548 homo sapien
16	51	50.0	89	7 O19549	O19549 homo sapien
17	51	50.0	89	7 O19550	O19550 homo sapien
18	51	50.0	89	7 O19551	O19551 homo sapien
19	51	50.0	89	7 O19640	O19640 homo sapien
20	51	50.0	89	7 O77967	O77967 homo sapien

21	51	50.0	89	7 O78174	O78174 homo sapien
22	51	50.0	89	7 O19638	O19638 homo sapien
23	51	50.0	89	7 P79487	P79487 homo sapien
24	51	50.0	89	7 O19587	O19587 homo sapien
25	51	50.0	89	7 O19576	O19576 homo sapien
26	51	50.0	89	7 O19577	O19577 homo sapien
27	51	50.0	89	7 O19581	O19581 homo sapien
28	51	50.0	89	7 O19583	O19583 homo sapien
29	51	50.0	112	7 O92671	O92671 homo sapien
30	51	50.0	134	7 Q29677	Q29677 homo sapien
31	51	50.0	137	7 Q29660	Q29660 homo sapien
32	51	50.0	137	7 Q29663	Q29663 homo sapien
33	51	50.0	137	7 Q29665	Q29665 homo sapien
34	51	50.0	137	7 Q29664	Q29664 homo sapien
35	51	50.0	147	7 Q29707	Q29707 homo sapien
36	51	50.0	165	7 P79665	P79665 homo sapien
37	51	50.0	165	7 P79666	P79666 homo sapien
38	51	50.0	166	7 O19777	O19777 homo sapien
39	51	50.0	166	7 O19778	O19778 homo sapien
40	51	50.0	172	7 O19776	O19776 homo sapien
41	51	50.0	176	7 Q29662	Q29662 homo sapien
42	51	50.0	179	7 Q29676	Q29676 homo sapien
43	51	50.0	180	7 Q29678	Q29678 homo sapien
44	51	50.0	180	7 O77960	O77960 homo sapien
45	51	50.0	181	7 Q29716	Q29716 homo sapien

ALIGNMENTS

```

RESULT 1
O19523      PRELIMINARY;          PRT;      81 AA.
AC  O19523;
DT  01-JAN-1998 (TRENBLrel. 05, Created)
DT  01-JAN-1998 (TRENBLrel. 05, Last sequence update)
DT  01-NOV-1998 (TRENBLrel. 08, Last annotation update)
DE  MHC CLASS I ANTIGEN HLA-B (FRAGMENT).
GN  HLA-B.
OS  Homo sapiens (Human).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC  Eutheria; Primates; Catarrhini; Hominidae; Homo.
RN  [1]
RP  CHANDANAYINGTONG D., SIRIKONG M., LUANGTRAKOOL K., SRINAK D.,
RA  RUNGROUNG E., BECHANDRA S.;
RL  Submitted (JUL-1997) to the EMBL/GenBank/DBJ databases.
DR  EMBL; AF014769; AAB67807.1;
DR  PFAM; PF00129; MHC_I; 1.
KW  MHC.
FT  NON_TER 1 1
FT  NON_TER 81 81
SQ  SEQUENCE 81 AA; 9405 MW; 073087CE CRC32;

Query Match      50.0%; Score 51; DB 7; Length 81;
Best Local Similarity 100.0%; Pred. No. 1.2;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  11 RESLNLRGY 20
Db  66 RESLNLRGY 75

RESULT 2
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AC  O19525;
DT  01-JAN-1998 (TRENBLrel. 05, Created)
DT  01-JAN-1998 (TRENBLrel. 05, Last sequence update)
DT  01-NOV-1998 (TRENBLrel. 08, Last annotation update)
DE  MHC CLASS I ANTIGEN HLA-B (FRAGMENT).
GN  HLA-B.

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OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Primates; Catarrhini; Hominidae; Homo.
[1]
RN SEQUENCE FROM N.A.
RA CHANDANAYINGYONG D., SIRIKONG M., LUANGTRAKOOL K., SRINAK D.,
RA RUNGRONG E., BEJCHANDRA S.;
RL Submitted (JUL-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF014771; AAB67809.1; -
DR PFAM; PF00129; MHC_I; 1.
KW MHC.
FT NON_TER 1
FT NON_TER 81
SQ SEQUENCE 81 AA; 9405 MW; 073087CE CRC32;

Query Match 50.0%; Score 51; DB 7; Length 81;
Best Local Similarity 100.0%; Pred. No. 1.2;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 RESLRNLRGY 20
DB 66 RESLRNLRGY 75

RESULT 3
ID O19527 PRELIMINARY; PRT; 81 AA.
AC O19527;
DT 01-JAN-1998 (TREMBLrel. 05, Created)
DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
DT 01-NOV-1998 (TREMBLrel. 08, Last annotation update)
DE MHC CLASS I ANTIGEN HLA-B (FRAGMENT).
GN HLA-B.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Primates; Catarrhini; Hominidae; Homo.
[1]
RN SEQUENCE FROM N.A.
RA CHANDANAYINGYONG D., SIRIKONG M., LUANGTRAKOOL K., SRINAK D.,
RA RUNGRONG E., BEJCHANDRA S.;
RL Submitted (JUL-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF014773; AAB67811.1; -
DR PFAM; PF00129; MHC_I; 1.
KW MHC.
FT NON_TER 1
FT NON_TER 81
SQ SEQUENCE 81 AA; 9405 MW; 073087CE CRC32;

Query Match 50.0%; Score 51; DB 7; Length 81;
Best Local Similarity 100.0%; Pred. No. 1.2;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 RESLRNLRGY 20
DB 66 RESLRNLRGY 75

RESULT 4
ID O19529 PRELIMINARY; PRT; 81 AA.
AC O19529;
DT 01-JAN-1998 (TREMBLrel. 05, Created)
DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
DT 01-NOV-1998 (TREMBLrel. 08, Last annotation update)
DE MHC CLASS I ANTIGEN HLA-B (FRAGMENT).
GN HLA-B.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Primates; Catarrhini; Hominidae; Homo.
[1]
RN SEQUENCE FROM N.A.
RA CHANDANAYINGYONG D., SIRIKONG M., LUANGTRAKOOL K., SRINAK D.,
RA RUNGRONG E., BEJCHANDRA S.;
RL Submitted (JUL-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF014773; AAB67811.1; -
DR PFAM; PF00129; MHC_I; 1.

RA CHANDANAYINGYONG D., SIRIKONG M., LUANGTRAKOOL K., SRINAK D.,
RA RUNGRONG E., BEJCHANDRA S.;
RL Submitted (JUL-1997) to the EMBL/GenBank/DBJ databases.
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DR PFAM; PF00129; MHC_I; 1.
KW MHC.
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FT NON_TER 81
SQ SEQUENCE 81 AA; 9405 MW; 073087CE CRC32;

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Best Local Similarity 100.0%; Pred. No. 1.2;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 RESLRNLRGY 20
DB 66 RESLRNLRGY 75

RESULT 5
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AC O19531;
DT 01-JAN-1998 (TREMBLrel. 05, Created)
DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
DT 01-NOV-1998 (TREMBLrel. 08, Last annotation update)
DE MHC CLASS I ANTIGEN HLA-B (FRAGMENT).
GN HLA-B.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Primates; Catarrhini; Hominidae; Homo.
[1]
RN SEQUENCE FROM N.A.
RA CHANDANAYINGYONG D., SIRIKONG M., LUANGTRAKOOL K., SRINAK D.,
RA RUNGRONG E., BEJCHANDRA S.;
RL Submitted (JUL-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF014777; AAB67815.1; -
DR PFAM; PF00129; MHC_I; 1.
KW MHC.
FT NON_TER 1
FT NON_TER 81
SQ SEQUENCE 81 AA; 9405 MW; 073087CE CRC32;

Query Match 50.0%; Score 51; DB 7; Length 81;
Best Local Similarity 100.0%; Pred. No. 1.2;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 RESLRNLRGY 20
DB 66 RESLRNLRGY 75

RESULT 6
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AC O19533;
DT 01-JAN-1998 (TREMBLrel. 05, Created)
DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
DT 01-NOV-1998 (TREMBLrel. 08, Last annotation update)
DE MHC CLASS I ANTIGEN HLA-B (FRAGMENT).
GN HLA-B.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Primates; Catarrhini; Hominidae; Homo.
[1]
RN SEQUENCE FROM N.A.
RA CHANDANAYINGYONG D., SIRIKONG M., LUANGTRAKOOL K., SRINAK D.,
RA RUNGRONG E., BEJCHANDRA S.;
RL Submitted (JUL-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF014775; AAB67817.1; -
DR PFAM; PF00129; MHC_I; 1.

KW MHC.
 FT NON_TER 1
 FT NON_TER 81
 SQ SEQUENCE 81 AA; 9405 MW; 073087CE CRC32;

Query Match 50.0%; Score 51; DB 7; Length 81;
 Best Local Similarity 100.0%; Pred. No. 1.2;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 RESLNLRGY 20
 Db 66 RESLNLRGY 75

RESULT 7
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AC O19535;
 DT 01-JAN-1998 (TREMBlrel. 05, Created)
 DT 01-JAN-1998 (TREMBlrel. 05, Last sequence update)
 DT 01-NOV-1998 (TREMBlrel. 08, Last annotation update)
 DE MHC CLASS I ANTIGEN HLA-B (FRAGMENT).
 GN HLA-B.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Eutheria; Primates; Catarrhini; Hominidae; Homo.
 RN [1]
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 RA CHANDANAYINGYONG D., SIRIKONG M., LUANGTRAKOOL K., SRINAK D.,
 RA RUNGROUNG E., BEJCHANDRA S.;
 RL Submitted (JUL-1997) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF014781; AAB67819.1;
 DR PFAM; PF00129; MHC_I; 1.
 KW MHC.
 FT NON_TER 1
 FT NON_TER 81
 SQ SEQUENCE 81 AA; 9405 MW; 073087CE CRC32;

Query Match 50.0%; Score 51; DB 7; Length 81;
 Best Local Similarity 100.0%; Pred. No. 1.2;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 RESLNLRGY 20
 Db 66 RESLNLRGY 75

RESULT 8
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AC O19537;
 DT 01-JAN-1998 (TREMBlrel. 05, Created)
 DT 01-JAN-1998 (TREMBlrel. 05, Last sequence update)
 DT 01-NOV-1998 (TREMBlrel. 08, Last annotation update)
 DE MHC CLASS I ANTIGEN HLA-B (FRAGMENT).
 GN HLA-B.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Eutheria; Primates; Catarrhini; Hominidae; Homo.
 RN [1]
 RP SEQUENCE FROM N.A.
 RA CHANDANAYINGYONG D., SIRIKONG M., LUANGTRAKOOL K., SRINAK D.,
 RA RUNGROUNG E., BEJCHANDRA S.;
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 DR EMBL; AF014783; AAB67821.1;
 DR PFAM; PF00129; MHC_I; 1.
 KW MHC.
 FT NON_TER 1
 FT NON_TER 81
 SQ SEQUENCE 81 AA; 9405 MW; 073087CE CRC32;

Query Match 50.0%; Score 51; DB 7; Length 81;
 Best Local Similarity 100.0%; Pred. No. 1.2;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 RESLNLRGY 20
 Db 66 RESLNLRGY 75

RESULT 9
 O19539 PRELIMINARY; PRT; 83 AA.

AC O19539;
 DT 01-JAN-1998 (TREMBlrel. 05, Created)
 DT 01-JAN-1998 (TREMBlrel. 05, Last sequence update)
 DT 01-NOV-1998 (TREMBlrel. 08, Last annotation update)
 DE MHC CLASS I ANTIGEN HLA-B (FRAGMENT).
 GN HLA-B.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Eutheria; Primates; Catarrhini; Hominidae; Homo.
 RN [1]
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 RA CHANDANAYINGYONG D., SIRIKONG M., LUANGTRAKOOL K., SRINAK D.,
 RA RUNGROUNG E., BEJCHANDRA S.;
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 DR EMBL; AF014785; AAB67823.1;
 DR PFAM; PF00129; MHC_I; 1.
 KW MHC.
 FT NON_TER 1
 FT NON_TER 83
 SQ SEQUENCE 83 AA; 9731 MW; 24B8D666 CRC32;

Query Match 50.0%; Score 51; DB 7; Length 83;
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 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 RESLNLRGY 20
 Db 58 RESLNLRGY 77

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AC O19541;
 DT 01-JAN-1998 (TREMBlrel. 05, Created)
 DT 01-JAN-1998 (TREMBlrel. 05, Last sequence update)
 DT 01-NOV-1998 (TREMBlrel. 08, Last annotation update)
 DE MHC CLASS I ANTIGEN HLA-B (FRAGMENT).
 GN HLA-B.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Eutheria; Primates; Catarrhini; Hominidae; Homo.
 RN [1]
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 RA CHANDANAYINGYONG D., SIRIKONG M., LUANGTRAKOOL K., SRINAK D.,
 RA RUNGROUNG E., BEJCHANDRA S.;
 RL Submitted (JUL-1997) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF014787; AAB67825.1;
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 FT NON_TER 1
 FT NON_TER 83
 SQ SEQUENCE 83 AA; 9731 MW; 24B8D666 CRC32;

Query Match 50.0%; Score 51; DB 7; Length 83;
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 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 RESLNLRGY 20
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 Db 68 RESLNLRGY 77

RESULT 11

O19543 PRELIMINARY; PRT; 83 AA.
 AC O19543;
 DT 01-JAN-1998 (TREMBLrel. 05, Created)
 DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
 DT 01-NOV-1998 (TREMBLrel. 08, Last annotation update)
 DE MHC CLASS I ANTIGEN HLA-B (FRAGMENT).
 GN HLA-B.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Eutheria; Primates; Catarrhini; Hominiidae; Homo.
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 RA CHANDANAYONG D., SIRIKONG M., LUANGTRAKOOL K., SRINAK D.,
 RA RUNGROUNG E., BEJCHANDRA S.,
 RL Submitted (JUL-1997) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF014789; AAB67827.1; -.
 DR PFAM; PF00129; MHC_I; 1.
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 FT NON_TER 1 1
 FT NON_TER 83 83
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Query Match 50.0%; Score 51; DB 7; Length 83;
 Best Local Similarity 100.0%; Pred. No. 1.2;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 Db 68 RESLNLRGY 77

RESULT 12

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 AC O9Y452;
 DT 01-NOV-1999 (TREMBLrel. 12, Created)
 DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)
 DT 01-NOV-1999 (TREMBLrel. 12, Last annotation update)
 DE HUMAN LEUCOCYTE ANTIGEN B (FRAGMENT).
 GN HLA-B.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 RN [1]
 RP SEQUENCE FROM N.A.
 RA CARTER V., DUNN P.P.;
 FT "Identification of a novel HLA-B*07 allele."
 RL Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AJ237594; CAB40714.1; -.
 FT NON_TER 1 1
 FT NON_TER 89 89
 SQ SEQUENCE 89 AA; 10609 MW; 659B735B CRC32;

Query Match 50.0%; Score 51; DB 4; Length 89;
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Qy 11 RESLNLRGY 20
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 Db 74 RESLNLRGY 83

RESULT 13

P79615 PRELIMINARY; PRT; 89 AA.
 AC P79615;
 DT 01-MAY-1997 (TREMBLrel. 03, Created)
 DT 01-MAY-1997 (TREMBLrel. 03, Last sequence update)
 DT 01-NOV-1998 (TREMBLrel. 08, Last annotation update)
 DE MHC CLASS I HLA-B (FRAGMENT).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 RN [1]
 RP SEQUENCE FROM N.A.
 RA CHOPEK M., CAO K., ZHANG G.H.;
 RL Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.
 DR EMBL; U88249; AAB48493.1; -.
 DR PFAM; PF00129; MHC_I; 1.
 KW MHC.
 FT NON_TER 1 1
 FT NON_TER 89 89
 SQ SEQUENCE 89 AA; 10489 MW; A7D3DF93 CRC32;

Query Match 50.0%; Score 51; DB 7; Length 89;
 Best Local Similarity 100.0%; Pred. No. 1.3;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 RESLNLRGY 20
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 Db 74 RESLNLRGY 83

RESULT 14

P79620 PRELIMINARY; PRT; 89 AA.
 AC P79620;
 DT 01-MAY-1997 (TREMBLrel. 03, Created)
 DT 01-MAY-1997 (TREMBLrel. 03, Last sequence update)
 DT 01-NOV-1998 (TREMBLrel. 08, Last annotation update)
 DE MHC CLASS I HLA-B (FRAGMENT).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 RN [1]
 RP SEQUENCE FROM N.A.
 RA CHOPEK M., CAO K., ZHANG G.H.;
 RL Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.
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 KW MHC.
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 FT NON_TER 89 89
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Query Match 50.0%; Score 51; DB 7; Length 89;
 Best Local Similarity 100.0%; Pred. No. 1.3;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 RESLNLRGY 20
 |||||
 Db 74 RESLNLRGY 83

RESULT 15

O19548 PRELIMINARY; PRT; 89 AA.
 AC O19548;
 DT 01-JAN-1998 (TREMBLrel. 05, Created)
 DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
 DT 01-NOV-1998 (TREMBLrel. 08, Last annotation update)
 DE MHC CLASS I ANTIGEN (FRAGMENT).
 GN HLA-B.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;

OC Eutheria; Primates; Catarrhini; Hominoidea; Homo.
RN [1]
RP SEQUENCE FROM N.A.
RA CAO K., BURDETT L., ZHANG H., FERNANDEZ-VINA M.;
EL Submitted (JUL-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF016299; AAB69444.1; -.
DR PFAM; PF00129; MHC_I; 1.
KW MHC.
FT NON_TER 1
FT NON_TER 89
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Query Match 50.0%; Score 51; DB 7; Length 89;
Best Local Similarity 100.0%; Pred. No. 1.3;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 RESLNLRGY 20
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Db 74 RESLNLRGY 83

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Job time: 21500 sec

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Genes were identified by a combination of three methods: Gene prediction programs including GRAIL (available by anonymous ftp from arthur.epm.ornl.gov), Genefinder (Phil Green, University of Washington), Genscan (Chris Burge, <http://gnomic.stanford.edu/~chris/GENSCANW.html>), and NetPlantGene (<http://www.cbs.dtu.dk/netgene/cbsnetgene.html>), searches of the complete sequence against a peptide database and the Arabidopsis EST database at TIGR (<http://www.tigr.org/tdb/at/at.html>). Annotated genes are named to indicate the level of evidence for their annotation. Genes with similarity to other proteins are named after the database hits. Genes without significant peptide similarity but with EST similarity are named as 'unknown' proteins. Genes without protein or EST similarity, that are predicted by more than two gene prediction programs over most of their length are annotated as 'hypothetical' proteins. Genes encoding tRNAs are predicted by tRNAscan-SE (Sean Eddy,

http://genome.wustl.edu/eddy/TrnScan-SE/. Simple repeats are identified by repeatmasker (Arian Smit).
http://ftp.genome.washington.edu/RW/RepeatMasker.html). Regions of genomic sequence that are not annotated as genes but have predicted exons by GRAIL are annotated as misc features.

FEATURES

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SEAAQLTLELDFORFKLDGLDKLFLGLEAVARTAGISICQRYKALELLELSTGLMA
CKEVPVPMPLNKRKDDGLIEDIQRIRVIGKLMYLTITRPDIITFAVNLQCFSSA
PRTHLTAAVRVQYIKGTGVLFSASDLTKGFADSNWASQDSRRSTSTFMF
VGPLTSWRSKQKQHTVSRSAEYRALATCEMWLFTLLVLSQASPPVPTLYSDS
TAATYATNPVFERHKKHLKDCHTVRERLDNGELKLLHVRTEDQVADILTRPLFYQ
FEHLKMSILNIFSCSS"
10299..10369
/rpt_family="(GAAA)n"
join(<13346..13547,13635..>13735)
/genes="F7H1.3"
<13346..>13735
/genes="F7H1.3"
join(13346..13547,13635..13735)
/genes="F7H1.3"
/codon_start=1
/product="similar to replication protein A1"
/db_xref="GI:4678198"
/translation="MVPGEWKATENGLTYAKFKATNHRKMGFMATKTRVRMEPLSD
SYLSTLSFTDVLVTGLNQNLIDVVGVQIVNGEMETINVHNKPTKKINFELDRHK"

repeat_region
14805..14919
/rpt_family="(CAT)n"
repeat_region
18429..18462
/rpt_family="(GAA)n"
<21092..>21322
/genes="F7H1.4"
<21092..>21322
/genes="F7H1.4"
/notes="predicted by genscan and genefinder"
21092..21322
/genes="F7H1.4"
/notes="hypothetical protein"
/codon_start=1
/protein_id="AAD26945.1"
/db_xref="GI:4678199"
/translation="MEALVVVHKVASEGGRRPKTTVSDSGSHREKGSFQVKDSPE
NMYATCKVDSLRSFSSSYNQERQSEQR"
complement(21381..21407)
/rpt_family="POLY_A"
complement(<21932..>22627)
/genes="F7H1.5"
complement(<21932..>22627)
/genes="F7H1.5"
/notes="predicted by genscan and genefinder"
complement(21932..22627)
/genes="F7H1.5"
/notes="hypothetical protein"
/codon_start=1
/protein_id="AAD26946.1"
/db_xref="GI:4678200"
/translation="MERNVVKMLKRVISVFLSIGTVLMVIMLOTPKTCISPEAPSKP
HFFPRSTCDSPRQHLPLPKNARIWSSGANKSRYSFSTVFLRDLGFIQNHHTKA
LCISAGAGHMAALSOIGLSDVTAVELVDSIPLVKRADPHNLPEFGVDFDEAFTALA
EALFPQFVEEMERTVRRGFCVSVDECGDDVDIARLFHNSKVVDVAVNTLESGK
KTSILFKVQDSPT"
join(<23753..24059,24489..>25330)
/genes="F7H1.6"
<23753..>25330
/genes="F7H1.6"
/notes="predicted by genscan and genefinder"
join(23753..24059,24489..25330)
/genes="F7H1.6"
/notes="hypothetical protein"
/codon_start=1
/protein_id="AAD26947.1"
/db_xref="GI:4678201"
/translation="MIGFNSDMKEHIREANKGEIHCHEPHSKSONELTELLANDTKM
MLKKIKDKRYSVILDSIPDSVRKEQMTFLRCVDVSTCSKIEBFFLFLHKDKR
EYTDNPHGRSDVESLSTHETGIGGFELFGIMLWYDLAAVNVSKSIOFEDMDLEV
AISOGLGVLYKNYKTEFEKAVESTQIAIEMKIAPVFKKSKKKQFVEDVEKI
DSKTAESFRIDYFINIMQAIMCIEIRFEQVQYQIFGFLGVKRLKVAEDDELK
TSCMKLEASLRKHDSVDGDELMELEKLLKDVLPKEITKPVLEVLKFLKIMDSYPT
WYARLLTIPVSVALAERTFSKLKILKYLKSLRSTMSQERLNGALISV"
<28186..>28689
/genes="F7H1.7"
<28186..>28689
/genes="F7H1.7"
/notes="predicted by genscan"
28186..28689
/genes="F7H1.7"
/notes="hypothetical protein"

alignment_scores
Quality: 52.00 Length: 17
Ratio: 3.467 Gaps: 0
Percent Similarity: 88.235 Percent Identity: 52.941
alignment_block
US-08-653-294-27 x ATAC007134
Align seg 1/1 to: ATAC007134 from: 1 to: 84544
4 LeuAsnArgLeuSerGluArgArgGluSerLeuArgAsnLeuArgGlyTy 20
```

```

:::|||||
78760 AATAATGATCAAGCCAGGCGTAACCAATTGAATAATCTTGGGTA 78809

```

```

20 r 20

```

```

78810 T 78810

```

```

seq_name: gb_htg6:AC010932

```

```

seq_documentation_block:
LOCUS AC010932 203273 bp DNA HTG 30-NOV-1999
DEFINITION Homo sapiens chromosome 15 clone RP11-296E22 map 15, *** SEQUENCING
IN PROGRESS ***, 36 unordered pieces.
ACCESSION AC010932
VERSION AC010932.2 GI:6479157
KEYWORDS HTG; HTGS_PHASE1.
SOURCE human.

```

ORGANISM

```

Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.

```

```

1 (bases 1 to 203273)

```

```

Birken, B., Linton, L., Nusbaum, C. and Lander, E.

```

```

Homo sapiens chromosome 15, clone RP11-296E22

```

```

Unpublished

```

```

2 (bases 1 to 203273)

```

```

Birken, B., Linton, L., Nusbaum, C., Lander, E., Allen, N., Anderson, M.,
Balgwin, J., Barna, N., Beckerly, R., Boguslavskiy, L., Boukhgalter, B.,
Brown, A., Castle, A., Collangelo, M., Collins, S., Collymore, A.,
Cooke, P., DeArelano, K., Dewar, K., Domino, M., Donegan, L., Doyle, M.,
Ferreira, P., FitzHugh, W., Forrest, C., Funke, R., Gage, D.,
Galagan, J., Gardyna, S., Grant, G., Hagos, B., Heaford, A., Horton, L.,
Howland, J.C., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J.,
Lehoczy, J., Lien, C., Locke, K., Macdonald, P., Marquis, N.,
McEwan, P., McGurk, A., McKernan, K., McLaughlin, J., Meldrim, J.,
Morrow, J., Naylor, J., Norman, C.H., O'Connor, T., O'Donnell, P.,
Peterson, K., Pollara, V., Riley, R., Roy, A., Santos, R., Severy, P.,
Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J.,
Testaye, S., Tirrell, A., Vassiliev, H., Vo, A., Wheeler, J., Wu, X.,
Wyman, D., Ye, W.J., Zimmer, A. and Zody, M.

```

```

Direct Submission

```

```

Submitted (28-SEP-1999) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA

```

```

On Nov 30, 1999 this sequence version replaced gi:5931431.

```

```

All repeats were identified using RepeatMasker:

```

```

Smit, A.F.A. & Green, P. (1996-1997)

```

```

http://ftp.genome.washington.edu/RM/RepeatMasker.html

```

```

----- Genome Center

```

```

Center: Whitehead Institute/ MIT Center for Genome Research

```

```

Center code: WIBR

```

```

Web site: http://www-seq.wi.mit.edu

```

```

Contact: sequence_submission@genome.wi.mit.edu

```

```

----- Project Information

```

```

Center project name: L1684

```

```

Center clone name: 296_E_22

```

```

-----

```

```

* NOTE: This is a 'working draft' sequence. It currently
* consists of 36 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

```

```

1 1375: contig of 1375 bp in length

```

```

1376 gap of unknown length

```

```

3332: contig of 1957 bp in length

```

```

3333 gap of unknown length

```

```

4414: contig of 1082 bp in length

```

```

4415 gap of unknown length

```

```

6085: contig of 1671 bp in length

```

```

6086 gap of unknown length

```

```

7636: contig of 1551 bp in length

```

```

gap of unknown length

```

```

7637 9176: contig of 1540 bp in length
9177 gap of unknown length
11451: contig of 2275 bp in length
11452 gap of unknown length
14012: contig of 2561 bp in length
14013 gap of unknown length
15805: contig of 1793 bp in length
15806 gap of unknown length
17914: contig of 2109 bp in length
17915 gap of unknown length
20644: contig of 2730 bp in length
20645 gap of unknown length
23409: contig of 2765 bp in length
23410 gap of unknown length
26283: contig of 2874 bp in length
26284 gap of unknown length
28593: contig of 2310 bp in length
28594 gap of unknown length
31564: contig of 2971 bp in length
31565 gap of unknown length
34023: contig of 2459 bp in length
34024 gap of unknown length
36890: contig of 2867 bp in length
36891 gap of unknown length
41485: contig of 4595 bp in length
41486 gap of unknown length
45667: contig of 4182 bp in length
45668 gap of unknown length
49439: contig of 3771 bp in length
49439 gap of unknown length
53273: contig of 3835 bp in length
53274 gap of unknown length
56613: contig of 3340 bp in length
56614 gap of unknown length
61902: contig of 5289 bp in length
61903 gap of unknown length
67950: contig of 6048 bp in length
67951 gap of unknown length
74487: contig of 6537 bp in length
74488 gap of unknown length
82190: contig of 7703 bp in length
82191 gap of unknown length
91448: contig of 9258 bp in length
91449 gap of unknown length
98969: contig of 7521 bp in length
98970 gap of unknown length
109518: contig of 10549 bp in length
109519 gap of unknown length
119016: contig of 9498 bp in length
119017 gap of unknown length
127923: contig of 8907 bp in length
127924 gap of unknown length
139858: contig of 11935 bp in length
139859 gap of unknown length
152524: contig of 12666 bp in length
152525 gap of unknown length
164676: contig of 12152 bp in length
164677 gap of unknown length
183255: contig of 18579 bp in length
183256 gap of unknown length
203273: contig of 20018 bp in length.

```

FEATURES

Location/Qualifiers

```

1. 203273
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="15"
/map="15"
/clone="RP11-296E22"
/clone_lib="RPC1-11 Human Male BAC"
54651 a 48192 c 46411 g 53915 t 104 others

```

BASE COUNT

ORIGIN

```

alignment_scores:
  Quality: 51.50      Length: 23
  Ratio: 2.861        Gaps: 1
  Percent Similarity: 52.174

alignment_block:
  US-08-653-294-27 x AC010932/rev ..
  Align seg 1/1 to reverse of: AC010932 from: 1 to: 203273

  1 TyrGlyArgLeuAsnArgLeuSerGluArgGlyTyr.....Le 14
  ||||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
  24858 TATGCAGGAATGGGAGATCTCAGATAAAGATATCTCTCTGTACCGT 24809

  14 uArgAsnLeuArgGlyTyr 20
  ||||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
  24808 CAAAATCTCAGAGGCTAC 24790

seq_name: gb_pr2: HSHLABK1

seq_documentation_block:
LOCUS HSHLABK1 243 bp DNA PRI 26-MAR-1997
DEFINITION Human cell line THAI DCH022 MHC class I HLA-B gene (allele
HLA-B*1521), exon 2.
ACCESSION U91332
VERSION U91332.1 GI:1906671
KEYWORDS
SEGMENT
SOURCE
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 243)
AUTHORS Chandanayingyong,D., Sirikong,M., Srinak,D., Longta,K.,
Rungroung,E., Bejchandra,S., Juji,T., Tokunaga,K. and
Grosse-Wilde,H.
TITLE B15 alleles (B*1525)
JOURNAL Unpublished
REFERENCE
2 (bases 1 to 243)
AUTHORS Chandanayingyong,D., Sirikong,M., Srinak,D., Longta,K.,
Rungroung,E., Bejchandra,S., Juji,T., Tokunaga,K. and
Grosse-Wilde,H.
TITLE Direct Submission
JOURNAL Submitted (26-FEB-1997) Transfusion Medicine, Faculty of Medicine,
Siriraj Hospital, Mahidol University, Prannok Road, Bangkok 10700,
Thailand
FEATURES
source Location/Qualifiers
1..243
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="6"
/map="6p21"
/cell_type="lymphoblastoid"
/cell_line="THAI DCH022"
1..243
/gene="HLA-B"
/note="similar to exon 2 of B*1501"
/number=2
BASE COUNT 52 a 79 c 84 g 28 t
ORIGIN
alignment_scores:
  Quality: 51.00      Length: 10
  Ratio: 5.100        Gaps: 0
  Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
  US-08-653-294-27 x HSHLABM1 ..
  Align seg 1/1 to: HSHLABM1 from: 1 to: 243

  11 ArgGluSerLeuArgAsnLeuArgGlyTyr 20
  ||||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
  195 CGAGAGAGCCTCGGAACTCGCGGCTAC 224

seq_name: gb_pr2: HSHLABO1

seq_documentation_block:
LOCUS HSHLABO1 243 bp DNA PRI 26-MAR-1997
DEFINITION Human cell line THAI DCH012 MHC class I HLA-B gene (allele
HLA-B*1525), exon 2.
ACCESSION U91336
VERSION U91336.1 GI:1906679
KEYWORDS
SEGMENT
SOURCE
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 243)

```


5

```

/feature="HLA-B"
/feature="2"
/number=2
<1..>246
/feature="HLA-B"
/codon_start=3
/product="MHC class I antigen HLA-B"
/protein_id="AAB67809.1"
/db_xref="GI:2345108"
/translation="TAMSPGGRGEPRFIAVGVDDTQFVRFSDAASPRMAPRAPWIE
QEGPEYWDRTQISKNTQTYRESLRNLRGYNQSEA"
BASE COUNT      55 a      81 c      82 g      28 t
ORIGIN

```

```

alignment_scores:
  Quality: 51.00      Length: 10
  Ratio: 5.100      Gaps: 0
  Percent Similarity: 100.000      Percent Identity: 100.000

```

```

alignment_block:
US-08-653-294-27 x AF014771 ..

```

```

Align seg 1/1 to: AF014771 from: 1 to: 246

```

```

11 ArgGlusSerLeuArgAsnLeuArgGlyTyr 20
|||||
198 CGAGAGAGCCTGCGGACCTGCGGCGCTAC 227

```

```

seq_name: gb_pr2:AF014773

```

```

seq_documentation_block:
LOCUS AF014773 246 bp DNA PRI 27-AUG-1997
DEFINITION Homo sapiens MHC class I antigen HLA-B gene (HLA-B*1502 allele),
exon 2 and partial cds.

```

```

ACCESSION AF014773
VERSION AF014773.1 GI:2345111
KEYWORDS
SOURCE human.

```

```

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 246)
AUTHORS Chandanayingyong,D., Sirikong,M., Luangtrakool,K., Srinak,D.,
Rungroung,E. and Bejchandra,S.
TITLE B15 alleles (B*1502)
JOURNAL Unpublished

```

```

REFERENCE 2 (bases 1 to 246)
Chandanayingyong,D., Sirikong,M., Luangtrakool,K., Srinak,D.,
Rungroung,E. and Bejchandra,S.
Direct Submission

```

```

TITLE Submitted (18-JUL-1997) Transfusion Medicine, Faculty of Medicine,
Siriraj Hospital, Mahidol University, Prannok Road, Bangkok 10700,
Thailand

```

```

FEATURES
Source Location/Qualifiers
1..246
/organism="Homo sapiens"
/db_xref="taxon:9606"
/cell_line="Thai DCH3086"
/chromosome="6"
/map="6p21"
/cell_type="lymphoblastoid"
<1..>246
/feature="HLA-B"
/allele="HLA-B*1502"

```

```

gene

```

```

exon

```

```

CDS

```

```

/codon_start=3
/product="MHC class I antigen HLA-B"

```

```

/protein_id="AAB67811.1"
/db_xref="GI:2345112"
/translation="TAMSPGGRGEPRFIAVGVDDTQFVRFSDAASPRMAPRAPWIE
QEGPEYWDRTQISKNTQTYRESLRNLRGYNQSEA"
BASE COUNT      55 a      81 c      82 g      28 t
ORIGIN

```

```

alignment_scores:
  Quality: 51.00      Length: 10
  Ratio: 5.100      Gaps: 0
  Percent Similarity: 100.000      Percent Identity: 100.000

```

```

alignment_block:
US-08-653-294-27 x AF014773 ..

```

```

Align seg 1/1 to: AF014773 from: 1 to: 246

```

```

11 ArgGlusSerLeuArgAsnLeuArgGlyTyr 20
|||||
198 CGAGAGAGCCTGCGGACCTGCGGCGCTAC 227

```

```

seq_name: gb_pr2:AF014775

```

```

seq_documentation_block:
LOCUS AF014775 246 bp DNA PRI 27-AUG-1997
DEFINITION Homo sapiens MHC class I antigen HLA-B gene (HLA-B*1502 allele),
exon 2 and partial cds.

```

```

ACCESSION AF014775
VERSION AF014775.1 GI:2345115
KEYWORDS
SOURCE human.

```

```

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 246)
AUTHORS Chandanayingyong,D., Sirikong,M., Luangtrakool,K., Srinak,D.,
Rungroung,E. and Bejchandra,S.
TITLE B15 alleles (B*1502)
JOURNAL Unpublished

```

```

REFERENCE 2 (bases 1 to 246)
Chandanayingyong,D., Sirikong,M., Luangtrakool,K., Srinak,D.,
Rungroung,E. and Bejchandra,S.
Direct Submission

```

```

TITLE Submitted (18-JUL-1997) Transfusion Medicine, Faculty of Medicine,
Siriraj Hospital, Mahidol University, Prannok Road, Bangkok 10700,
Thailand

```

```

FEATURES
source Location/Qualifiers
1..246
/organism="Homo sapiens"
/db_xref="taxon:9606"
/cell_line="Thai DCH018"
/chromosome="6"
/map="6p21"
/cell_type="lymphoblastoid"
<1..>246
/feature="HLA-B"
/allele="HLA-B*1502"

```

```

gene

```

```

exon

```

```

CDS

```

```

/codon_start=3
/product="MHC class I antigen HLA-B"
/protein_id="AAB67811.1"
/db_xref="GI:2345116"
/translation="TAMSPGGRGEPRFIAVGVDDTQFVRFSDAASPRMAPRAPWIE
QEGPEYWDRTQISKNTQTYRESLRNLRGYNQSEA"

```

```

BASE COUNT      55 a      81 c      82 g      28 t
ORIGIN

```

alignment_scores:
 Quality: 51.00 Length: 10
 Ratio: 5.100 Gaps: 0
 Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:

US-08-653-294-27 x AF014775 ..

Align seg 1/1 to: AF014775 from: 1 to: 246

11 ArgGluSerLeuArgAsnLeuArgGlyTyr 20
 |||||||
 198 CGAGAGACCTGCGGACCTGCGGGCTAC 227

seq_name: gb_pr2:AF014777

seq_documentation_block: 246 bp DNA PRI 27-AUG-1997
 LOCUS AF014777 Homo sapiens MHC class I antigen HLA-B gene (HLA-B*1502 allele),
 DEFINITION exon 2 and partial cds.

ACCESSION AF014777 GI:2345119

VERSION AF014777

KEYWORDS human.

SOURCE

ORGANISM

Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;

REFERENCE 1 (bases 1 to 246)
 Eutheria; Primates; Catarrhini; Hominidae; Homo.

AUTHORS Chandanayingyong,D., Sirikong,M., Luangtrakool,K., Srinak,D.,
 Rungroung,E. and Bejchandra,S.

TITLE B15 alleles (B*1502)

JOURNAL Unpublished

REFERENCE 2 (bases 1 to 246)
 Chandanayingyong,D., Sirikong,M., Luangtrakool,K., Srinak,D.,
 Rungroung,E. and Bejchandra,S.

AUTHORS Direct Submission

TITLE Submitted (18-JUL-1997) Transfusion Medicine, Faculty of Medicine,
 JOURNAL Siriraj Hospital, Mahidol University, Prannok Road, Bangkok 10700,
 Thailand

FEATURES Location/Qualifiers

source
 1..246
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /cell_line="Thai DCH017"
 /chromosome="6"
 /map="6p21"
 /cell_type="lymphoblastoid"
 <1..>246
 /gene="HLA-B"
 /allele="HLA-B*1502"
 /note="2"
 /number=2
 <1..>246
 /gene="HLA-B"
 /codon_start=3
 /product="MHC class I antigen HLA-B"
 /protein_id="AAB67815.1"
 /db_xref="GI:2345120"
 /translation="TAMSRPGRGEPRFIAVGVDQTFVRFSDAASPRMAPRAPWIE
 QEGPEYWDNTQISKNTQTYRESLNLRGYNQSEA"

gene

exon

CDS

BASE COUNT 55 a 81 c 82 g 28 t

ORIGIN

alignment_scores:
 Quality: 51.00 Length: 10
 Ratio: 5.100 Gaps: 0
 Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:

US-08-653-294-27 x AF014775 ..

Align seg 1/1 to: AF014775 from: 1 to: 246

11 ArgGluSerLeuArgAsnLeuArgGlyTyr 20
 |||||||
 198 CGAGAGACCTGCGGACCTGCGGGCTAC 227

seq_name: gb_pr2:AF014777

seq_documentation_block: 246 bp DNA PRI 27-AUG-1997
 LOCUS AF014777 Homo sapiens MHC class I antigen HLA-B gene (HLA-B*1502 allele),
 DEFINITION exon 2 and partial cds.

ACCESSION AF014777 GI:2345119

VERSION AF014777

KEYWORDS human.

SOURCE

ORGANISM

Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;

REFERENCE 1 (bases 1 to 246)
 Eutheria; Primates; Catarrhini; Hominidae; Homo.

AUTHORS Chandanayingyong,D., Sirikong,M., Luangtrakool,K., Srinak,D.,
 Rungroung,E. and Bejchandra,S.

TITLE B15 alleles (B*1502)

JOURNAL Unpublished

REFERENCE 2 (bases 1 to 246)
 Chandanayingyong,D., Sirikong,M., Luangtrakool,K., Srinak,D.,
 Rungroung,E. and Bejchandra,S.

TITLE Submitted (18-JUL-1997) Transfusion Medicine, Faculty of Medicine,
 JOURNAL Siriraj Hospital, Mahidol University, Prannok Road, Bangkok 10700,
 Thailand

FEATURES Location/Qualifiers

source
 1..246
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /cell_line="Thai DCH017"
 /chromosome="6"
 /map="6p21"
 /cell_type="lymphoblastoid"
 <1..>246
 /gene="HLA-B"
 /allele="HLA-B*1502"
 /note="2"
 /number=2
 <1..>246
 /gene="HLA-B"
 /codon_start=3
 /product="MHC class I antigen HLA-B"
 /protein_id="AAB67815.1"
 /db_xref="GI:2345120"
 /translation="TAMSRPGRGEPRFIAVGVDQTFVRFSDAASPRMAPRAPWIE
 QEGPEYWDNTQISKNTQTYRESLNLRGYNQSEA"

US-08-653-294-27 x AF014777 ..

Align seg 1/1 to: AF014777 from: 1 to: 246

11 ArgGluSerLeuArgAsnLeuArgGlyTyr 20
 |||||||
 198 CGAGAGACCTGCGGACCTGCGGGCTAC 227

seq_name: gb_pr2:AF014779

seq_documentation_block: 246 bp DNA PRI 27-AUG-1997
 LOCUS AF014779 Homo sapiens MHC class I antigen HLA-B gene (HLA-B*1502 allele),
 DEFINITION exon 2 and partial cds.

ACCESSION AF014779 GI:2345123

VERSION AF014779

KEYWORDS human.

SOURCE

ORGANISM

Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;

REFERENCE 1 (bases 1 to 246)
 Eutheria; Primates; Catarrhini; Hominidae; Homo.

AUTHORS Chandanayingyong,D., Sirikong,M., Luangtrakool,K., Srinak,D.,
 Rungroung,E. and Bejchandra,S.

TITLE B15 alleles (B*1502)

JOURNAL Unpublished

REFERENCE 2 (bases 1 to 246)
 Chandanayingyong,D., Sirikong,M., Luangtrakool,K., Srinak,D.,
 Rungroung,E. and Bejchandra,S.

AUTHORS Direct Submission

TITLE Submitted (18-JUL-1997) Transfusion Medicine, Faculty of Medicine,
 JOURNAL Siriraj Hospital, Mahidol University, Prannok Road, Bangkok 10700,
 Thailand

FEATURES Location/Qualifiers

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BASE COUNT 55 a 81 c 82 g 28 t

ORIGIN

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DEFINITION Homo sapiens MHC class I antigen HLA-B gene (HLA-B*1502 allele),
exon 2 and partial cds.
ACCESSION AF014781
VERSION AF014781.1 GI:2345127
KEYWORDS
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ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 246)
Chandanayingyong,D., Sirikong,M., Luangtrakool,K., Srinak,D.,
Rungroung,E. and Bejchandra,S.
B15 alleles (B*1502)
TITLE
JOURNAL
AUTHORS
REFERENCE
2 (bases 1 to 246)
Chandanayingyong,D., Sirikong,M., Luangtrakool,K., Srinak,D.,
Rungroung,E. and Bejchandra,S.
Direct Submission
TITLE
JOURNAL
AUTHORS
REFERENCE
18-JUL-1997 Transfusion Medicine, Faculty of Medicine,
Siriraj Hospital, Mahidol University, Prannok Road, Bangkok 10700,
Thailand
FEATURES
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seq_documentation_block:
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DEFINITION Homo sapiens MHC class I antigen HLA-B gene (HLA-B*1525 allele),
exon 2 and partial cds.
ACCESSION AF014783
VERSION AF014783.1 GI:2345135
KEYWORDS
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ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 246)
Chandanayingyong,D., Sirikong,M., Luangtrakool,K., Srinak,D.,
Rungroung,E. and Bejchandra,S.
B15 alleles (B*1502)
TITLE
JOURNAL
AUTHORS
REFERENCE
2 (bases 1 to 246)
Chandanayingyong,D., Sirikong,M., Luangtrakool,K., Srinak,D.,
Rungroung,E. and Bejchandra,S.
Direct Submission
TITLE
JOURNAL
AUTHORS
REFERENCE
18-JUL-1997 Transfusion Medicine, Faculty of Medicine,
Siriraj Hospital, Mahidol University, Prannok Road, Bangkok 10700,
Thailand
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LOCUS AF014783 246 bp DNA PRI 27-AUG-1997
DEFINITION Homo sapiens MHC class I antigen HLA-B gene (HLA-B*1502 allele),
exon 2 and partial cds.
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REFERENCE
AUTHORS 1 (bases 1 to 250)
          Chandanayingyong,D., Sirikong,M., Luangtrakool,K., Srinak,D.,
          Rungroung,E. and Bejchandra,S.
TITLE
JOURNAL B15 alleles (B*1525)
          Unpublished
REFERENCE
AUTHORS 2 (bases 1 to 250)
          Chandanayingyong,D., Sirikong,M., Luangtrakool,K., Srinak,D.,
          Rungroung,E. and Bejchandra,S.
TITLE
JOURNAL Direct Submission
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          Siriraj Hospital, Mahidol University, Prannok Road, Bangkok 10700,
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DEFINITION Homo sapiens MHC class I antigen HLA-B gene (HLA-B*1525 allele),
exon 2, and partial cds.
ACCESSION AF014787
VERSION AF014787.1 GI:2345139
KEYWORDS
SOURCE human.
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS 1 (bases 1 to 250)
          Chandanayingyong,D., Sirikong,M., Luangtrakool,K., Srinak,D.,
          Rungroung,E. and Bejchandra,S.
TITLE
JOURNAL B15 alleles (B*1525)
          Unpublished
REFERENCE
AUTHORS 2 (bases 1 to 250)
          Chandanayingyong,D., Sirikong,M., Luangtrakool,K., Srinak,D.,
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TITLE
JOURNAL Direct Submission
          Submitted (18-JUL-1997) Transfusion Medicine, Faculty of Medicine,
          Siriraj Hospital, Mahidol University, Prannok Road, Bangkok 10700,
          Thailand
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DEFINITION Homo sapiens MHC class I antigen HLA-B gene (HLA-B*1525 allele),
exon 2, and partial cds.
ACCESSION AF014787
VERSION AF014787.1 GI:2345139
KEYWORDS
SOURCE human.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
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AUTHORS 1 (bases 1 to 250)
          Chandanayingyong,D., Sirikong,M., Luangtrakool,K., Srinak,D.,
          Rungroung,E. and Bejchandra,S.
TITLE
JOURNAL B15 alleles (B*1525)
          Unpublished
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AUTHORS 2 (bases 1 to 250)
          Chandanayingyong,D., Sirikong,M., Luangtrakool,K., Srinak,D.,
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TITLE
JOURNAL Direct Submission
          Submitted (18-JUL-1997) Transfusion Medicine, Faculty of Medicine,
          Siriraj Hospital, Mahidol University, Prannok Road, Bangkok 10700,
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202 CGAGAGAGCCTGCGGAACTGCGCGGCTAC 231

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Date: Feb 8, 2000 7:31 PM
About: Results were produced by the GenCore software, version 4.5,
Copyright (c) 1993-2000 CompuGen Ltd.

Command line parameters:
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Search information block:

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Database: N_Geneseq_36:*
Database sequences: 311585
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N_Geneseq_36:Q75974	-	51.00	124.88	23.49	4059	HLA-B7 expression vector. New
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N_Geneseq_36:Q771145	+	48.00	119.62	46.11	2675	DNA encoding human CRP1TO-rela
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N_Geneseq_36:Q781924	+	48.00	119.62	46.11	2675	Human CRP1TO-related gene (CR-
N_Geneseq_36:Q22495	+	48.00	119.22	119.26	5761	Human CRP1TO gene CR-1. New CR
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N_Geneseq_36:Q17562	+	47.50	121.81	34.85	1818	Coding sequence for the alpha
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N_Geneseq_36:Q89291	+	46.00	134.93	6.48	289	EST clone CG336. New polynucleo
N_Geneseq_36:Q82783	-	46.00	125.78	20.94	745	Clone dn809.5 isolated from hum
N_Geneseq_36:Q99594	+	46.00	117.00	64.56	1849	Mouse TIE-2 receptor ligand 3
N_Geneseq_36:Q11549	+	46.00	97.74	763.38	13585	Tumour rejection antigen prec
N_Geneseq_36:Q08510	+	45.00	112.31	117.87	2182	Sequence of amylase gene and u
N_Geneseq_36:Q17563	+	44.50	111.99	122.69	1920	Coding sequence for the alpha
N_Geneseq_36:Q90017	+	44.00	137.55	4.63	116	EST clone CE242. New polynucleo
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N_Geneseq_36:Q12984	-	43.00	86.24	3.3e+03	17087	Enterococcus faecalis genome
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N_Geneseq_36:X20250	+	43.00	68.14	3.3e+04	111309	Borrelia burgdorferi polynud

N_Geneseq_36:X41493 - 42.50 120.57 40.82 416 ! Human secreted protein 5' ES
N_Geneseq_36:N50226 + 42.50 81.18 6.4e+03 24593 ! Sequence of opine synthase
N_Geneseq_36:N50182 + 42.50 81.18 6.4e+03 24596 ! Complete nucleotide sequen
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ID Q12115 standard; DNA; 1089 BP.

AC Q12115;

DT 29-AUG-1991 (first entry)

DE HLA-B35 exon.

KW Human leukocyte antigen; probe; major histocompatibility complex;

OS Homo sapiens.

PH Key Location/Qualifiers

FT cds 1..1089

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PN J03112486-A.

PD 14-MAY-1991.

PE 22-SEP-1989; 247697

PR 22-SEP-1989; JP-247697.

PA (OLYU) OLYMPUS OPTICAL KK.

DR WPI; 91-182991/25.

DR P-PSDB; R12464.

PT HLA-B35 gene - used in DNA probe and transformant cells for

PT immunising animals, for developing monoclonal antibody.

PS Claim 1; Page 1; lipp; Japanese.

CC Probes comprising part of the sequence can be used to identify

CC Class I genes. The DNA can be expressed for immunisation of

CC animals and prodn. of monoclonal antibodies specific for the

CC HLA-B35 antigen. See also J03112485 and J03112487.

SQ Sequence . 1089 BP; 221 A; 336 C; 359 G; 173 T;

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ID Q75974 standard; cDNA; 4059 BP.

AC Q75974;

DT 23-AUG-1995 (first entry)

DE pHLA-B7 expression vector.

KW expression vector; pHLA-B7; heavy human HLA-B7; bicistronic mRNA;

KW light beta-2 microglobulin; class I major histocompatibility complex;

KW MHC; human leukocyte antigen; HLA; covalently closed circular DNA; ds.

OS Synthetic.

PH Key Location/Qualifiers

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FT replication"

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FT the gene is taken from the transposable element

FT tn303"

FT complement (1410..1177)

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FT /note= "SV40 polyA signal sequence"

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FT 07-JUN-1993; US-074344.
FT (UNMI ) UNIV MICHIGAN.
FT (VICA-) VICAL INC.
FT PI Lew D, Marquet M, Nabel EG, Nabel GJ;
FT WPI; 95-036494/05.
FT New vectors for gene therapy, partic for tumours - comprising
FT genetic material encoding one or more cistron(s) which express
FT immunogenic or therapeutic peptide(s)
FT PS Claim 9; Page 42-43; 50pp; English.
FT CC This HLA-B7 antigen encoding plasmid was developed to incorporate many
FT advantageous features, eg. the kanamycin resistance gene. The
FT eradication of two open reading frames encoding portions of SV40 viral
FT proteins lowers the risk of tumorigenicity. The vector may also operate
FT as a cassette into which cistrons may be inserted and removed at will
FT for the transcription and subsequent translation of peptides of interest.
FT The vector is used partic. for the treatment of neoplastic disease,
FT eg. melanoma, and provides enhanced gene delivery and expression
FT in vivo.
FT SQ Sequence 4059 BP; 975 A; 1051 C; 1033 G; 1000 T;

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alignment_block:
US-08-653-294-27 x Q75974/rev ..
Align seg 1/1 to reverse of: Q75974 from: 1 to: 4059
11 ArgGluSerLeuArgAsnLeuArgGlyTyr 20
|||||
2589 CGAGAGAGCCTGCGGACCTCGCGGCTAC 2560

seq_name: N_Geneseq_36:Q75973
seq_documentation_block:
ID Q75973 standard: cDNA; 4965 BP.
AC Q75973;
DT 23-AUG-1995 (first entry)
DE pHLA-B7/beta-2 microglobulin expression vector.
KW expression vector; pHLA-B7/beta-2 microglobulin; heavy human HLA-B7;
KW light beta-2 microglobulin; class I major histocompatibility complex;
KW MHC; bicistronic mRNA; human leukocyte antigen; HLA;
KW covalently closed circular DNA; ds.
OS Synthetic.
FH Key Location/Qualifiers
FT ltr 1..529
FT /tag= a
FT /note= "Rous sarcoma virus LTR promoter domain, derived
FT for the Schmidt-Rupin strain nucleotides
FT 8673-9146. This region also includes a 56 bp
FT region of a synthetic oligonucleotide which

```

```

FT modifies this regulatory sequence to effect a
FT higher level of expression of downstream
FT sequences. The oligonucleotide removes a
FT polyadenylation signal sequence originally found
FT in the RSV DNA sequence."
FT 531..534
FT /tag= b
FT /label= consensus_Kozak_signal_sequence
FT 535..1620
FT /tag= c
FT /note= "HLA-B7 heavy chain open reading frame"
FT 535..606
FT /tag= d
FT /note= "encodes putative signal peptide of the
FT HLA-B7 heavy chain"
FT 607..1620
FT /tag= e
FT /note= "encodes putative HLA-B7 heavy chain mature
FT peptide"
FT 1621..1853
FT /tag= f
FT /note= "3' untranslated sequence of HLA-B7 heavy
FT chain mRNA"
FT 1854..1888
FT /tag= g
FT /note= "Multiple cloning site, forms a junction
FT between the HLA-B7 sequence and the EMCV-CITE
FT sequence, and is used to facilitate subcloning"
FT 1889..2479
FT /tag= h
FT /note= "murine encephalomyocarditis CAP-independent
FT translational enhancer (EMCV-CITE); taken from
FT nucleotides 255-843 of cloned EMCV genomic DNA.
FT It is a non-coding regulatory sequence functioning
FT as an internal entry point for the eukaryotic
FT ribosomal subunits when located within a mRNA
FT the beta-2 microglobulin, downstream of the HLA-B7
FT stop codon on this bicistronic mRNA to be
FT recognised by the ribosome"
FT 2480..2839
FT /tag= i
FT /note= "encodes beta-2 microglobulin; this cDNA is
FT deriv. from chimpanzee (differs to the human
FT cDNA by only 4 bases)"
FT 2840..2846
FT /tag= j
FT /note= "3' untranslated region of the beta-2
FT microglobulin mRNA"
FT 2847..2870
FT /tag= k
FT /note= "synthetic linker"
FT 3'UTR ..3111
FT /tag= l
FT /note= "bovine growth hormone 3'UTR and transcriptional
FT terminator; it starts at a blunt-ended BglI site
FT within the 3'UTR of the mRNA coding sequence"
FT 2979..2984
FT /tag= m
FT 3112..3151
FT /tag= n
FT /note= "synthetic linker to facilitate cloning"
FT complement (3151..3967)
FT /tag= o
FT /note= "kanamycin resistance gene open reading frame;
FT the gene is taken from the transposable element
FT Tn903"
FT 4014..4965
FT /tag= p
FT /note= "pBR322 backbone contg. bacterial origin of
FT replication, it represents nucleotides 2244-3193"
FT
FT W09429469-A.
FT 22-DEC-1994.

```



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PF 27-MAY-1994; U06069.
PR 07-JUN-1993; US-074344.
PA (UNMI ) UNIV MICHIGAN.
PA (VICA-) VICAL INC.
PI Lew D., Marquet M., Nabel EG, Nabel GJ;
DR WPI; 95-036494/05.
PT New vectors for gene therapy, partic for tumours - comprising
PT genetic material encoding one or more cistron(s) which express
PT immunogenic or therapeutic peptide(s)
PS Claim 8; Page 41-42; 50pp; English.
CC The pHA-B7/beta-2 microglobulin plasmid expression vector, in addition
CC to the kanamycin resistance gene, contains the plasmid DNA encoding the
CC heavy (human HLA-B7) and light (beta-2 microglobulin) proteins of a
CC class I major histocompatibility complex (MHC) antigen. The plasmid is
CC designed to express these two proteins via a bicistronic mRNA in
CC eukaryotic cells. Initiation of transcription of the mRNA is dependent
CC on a Kous Sarcoma Virus (RSV) promoter sequence deriv. from the 3' long
CC terminal repeat. Termination of transcription is dependent upon the
CC polyadenylation signal sequence deriv. from the bovine growth hormone
CC gene. Eukaryotic cell translation of the heavy chain is regulated by the
CC 5' cap-dependent protein start site. Translation of the light chain is
CC controlled by the CITE. Finally the replication of the plasmid in
CC bacterial cells is controlled by the presence of a bacterial origin of
CC replication. The vector is used partic. for the treatment of neoplastic
CC disease, eg. melanoma, and provides enhanced gene delivery and expression
CC in vivo.
SQ Sequence 4965 BP; 1171 A; 1293 C; 1338 G; 1163 T;

alignment_scores:
  Quality: 51.00      Length: 10
  Ratio: 5.100      Gaps: 0
Percent Similarity: 100.000      Percent Identity: 100.000

alignment_block:
US-08-653-294-27 x Q75973 ..
Align seg 1/1 to: Q75973 from: 1 to: 4965

11 ArgGluSerLeuArgAsnLeuArgGlyTyr 20
|||||
829 CGAGAGAGCGCTGCGGAACCTGCGCGCTAC 858

seq_name: N_Geneseq_36:Q22494

seq_documentation_block:
ID Q22494 standard; DNA; 2675 BP.
AC Q22494;
DT 28-AUG-1992 (first entry)
DE Human CRIPTO-related gene CR-3.
KW cell proliferation; tumour; CR-1; transforming growth factor;
KW epidermal growth factor; ss.
OS Homo sapiens.
FH Key Location/Qualifiers
FT cds 809..1375
FT /*tag= a
FT /product= CR-3
PN US7749001-A.
PD 25-FEB-1992.
PF 23-AUG-1991; 749001.
PR 23-AUG-1991; US-749001.
PA (USSH ) US DEPT HEALTH & HUMAN.
PI Salomon D, Persico M;
DR WPI; 92-123675/15.
DR P-PSDB: R22547.
PT New CRIPTO gene CR-1 and CRIPTO-related gene CR-3 genomic DNA -
PT CR-3 protein and anti-CR-3 antibodies, useful in immunoassay to
PT detect CR-3 as tumour specific marker
PS Disclosure; Page 29; 44pp; English.
CC The CR-3 nucleotide sequence was isolated from a human genomic
CC library using a labelled DNA fragment containing 800bp upstream of
CC the translation initiation site of CR-1. Clones were isolated which
CC contained the 5' cDNA non-coding region of CR-3. One clone was

```

```

CC sequenced and found to include a complete CRIPTO cDNA lacking
CC introns and containing a poly(A) tract at the 3' end. Seven single
CC base pair substitutions were observed in the coding region (C.f.
CC CR-1 sequence in Ciccodicola A. et al., EMBO J.8:1987-1991(1989)),
CC six of which gave rise to amino acid changes. The 3' non-coding
CC sequence is less similar (97% identical) to CR-1. Most of the
CC differences occur in the inverted Alu sequence. The unusual poly(A)
CC addition site ACTAAA found in the CR-1 gene is also conserved in
CC CR-3. The similarity between CR-1 and CR-3 extends for 697
CC nucleotides upstream of the initiator AUG where it is possible to
CC observe 7 base pair substitutions and 6 nucleotide deletions.
CC The 14 "Others" in the sequence represent nucleotides whose
CC identity, although determined by the inventors, was unclear in
CC the sequence printed in the specification.
SQ Sequence 2675 BP; 738 A; 611 C; 553 G; 759 T;

alignment_scores:
  Quality: 48.00      Length: 21
  Ratio: 3.200      Gaps: 1
Percent Similarity: 71.429      Percent Identity: 57.143

alignment_block:
US-08-653-294-27 x Q22494 ..
Align seg 1/1 to: Q22494 from: 1 to: 2675

2 GlyArgLeuAsnArgLeuSerGlu.....ArgArgGluSerLeuArgAs 16
|||||
2161 GCGAGACTGGGTAGGAAGAGAGAGCAATAGAGAGAGAGAGGTTGAAAAA 2210

16 nLeuArgGlyTyr 20
|||||
2211 CAAATGGGTTTAC 2223

seq_name: N_Geneseq_36:T71145

seq_documentation_block:
ID T71145 standard; DNA; 2675 BP.
AC T71145;
DT 19-AUG-1997 (first entry)
DE DNA encoding human CRIPTO-related gene product, CR-3.
KW CRIPTO; CR1; CR3; epidermal growth factor superfamily; EGF; mitogen;
KW tumour marker; epithelium; mesenchyme; diagnosis; prognosis; ss.
OS Homo sapiens.
FH Key Location/Qualifiers
FT cds 809..1375
FT /*tag= a
FT /product= CR-3
PN US5620866-A.
PD 15-APR-1997.
PF 23-AUG-1991; 749001.
PR 23-AUG-1991; US-749001.
PR 17-NOV-1993; US-154198.
PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.
PI Persico MG, Salomon DS;
DR WPI; 97-235180/21.
DR P-PSDB: W19980.
PT New DNA encoding the human CRIPTO-related gene product CR-3 - used
PT to produce recombinant protein, useful for preparation of diagnostic
PT antibodies
PS Claim 1; Column 17-20; 25pp; English.
CC T71145 encodes a human CRIPTO-related gene product CR-3. CR-3 is
CC thought to be a tumour-specific marker and as such DNA and amino
CC acid sequences of CR-3 and derivatives can be used in the
CC diagnosis, prognosis and possibly treatment of some types of cancer.
CC CR-3 includes a region homologous to products of the epidermal
CC growth factor superfamily of genes and it may be a mitogen involved
CC in regulating proliferation, differentiation and transformation of
CC mesenchymal and epithelial cells.
SQ Sequence 2675 BP; 739 A; 618 C; 555 G; 763 T;

```


Align seg 1/1 to reverse of: X12977 from: 1 to: 1346

1 TvrGlyArgLeuAsnArgLeuSerGluArgGluSerLeuArgAsnLe 17
 |||||
 1202 TAATGGAGATTAGAAAGTTCGTCATTTAAAGACAGTATCGAAATT 1153
 :
 17 uArgGly 19
 :
 1152 TAAAGGC 1146

seq_name: N_Geneseq_36:V89291

seq_documentation_block:

ID V89291 standard; cDNA: 289 BP.
 AC V89291;
 DE EST clone CG336.
 KW Human; secreted protein; expressed sequence tag; EST; haematopoiesis;
 KW tissue growth; activin; inhibin; chemotaxis; chemokinesis; haemostatic;
 KW receptor; ligand; thrombolytic; anti-inflammatory; cadherin; anti-tumour;
 KW gene therapy; ss.
 OS Homo sapiens.
 PN W09845436-A2.
 PD 15-OCT-1998.
 PF 10-APR-1998; U06955.
 PR 10-APR-1997; US-838821.
 PA (GEMV) GENETICS INST INC.
 PI Agostino MJ, Jacobs K, Lavallie ER, McCoy JM, Merberg D,
 PI Racie LA, Spaulding V, Treacy M;
 DR WPI: 99-070077/06.
 PT New polynucleotides encoding human secreted proteins - derived from
 PT e.g. human blood, kidney, foetal lung, placenta, testes, brain,
 PT ovary, pituitary, retina and colon cDNA libraries.
 PS Claim 1: Page 171; 618pp; English.
 CC The present sequence represents a human expressed sequence tag (EST).
 CC The polynucleotide, which is a secreted EST, and the encoded protein
 CC are predicted to have useful biological activities which would make
 CC them suitable for treating, preventing or ameliorating medical
 CC conditions in humans and animals, although no supporting data is
 CC given. Suggested activities include nutritional activity, immune
 CC stimulating or suppressing activity, haematopoiesis regulating
 CC activity, tissue growth activity, activin/inhibin activity,
 CC chemotactic/chemokinetic activity, haemostatic and thrombolytic
 CC activity, receptor/ligand activity, anti-inflammatory activity,
 CC cadherin/tumour invasion suppressor activity, tumour inhibition
 CC activity. The polynucleotide may also be useful for gene therapy.
 SQ Sequence 289 BP; 63 A; 63 C; 63 G; 100 T;

alignment_scores:

Quality: 46.00 Length: 13
 Ratio: 4.182 Gaps: 0
 Percent Similarity: 84.615 Percent Identity: 76.923

alignment_block:

US-08-653-294-27 x V89291 ..

Align seg 1/1 to: V89291 from: 1 to: 289

3 ArgLeuAsnArgLeuSerGluArgGluSerLeuArg 15
 |||||
 74 AGAGTCAACAGGCTAAGTGAGAGGAGGAGGATGCTACGC 112

seq_name: N_Geneseq_36:V82783

seq_documentation_block:

ID V82783 standard; cDNA: 745 BP.
 AC V82783;
 DE 25-FEB-1999 (first entry)
 DE Clone dn809_5 isolated from human foetal brain cDNA library.
 KW Secreted protein; nutritional activity; immune stimulating; vaccine;
 KW suppressing activity; haematopoiesis regulating activity;
 KW tissue growth activity; activin; inhibin activity; chemotactaxis;

KW chemokinetic activity; haemostasis; thrombolytic activity; receptor;
 KW ligand; anti-inflammatory; cadherin; tumour invasion suppressor;
 KW tumour inhibition; gene therapy; ds.
 OS Homo sapiens.
 PN W09842739-A2.
 PD 01-OCT-1998.
 PF 20-MAR-1998; U05653.
 PR 19-MAR-1998; US-044466.
 PR 21-MAR-1997; US-822167.
 PA (GEMV) GENETICS INST INC.
 PI Agostino MJ, Jacobs K, Lavallie ER, McCoy JM, Merberg D,
 PI Racie LA, Spaulding V, Treacy M;
 DR WPI: 98-609890/51.
 DR P-PSDB; W85461.
 PT New polynucleotides encoding secreted human proteins - derived from
 PT human foetal brain, adult brain, foetal kidney, placenta or adult
 PT pineal gland cDNA libraries.
 PS Claim 26; Page 80; 113pp; English.
 CC The present sequence encodes a secreted protein. The polynucleotide and
 CC secreted protein are predicted to have biological activities which would
 CC make them suitable for treating, preventing or ameliorating medical
 CC conditions in humans and animals, although no supporting data is given.
 CC Suggested activities include nutritional activity, immune stimulating
 CC (e.g. as vaccines) or suppressing activity, haematopoiesis regulating
 CC activity, tissue growth activity, activin/inhibin activity,
 CC chemotactic/chemokinetic activity, haemostatic and thrombolytic activity,
 CC receptor/ligand activity, anti-inflammatory activity, cadherin/tumour
 CC invasion suppressor activity, and tumour inhibition activity (no data is
 CC given in the specification to support these activities). The
 CC polynucleotide is also stated to be useful for gene therapy.
 SQ Sequence 745 BP; 179 A; 229 C; 176 G; 161 T;

alignment_scores:

Quality: 46.00 Length: 13
 Ratio: 4.182 Gaps: 0
 Percent Similarity: 84.615 Percent Identity: 76.923

alignment_block:

US-08-653-294-27 x V82783/rev ..

Align seg 1/1 to reverse of: V82783 from: 1 to: 745

3 ArgLeuAsnArgLeuSerGluArgGluSerLeuArg 15
 |||||
 123 AGAGTCAACAGGCTAAGTGAGAGGAGGAGGATGCTACGC 85

seq_name: N_Geneseq_36:T99594

seq_documentation_block:

ID T99594 standard; cDNA: 1849 BP.
 AC T99594;
 DE 22-JUN-1998 (first entry)
 DE Mouse TIE-2 receptor ligand 3 cDNA.
 KW TIE-2 receptor ligand; TIE ligand-3; tyrosine kinase; mouse;
 KW angiogenesis; vascularisation; blood vessel growth; tumour;
 KW therapy; receptorbody; ss.
 OS Mus musculus.
 FH Key Location/Qualifiers
 FT CDS 47..1576 /*tag= a
 FT WO9748804-A2.
 PD 24-DEC-1997.
 PF 19-JUN-1997; U10728.
 PR 02-AUG-1996; US-022999.
 PR 19-JUN-1996; US-665926.
 PR 02-JUL-1996; US-021087.
 PA (REGG-) REGENERON PHARM INC.
 PI Jones PF, Valenzuela DM, Yancopoulos GD;
 DR WPI: 98-063143/06.
 DR P-PSDB; W26792.
 PT DNA encoding TIE ligands 3 and 4 - useful for, e.g. blocking blood
 PT vessel growth and promoting neovascularisation, etc.

CC The tumour rejection antigen precursor (TRAP) is processed to a
CC tumour rejection antigen (TRA) presented by HLA-A2 molecules. TRA
CC is used to generate cytotoxic T lymphocytes for treating cancer (esp.
CC melanoma). It can also be used to raise specific antibodies, and
CC when complexed with HLA-A2, it can be used to produce vaccines.
CC Cytotoxic T lymphocytes so generated can be used in adoptive
CC transfer or generated, or they can be generated *in vivo* by using a
CC vector containing the appropriate gene or using TRA or TRAP together
CC with an adjuvant that facilitates entry into HLA-A2 presenting cells
CC Diagnostic methods involving the detection of expression of TRAP
CC can be used in the detection of cancers.
SQ Sequence 13595 BP; 3827 A; 2859 C; 2968 G; 3894 T;

```
alignment_scores:
  Quality: 46.00
  Ratio: 3.538
  Percent Similarity: 81.250
  Percent Identity: 56.250
  Gaps: 0
  Length: 16
```

```
alignment_block:
US-08-653-294-27 x T11549
..
```

4 LeuAsnArgLeuSerGluArgArgGluSerLeuArgAsnLeuArgGly 19
:::|||||::||| ::||| |||:: |::::|
246 ATCAACAGAAATTCTCGCAACGTTTGTCAGTCTCCACGCTCAGGG 293

19 Y^{Tyr} 20
|:::

757 CCAT 760

seq_name: N_Geneseq_36:T11549

seq_documentation_block:
ID T11549 standard; DNA; 13585 BP.

TII349;

DE 18-APR-1996 (first entry)
DT Tumour rejection antigen precursor coding sequence.
DE
KW Tumour rejection antigen precursor; TRAP; TRA; melanoma; cancer;
KW tumour; treatment; detection; vaccine; HLA-A2; adoptive transfer;
KW T cell; T lymphocyte; human leukocyte antigen; ds.
DE

US	HOMO	SAPTEMS
FH		Key

FH	key	Location/Qualifiers
FT	misc_feature	2685

FT misc_feature

FT	/*tag=	a	/note=	"Identified nucleotide."
FT				

FT		/note= "Unic
FT	misc feature	9422 9456

```
FT misc_feature 9422..9456
FT /*tag= b
FT /note= "this region is 4.7-5.3 kilobases in length
FT but the sequence of this region has not been
FT deduced "
```

FT	misc	deduce
FT	feature	11539

```
FT misc_feature 11539 /*tag= c /note= "identified nucleotide "
```

FT
PN
W09601557-A1

PN WO9601557-A1.
PD 25-JAN-1996

PD 25 - JAN - 1996.
 PE 27 - JUN - 1995: 1108153

PF 27-JUN-1995; U08153.
 PR 09-JUL-1994; US-272351

PR 08-JUL-1994; US-272351.
PR 10-JAN-1995; US-270319

PR 10-JAN-1995; US-370319.
PA (U)OW-1 TUDWIC INST CANCER RES

PA (LUDW-) LUDWIG INST CANCER RES.
 PI BOON-fallow T Brichard V Coulic D
 DO DIEN F.

PI Boon-falleur T, Brichard V, Coulie

PI Traversari C, Van

DR WPI; 96-097390/10.

PT Genomic DNA encoding a tumour rejection antigen precursor -

PT processed to antigen

PT diagnosing melanoma

PS Claim 3; Page 18-22; 41pp; English.

OM of: US-08-653-294-27 to: EST:* out_format : pfs
 Date: Feb 8, 2000 6:23 AM
 About: Results were produced by the GenCore software, version 4.5,
 Copyright (c) 1993-2000 Compugen Ltd.

Command line parameters:

-MODEL=framet_p2n.model -DEV=xlp
 -O=Cgml1/USPTO.spool/US08653294/runat_04022000.160700.15770/app_query.fasta.2
 -DB=EST -QFM=fastap -SUFFIX=rst -GAPOP=12.000 -GAPEXT=4.000
 -MINMATCH=0.100 -LOOPCL=0.000 -LOOPEXT=0.000 -QGAPOP=4.500
 -GAPEXT=0.050 -XGAPOP=10.000 -XGAPEXT=0.500 -FGAPOP=6.000
 -FGAEXT=7.000 -YGAPOP=10.000 -YGAPEXT=0.500 -DELOP=6.000
 -DELEX=7.000 -START=1 -MATRIX=blosum62 -TRANS=human40.cdi
 -LIST=45 -LOCALIGN=200 -THR SCORE=pct -ALIGN=15 -MODE=LOCAL
 -OUTFMT=pfs -NORM=ext -MINLEN=0 -MAXLEN=1000000 -USER=US08653294
 -NCPU=6 -ICPU=3 -NO_XLPXY -WAIT -THREADS=1

Search information block:

Query: US-08-653-294-27

Query length: 20

Database: EST.*

Database sequences: 4538634

Database length: 1887831982

Search time (sec): 7600.090000

score_list:

Sequence	Strd Orig	ZScore	Escore	Len	Documentation
gb_est12:AA319533	+	51.00	6.30	103	AA319533 EST21772 Adrenal gland
gb_est13:AA361477	+	51.00	135.06	189	AA361477 EST70761 T-cell lymph
gb_est13:AA352603	+	51.00	13.84	218	AA352603 EST60621 Activated T-c
gb_est12:AA294911	+	51.00	148.49	218	AA352603 EST60621 Activated T-c
gb_est13:AA352960	+	51.00	20.81	259	AA294911 EST100074 Pancreas tum
gb_est13:AA352960	+	51.00	146.33	270	AA32960 EST61101 Activated T-c
gb_est8:AA058454	+	51.00	33.38	373	AA058454 z167407.r1 Stratagene
gb_est11:AA224068	+	51.00	142.43	397	AA224068 z171102.r1 Stratagene
gb_est10:AA160317	+	51.00	37.14	405	AA160317 z056007.r1 Stratagene
gb_est9:AA100680	+	51.00	141.89	419	AA100680 z190502.r1 Stratagene
gb_est7:WA0489	+	51.00	39.77	427	WA0489 zc84b01.r1 Pancreatic is
gb_est12:AA310808	+	51.00	141.33	443	AA310808 EST161593 Jurkat T-cell
gb_est9:CI8310	+	51.00	140.62	456	CI8310 C18310 Human placenta ch
gb_est17:AA663896	+	51.00	140.54	479	AA663896 ae74d01.s1 Stratagene
gb_est35:AL039796	+	51.00	140.04	49.17	AL039796 DKFZ434B1912.r1 434
gb_est28:AT524732	+	51.00	138.55	59.53	AT524732 th12c03.x1 NCI_CGAP_C
gb_est37:AA008453	+	51.00	137.30	69.91	AA008453 w55d05.x1 NCI_CGAP_C
gb_est11:AA263135	+	51.00	136.56	76.85	AA263135 PM05598 KGI-a Lambda Z
gb_gss3:B20346	-	51.00	135.31	90.27	B20346 F1831-Sp6 IGF Arabidopsi
gb_gss10:AA248102	-	50.50	137.61	97.21	AA248102 HS_2015.A1_H09_MR CIT
gb_gss8:AA009853	+	50.00	139.60	52.03	B90159 CIT-HSP-2173M11.TF CIT-H
gb_gss3:B50728	-	50.00	138.93	56.72	B50728 CIT-HSP-63C12.IV CIT-HS
gb_gss13:AA0475632	+	50.00	134.64	98.38	AA0475632 CITBI-EI-2590L18.TF CIT
gb_gss13:AA0475628	+	50.00	133.50	113.75	AA0475628 CITBI-EI-2590L16.TF CIT
gb_gss12:AA0377514	-	49.50	137.00	72.62	AA0377514 RPCI-11-162P10.TJ RPCI
gb_est5:DT3898	-	49.00	140.37	47.14	D73898 CELK064C5F Yuji Kohara u
gb_est9:AA063950	+	49.00	136.57	76.80	AA063950 m143f02.r1 Stratagene
gb_gss11:AA029878	+	49.00	134.31	102.60	AA029878 HS_3005.B2.A11.T7 CIT
gb_est11:AA205710	-	49.00	133.77	109.92	AA05710 zq6a12.s1 Stratagene
gb_est34:AA1795124	+	48.50	142.17	37.46	AA1795124 sb7b04.y1 Gm-c1010 G
gb_est44:AA184423	-	48.00	138.77	57.91	AA331579 EST35512 Embryo, 8 wee
gb_est35:AA1827894	-	48.00	132.31	132.50	AA184423 f14a03.y1 Zebrafish a
gb_est10:AA129456	+	48.00	132.05	137.11	AA187894 w12b01.x1 Soares NFL
gb_gss15:AA0641570	+	48.00	131.56	146.03	AA129456 zn78c06.s1 Stratagene
gb_est21:AA1951979	+	48.00	131.07	155.48	AA041570 RPC93-EcoRI-319.TP RP
gb_est11:AA216757	-	48.00	130.72	162.65	AA216757 zq9b501.s1 Stratagene
gb_est44:AA187318	-	48.00	130.27	172.33	AA187318 ENLGH112771 Six-day Cd
gb_est15:AA526987	-	48.00	130.16	174.77	AA526987 n119b06.s1 NCI_CGAP_C
gb_gss11:AA0295324	+	48.00	129.78	183.36	AA0295324 HS_3111.A1_E09_MR CIT
gb_est34:AA0641860	+	48.00	128.63	212.68	AA0641860 RPCI93-EcoRI-6L21.TV H
gb_est34:AA1794913	+	47.50	131.30	151.00	AA1794913 sb73d11.y1 Gm-c1010 G

gb_est34:AA1794877 + 47.50 129.22 197.12 527 ! AT1794877 sb72h01.y1 Gm-c1010
 gb_est34:AA1795011 + 47.50 129.22 197.12 527 ! AT1795011 sb75a10.y1 Gm-c1010
 gb_gss6:AA0873097 + 47.50 128.80 207.84 549 ! AA0873097 V59C8 mTn-3xHA/lacZ

seq_name: gb_est12:AA319533

seq_documentation_block:

LOCUS AA319533 103 bp mRNA EST 19-APR-1997
 DEFINITION EST21772 Adrenal gland tumor Homo sapiens cDNA 5' end similar to
 similar to major histocompatibility complex, class I, B
 (GB:W6102), mRNA sequence.

ACCESSION AA319533

VERSION AA319533.1 GI:1971860

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;

Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 103)

AUTHORS

Adams,M.D., Kerlavage,A.R., Fleischmann,R.D., Feldner,R.A.,
 Bult,C.J., Lee,N.H., Kirkness,E.F., Weinstock,K.G., Gocayne,J.D.,
 White,O., Sutton,G., Blake,J.A., Brandon,R.C., Man-Wai,C.,
 Clayton,R.A., Cline,T.R., Cotton,M.D., Earle-Hughes,J., Fine,L.D.,
 Fitzgerald,L.M., Fitzhugh,W.M., Fritchman,J.L., Geoghagen,N.S.,
 Glodek,A., Gnehm,C.L., Hanna,M.C., Hedblom,E., Hinkle,F.S., Jr.,
 Kelley,J.M., Kelley,J.C., Liu,L.-I., Marmaros,S.M., Merrick,J.M.,
 Moreno-Palancas,R.F., McDonald,L.A., Nguyen,D.T., Pelligrino,S.M.,
 Phillips,C.A., Ryder,S.E., Scott,J.L., Saudek,D.M., Shirley,R.,
 Small,K.V., Spriggs,I.A., Uterback,T.R., Weidman,J.F., Li,Y.,
 Bednarek,D.P., Cao,L., Cepeda,M.A., Coleman,T.A., Collins,E.J.,
 Dimke,D., Feng,D.-F., Ferrie,A., Fischer,C., Hastings,E.J.,
 He,W.W., Hu,J.S., Greene,J.M., Gruber,J., Hudson,P., Kim,A.K.,
 Kozak,D.L., Kunsch,C., Hungjun,J., Li,H., Weissner,P.S., Olsen,H.,
 Raymond,L., Wei,Y.F., Wing,J., Xu,C., Yu,G.L., Ruben,S.M.,
 Dillion,P.J., Fannon,M.R., Rosen,C.A., Haseltine,W.A., Fields,C.,
 Fraser,C.M. and Venter,J.C.

TITLE

Initial assessment of human gene diversity and expression patterns
 based upon 83 million nucleotides of cDNA sequence

JOURNAL

MEDLINE

COMMENT On Sep 12, 1996 this sequence version replaced gi:1393672.

Other_ESTs: THC169519

Contact: Kerlavage, AR

Bioinformatics

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Fax: 3018699423

Email: arkerlavet@tigr.org

For clone availability, additional sequence and expression

information related to this EST, please check the TIGR Human Gene

Index (<http://www.tigr.org/tdb/hgi/hgi.html>)

Seq primer: M13 Reverse.

FEATURES

source

1..103

/organism="Homo sapiens"

/db_xref="ATCC (inhost):120083"

/db_xref="taxon:9606"

/clone_lib="Adrenal gland tumor"

/stage="adult"

/note="Organ: adrenal gland; Vector: pBluescript SK-;

Site:1: EcoRI; Site:2: XhoI"

BASE COUNT 26 a 35 c 29 g 13 t

ORIGIN

alignment_scores:

Quality: 51.00 Length: 10

Ratio: 5.100 Gaps: 0

Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:

US-08-653-294-27 x AA319533

Align seg 1/1 to: AA319533 from: 1 to: 103

11 ArgGlusSerLeuArgAsnLeuArgGlyTyr 20
|||||
27 CGAGAGCGCTCGCGAACCTTCGCGCTAC 56

seq_name: gb_est13:AA361477

seq_documentation_block: 189 bp mRNA EST 21-APR-1997
LOCUS AA361477 T-cell lymphoma Homo sapiens cDNA 5' end similar to
DEFINITION EST70761 T-cell lymphoma Homo sapiens cDNA 5' end similar to
similar to major histocompatibility complex, class I, Bw62.3, mRNA
sequence.

ACCESSION AA361477
VERSION AA361477.1 GI:2013795
KEYWORDS EST.

SOURCE human.

ORGANISM

REFERENCE 1 (bases 1 to 189)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.

AUTHORS

Adams,M.D., Kerlavage,A.R., Fleischmann,R.D., Fuldner,R.A.,
Bult,C.J., Lee,N.H., Kirkness,E.F., Weinstock,K.G., Gocayne,J.D.,
White,O., Sutton,G., Blake,J.A., Brandon,R.C., Man-Wai,C.,
Clayton,R.A., Cline,T.R., Cotton,M.D., Earle-Hughes,J., Fine,L.D.,
Fitzgerald,L.M., Fitzhugh,W.M., Fritchman,J.L., Geoghagen,N.S.,
Glodek,A., Gnehm,C.L., Hanna,M.C., Hedblom,E., Hinkle,P.S., Jr.,
Kelley,J.M., Kelley,J.C., Liu,L.-I., Marmaros,S.M., Merrick,J.M.,
Moreno-Palauques,R.F., McDonald,L.A., Nguyen,D.T., Pelligrino,S.M.,
Phillips,C.A., Ryder,S.E., Scott,J.L., Sauder,D.M., Shirley,R.,
Small,K.V., Spriggs,T.A., Utterback,T.R., Weidman,J.F., Li,Y.,
Bednarek,D.P., Cao,L., Cepeda,M.A., Coleman,T.A., Collins,E.J.,
Dimke,D., Feng,D.-F., Ferrie,A., Fischer,C., Hastings,G.A.,
He,W.W., Hu,J.S., Greene,J.M., Gruber,J., Hudson,P., Kim,A.K.,
Kozak,D.L., Kunsch,C., Hungjun,J., Li,H., Meissner,P.S., Olsen,H.,
Raymond,L., Wei,Y.F., Wing,J., Xu,C., Yu,G.L., Ruben,S.M.,
Dillion,P.J., Fannon,M.R., Rosen,C.A., Haseltine,W.A., Fields,C.,
Fraser,C.M. and Venter,J.C.

TITLE

Initial assessment of human gene diversity and expression patterns
based upon 83 million nucleotides of cDNA sequence

JOURNAL

MEDLINE

COMMENT

On Sep 12, 1996 this sequence version replaced gi:1404737.
Other_ESTs: THCI69519
Contact: Kerlavage, AR

Bioinformatics

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Email: arkerlav@tigr.org

For clone availability, additional sequence and expression
information related to this EST, please check the TIGR Human Gene
Index (<http://www.tigr.org/tdb/hgi/hgi.html>)

Seq primer: M13 Reverse.

FEATURES

Location/Qualifiers

1..189
/organism="Homo sapiens"
/db_xref="ATCC (inhost):165623"
/db_xref="taxon:9606"
/clone_lib="T-cell lymphoma"
/cell_type="T-lymphocyte"
/note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2:
XhoI"

BASE COUNT 45 a 60 c 55 g 25 t 4 others

ORIGIN

alignment_scores:

Quality: 51.00 Length: 10
Ratio: 5.100 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:

US-08-653-294-27 x AA361477

Align seg 1/1 to: AA361477 from: 1 to: 189

11 ArgGlusSerLeuArgAsnLeuArgGlyTyr 20
|||||
37 CGAGAGCGCTCGCGAACCTTCGCGCTAC 66

seq_name: gb_est13:AA352603

seq_documentation_block:

LOCUS AA352603 218 bp mRNA EST 21-APR-1997
DEFINITION EST760621 Activated T-cells XX Homo sapiens cDNA 5' end similar to
similar to major histocompatibility complex, class I, Bw62.3, mRNA
sequence.

ACCESSION AA352603

VERSION AA352603.1 GI:2004923

KEYWORDS EST.

SOURCE human.

ORGANISM

REFERENCE 1 (bases 1 to 218)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.

AUTHORS

Adams,M.D., Kerlavage,A.R., Fleischmann,R.D., Fuldner,R.A.,
Bult,C.J., Lee,N.H., Kirkness,E.F., Weinstock,K.G., Gocayne,J.D.,
White,O., Sutton,G., Blake,J.A., Brandon,R.C., Man-Wai,C.,
Clayton,R.A., Cline,T.R., Cotton,M.D., Earle-Hughes,J., Fine,L.D.,
Fitzgerald,L.M., Fitzhugh,W.M., Fritchman,J.L., Geoghagen,N.S.,
Glodek,A., Gnehm,C.L., Hanna,M.C., Hedblom,E., Hinkle,P.S., Jr.,
Kelley,J.M., Kelley,J.C., Liu,L.-I., Marmaros,S.M., Merrick,J.M.,
Moreno-Palauques,R.F., McDonald,L.A., Nguyen,D.T., Pelligrino,S.M.,
Phillips,C.A., Ryder,S.E., Scott,J.L., Sauder,D.M., Shirley,R.,
Small,K.V., Spriggs,T.A., Utterback,T.R., Weidman,J.F., Li,Y.,
Bednarek,D.P., Cao,L., Cepeda,M.A., Coleman,T.A., Collins,E.J.,
Dimke,D., Feng,D.-F., Ferrie,A., Fischer,C., Hastings,G.A.,
He,W.W., Hu,J.S., Greene,J.M., Gruber,J., Hudson,P., Kim,A.K.,
Kozak,D.L., Kunsch,C., Hungjun,J., Li,H., Meissner,P.S., Olsen,H.,
Raymond,L., Wei,Y.F., Wing,J., Xu,C., Yu,G.L., Ruben,S.M.,
Dillion,P.J., Fannon,M.R., Rosen,C.A., Haseltine,W.A., Fields,C.,
Fraser,C.M. and Venter,J.C.

Initial assessment of human gene diversity and expression patterns
based upon 83 million nucleotides of cDNA sequence

Nature 377 (6547 Suppl), 3-174 (1995)

JOURNAL

MEDLINE

COMMENT

On May 8, 1995 this sequence version replaced gi:800964.
Other_ESTs: THCI72938
Contact: Kerlavage, AR

Bioinformatics

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Email: arkerlav@tigr.org

For clone availability, additional sequence and expression
information related to this EST, please check the TIGR Human Gene
Index (<http://www.tigr.org/tdb/hgi/hgi.html>)

Seq primer: M13 Reverse.

FEATURES

Location/Qualifiers

1..218
/organism="Homo sapiens"
/db_xref="ATCC (inhost):152802"
/db_xref="taxon:9606"
/clone_lib="Activated T-cells XX"
/cell_type="T-lymphocyte"
/dev_stage="adult"
/note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2:
XhoI"

BASE COUNT

52 a 70 c 62 g 28 t 6 others

ORIGIN

alignment_scores:
 Quality: 51.00 Length: 10
 Ratio: 5.100 Gaps: 0
 Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
 US-08-653-294-27 x AA352603 ..

Align seg 1/1 to: AA352603 from: 1 to: 218

```

11 ArgGlusSerLeuArgAsnLeuArgGlyTyr 20
|||||
39 CGAGAGAGCCTGCGGAACCTGCGGCTAC 68

```

seq_name: gb_est12:AA294911

seq_documentation_block: 259 bp mRNA EST 18-APR-1997
 LOCUS AA294911
 DEFINITION EST100074 Pancreas tumor I Homo sapiens cDNA 5' end similar to similar to major histocompatibility complex, class I, Bw62.3, mRNA sequence.

ACCESSION AA294911
 VERSION AA294911.1 GI:1947266

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 259)

AUTHORS Adams,M.D., Kerlavage,A.R., Fleischmann,R.D., Fuldner,R.A., Bult,C.J., Lee,N.H., Kirkness,E.F., Weinstock,K.G., Gocayne,J.D., White,O., Sutton,G., Blake,J.A., Brandon,R.C., Man-Wai,C., Clayton,R.A., Cline,T.R., Cotton,M.D., Earle-Hughes,J., Fine,L.D., Fitzgerald,L.M., Fitzhugh,W.M., Fritchman,J.L., Geoghagen,N.S., Glodek,A., Gnehm,C.L., Hanna,M.C., Hedblom,E., Hinkle,P.S.Jr., Kelley,J.M., Kelley,J.C., Liu,L.-I., Marmaros,S.M., Merrick,J.M., Moreno-Palauques,R.F., McDonald,L.A., Nguyen,D.T., Pelligrino,S.M., Phillips,C.A., Ryder,S.E., Scott,J.L., Saudek,D.M., Shirley,R., Small,K.V., Spriggs,T.A., Utterback,T.R., Weidman,J.F., Li,Y., Bednarek,D.P., Cao,L., Cepeda,M.A., Coleman,T.A., Collins,E.J., Dimke,D., Feng,D.-F., Ferrie,A., Fischer,C., Hastings,G.A., He,W.W., Hu,J.S., Greene,J.M., Gruber,J., Hudson,P., Kim,A.K., Kozak,D.L., Kunsch,C., Hungjun,J., Li,H., Weissner,P.S., Olsen,H., Raymond,P.J., Wei,Y.F., Wing,J., Xu,C., Yu,G.L., Ruben,S.M., Dillion,P.J., Fannon,M.R., Rosen,C.A., Haseltine,W.A., Fields,C., Fraser,C.M. and Venter,J.C.

Initial assessment of human gene diversity and expression patterns based upon 83 million nucleotides of cDNA sequence

Nature 377 (6547 Suppl), 3-174 (1995)

12140200

On Nov 29, 1993 this sequence version replaced gi:430148.

COMMENT

JOURNAL

MEDLINE

COMMENT

Contact: Kerlavage, AR

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9712 Medical Center Drive, Rockville, MD 20850 USA

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Fax: 3018699423

Email: arkerlavetigr.org

For clone availability, additional sequence and expression

information related to this EST, please check the TIGR Human Gene

Index (<http://www.tigr.org/tdb/hgi/hgi.html>)

Seq primer: M13 Reverse.

Location/Qualifiers

1..259

/organism="Homo sapiens"

/db_xref="ATCC (inhost):190413"

/db_xref="taxon:9606"

/clone_lib="Pancreas tumor I"

/dev_stage="adult"

/note="Organ: pancreas; Vector: pBluescript SK-; Site_1:

EcoRI; Site_2: XhoI"

BASE COUNT 60 a 87 c 75 g 30 t 7 others

ORIGIN

alignment_scores:
 Quality: 51.00 Length: 10
 Ratio: 5.100 Gaps: 0
 Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:

US-08-653-294-27 x AA294911 ..

Align seg 1/1 to: AA294911 from: 1 to: 259

```

11 ArgGlusSerLeuArgAsnLeuArgGlyTyr 20
|||||
42 CGAGAGAGCCTGCGGAACCTGCGGCTAC 71

```

seq_name: gb_est13:AA352960

seq_documentation_block: 270 bp mRNA EST 21-APR-1997

LOCUS AA352960

DEFINITION EST61101 Activated T-cells XX Homo sapiens cDNA 5' end similar to similar to major histocompatibility complex, class I, B61, mRNA sequence.

ACCESSION AA352960.1 GI:2005353

VERSION AA352960

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 270)

AUTHORS Adams,M.D., Kerlavage,A.R., Fleischmann,R.D., Fuldner,R.A., Bult,C.J., Lee,N.H., Kirkness,E.F., Weinstock,K.G., Gocayne,J.D., White,O., Sutton,G., Blake,J.A., Brandon,R.C., Man-Wai,C., Clayton,R.A., Cline,T.R., Cotton,M.D., Earle-Hughes,J., Fine,L.D., Fitzgerald,L.M., Fitzhugh,W.M., Fritchman,J.L., Geoghagen,N.S., Glodek,A., Gnehm,C.L., Hanna,M.C., Hedblom,E., Hinkle,P.S.Jr., Kelley,J.M., Kelley,J.C., Liu,L.-I., Marmaros,S.M., Merrick,J.M., Moreno-Palauques,R.F., McDonald,L.A., Nguyen,D.T., Pelligrino,S.M., Phillips,C.A., Ryder,S.E., Scott,J.L., Saudek,D.M., Shirley,R., Small,K.V., Spriggs,T.A., Utterback,T.R., Weidman,J.F., Li,Y., Bednarek,D.P., Cao,L., Cepeda,M.A., Coleman,T.A., Collins,E.J., Dimke,D., Feng,D.-F., Ferrie,A., Fischer,C., Hastings,G.A., He,W.W., Hu,J.S., Greene,J.M., Gruber,J., Hudson,P., Kim,A.K., Kozak,D.L., Kunsch,C., Hungjun,J., Li,H., Weissner,P.S., Olsen,H., Raymond,P.J., Wei,Y.F., Wing,J., Xu,C., Yu,G.L., Ruben,S.M., Dillion,P.J., Fannon,M.R., Rosen,C.A., Haseltine,W.A., Fields,C., Fraser,C.M. and Venter,J.C.

Initial assessment of human gene diversity and expression patterns based upon 83 million nucleotides of cDNA sequence

Nature 377 (6547 Suppl), 3-174 (1995)

12140200

On May 8, 1995 this sequence version replaced gi:801269.

Other ESTs: THCI72938

Contact: Kerlavage, AR

Bioinformatics

The Institute for Genomic Research

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Email: arkerlavetigr.org

For clone availability, additional sequence and expression

information related to this EST, please check the TIGR Human Gene

Index (<http://www.tigr.org/tdb/hgi/hgi.html>)

Seq primer: M13 Reverse.

Location/Qualifiers

1..270

/organism="Homo sapiens"

/db_xref="ATCC (inhost):153240"

/db_xref="taxon:9606"

/clone_lib="Activated T-cells XX"

/cell_type="T-lymphocyte"

FEATURES

source

```

/dev_stage="adult"
/note="vector: pBluescript SK-; Site_1: EcoRI; Site_2:
XhoI"

```

```

BASE COUNT      62 a   80 c   88 g   35 t   5 others
ORIGIN

```

```

alignment_scores:
  Quality:      51.00      Length:      10
  Ratio:        5.100      Gaps:        0
Percent Similarity: 100.000 Percent Identity: 100.000

```

```

alignment_block:
US-08-653-294-27 x AA352960 ..

```

```

Align seg 1/1 to: AA352960 from: 1 to: 270

```

```

11 ArgGluSerLeuArgAsnLeuArgGlyTyr 20
|||||
182 CGAGAGAGCCTCGGAACCTCGCGGCTAC 211

```

```

seq_name: gb_est8:AA058454

```

```

seq_documentation_block:
LOCUS      AA058454      373 bp      mRNA      EST      01-DEC-1996
DEFINITION z167807.r1 Stratagene colon (#937204) Homo sapiens cDNA clone
IMAGE:509677 5' similar to gb:M24039_cds1 HLA CLASS I
HISTOCOMPATIBILITY ANTIGEN, B-18 B*1801 ALPHA (HUMAN);, mRNA
sequence.
ACCESSION      AA058454
VERSION        AA058454.1 GI:1551280
KEYWORDS       EST.
SOURCE         human.
ORGANISM       Homo sapiens

```

```

REFERENCE
AUTHORS      Hillier,L., Lennon,G., Becker,M., Bonaldo,M.F., Chiapelli,B.,
Chissoe,S., Dietrich,N., Dubuque,T., Favello,A., Gish,W.,
Hawkins,M., Hultman,M., Kucaba,T., Lacy,M., Le,M., Le,N.,
Mardis,E., Moore,B., Morris,M., Parsons,J., Prange,C., Rifkin,L.,
Rohlfing,T., Schellenberg,K., Soares,M.B., Tan,F., Thierry-Mieg,J.,
Trevasakis,E., Underwood,K., Wohlmann,P., Waterston,R., Wilson,R.
and Marra,M.

```

```

TITLE      Generation and analysis of 280,000 human expressed sequence tags
JOURNAL      Genome Res. 6 (9), 807-828 (1996)
MEDLINE      97044478
COMMENT      On Sep 12, 1996 this sequence version replaced gi:1393357.

```

```

Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810

```

```

Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 1592 Std Error: 0.00
Seq primer: -28M13 rev2 from Amersham
High quality sequence stop: 268.

```

```

Location/Qualifiers
1..373

```

```

/organism="Homo sapiens"
/db_xref="GDB:3813009"
/db_xref="taxon:9606"
/clone="IMAGE:509677"
/clone_lib="Stratagene colon (#937204)"
/lab_host="SOLR cells (kanamycin resistant)"
/note="Organ: colon; Vector: pBluescript SK-; Site_1:
EcoRI; Site_2: XhoI; Cloned unidirectionally. Primer:
Oligo dT. T-84 colonic epithelial cell line. Average
insert size: 1.0 kb; Uni-ZAP XR Vector; -5' adaptor
sequence: 5' GAATCGGCACGAG 3' -3' adaptor sequence: 5'
CTCGAGTTTTTTTTTTTTTT 3'"

```

```

FEATURES
source

```

```

BASE COUNT      73 a   119 c   116 g   57 t   8 others
ORIGIN

```

```

alignment_scores:
  Quality:      51.00      Length:      10
  Ratio:        5.100      Gaps:        0
Percent Similarity: 100.000 Percent Identity: 100.000

```

```

alignment_block:
US-08-653-294-27 x AA058454 ..

```

```

Align seg 1/1 to: AA058454 from: 1 to: 373

```

```

11 ArgGluSerLeuArgAsnLeuArgGlyTyr 20
|||||
229 CGAGAGAGCCTCGGAACCTCGCGGCTAC 258

```

```

seq_name: gb_est11:AA224068

```

```

seq_documentation_block:
LOCUS      AA224068      397 bp      mRNA      EST      19-FEB-1997
DEFINITION zrlif02.r1 Stratagene hnt neuron (#937233) Homo sapiens cDNA clone
IMAGE:648507 5' similar to gb:L22649_cds1 HLA CLASS I
HISTOCOMPATIBILITY ANTIGEN, B-39 B*3901 ALPHA (HUMAN);, mRNA
sequence.
ACCESSION      AA224068
VERSION        AA224068.1 GI:1844610
KEYWORDS       EST.
SOURCE         human.
ORGANISM       Homo sapiens

```

```

REFERENCE
AUTHORS      Hillier,L., Lennon,G., Becker,M., Bonaldo,M.F., Chiapelli,B.,
Chissoe,S., Dietrich,N., Dubuque,T., Favello,A., Gish,W.,
Hawkins,M., Hultman,M., Kucaba,T., Lacy,M., Le,M., Le,N.,
Mardis,E., Moore,B., Morris,M., Parsons,J., Prange,C., Rifkin,L.,
Rohlfing,T., Schellenberg,K., Soares,M.B., Tan,F., Thierry-Mieg,J.,
Trevasakis,E., Underwood,K., Wohlmann,P., Waterston,R., Wilson,R.
and Marra,M.

```

```

TITLE      Generation and analysis of 280,000 human expressed sequence tags
JOURNAL      Genome Res. 6 (9), 807-828 (1996)
MEDLINE      97044478
COMMENT      On Nov 29, 1993 this sequence version replaced gi:430429.
Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810

```

```

Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -28M13 rev1 ET from Amersham
High quality sequence stop: 295.

```

```

Location/Qualifiers
1..397

```

```

/organism="Homo sapiens"
/db_xref="GDB:558245"
/db_xref="taxon:9606"
/clone="IMAGE:648507"
/clone_lib="Stratagene hnt neuron (#937233)"
/lab_host="SOLR (kanamycin resistant)"
/note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2:
XhoI; Cloned unidirectionally. Primer: Oligo dT.
Differentially, post mitotic hnt neurons. Average insert
size: 1.5 kb; Uni-ZAP XR Vector; -5' adaptor sequence: 5'
GAATCGGCACGAG 3' -3' adaptor sequence: 5'
CTCGAGTTTTTTTTTTTTTT 3'"

```

```

FEATURES
source

```

```

BASE COUNT      77 a   129 c   131 g   56 t   4 others
ORIGIN

```

alignment_scores:
 Quality: 51.00 Length: 10
 Ratio: 5.100 Gaps: 0
 Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:

US-08-653-294-27 x AA224068 ..

Align seg 1/1 to: AA224068 from: 1 to: 397

11 ArgGluSerLeuArgAsnLeuArgGlyTyr 20
 |||||
 297 CGAGAGAGCGCTGCGNAACCTGCGGCTAC 326

seq_name: gb_est10:AA160317

seq_documentation_block: 405 bp mRNA EST 09-MAR-1998
 LOCUS AA160317
 DEFINITION z056c07.r1 Stratagene pancreas (#937208) Homo sapiens cDNA clone
 IMAGE:590892 5' similar to gb:U11265 HLA CLASS I HISTOCOMPATIBILITY
 ANTIGEN, B-35 B*3501 ALPHA (HUMAN);, mRNA sequence.

ACCESSION AA160317

VERSION AA160317.1 GI:1734956

KEYWORDS

EST.

SOURCE

human.

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;

Eutheria; Primates; Catarrhini; Homnidae; Homo.

1 (bases 1 to 405)

Hillier, L., Allen, M., Bowles, L., Dubuque, T., Geisel, G., Jost, S.,

Krizman, D., Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M.,

Martin, J., Moore, B., Schellenberg, K., Steptoe, M., Tan, F.,

Theising, B., White, Y., Wylie, T., Waterston, R. and Wilson, R.

WashU-NCI human EST Project

Unpublished (1997)

On Sep 12, 1996 this sequence version replaced gi:1406818.

Contact: Wilson RK

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800

Fax: 314 286 1810

Email: est@watson.wustl.edu

This clone is available royalty-free through LLNL; contact the

IMAGE Consortium (info@image.llnl.gov) for further information.

Insert Length: 1671 Std Error: 0.00

Seq primer: -28M13 rev2 from Amersham

High quality sequence stop: 332.

Location/Qualifiers

1..405

/organism="Homo sapiens"

/db_xref="GDB:4622278"

/db_xref="taxon:9606"

/clone="IMAGE:590892"

/clone_lib="Stratagene pancreas (#937208)"

/lab_host="SOLR cells (kanamycin resistant)"

/note="Organ: pancreas; Vector: pBluescript SK-; Site:1:

ECORI; Site:2: XhoI; Cloned unidirectionally. Primer:

Oligo dT. Pancreatic adenocarcinoma cell line. Average

insert size: 1.0 kb; Uni-ZAP XR Vector; -5' adaptor

sequence: 5' GAATTCGACGAG 3' -3' adaptor sequence: 5'

CTCAGATTTTTTTTTTTT 3"

BASE COUNT 80 a 132 c 132 g 58 t 3 others

ORIGIN

alignment_scores:

Quality: 51.00 Length: 10

Ratio: 5.100 Gaps: 0

Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:

US-08-653-294-27 x AA160317 ..

Align seg 1/1 to: AA160317 from: 1 to: 405

11 ArgGluSerLeuArgAsnLeuArgGlyTyr 20
 |||||
 281 CGAGAGAGCGCTGCGNAACCTGCGGCTAC 310

seq_name: gb_est9:AA100680

seq_documentation_block: 419 bp mRNA EST 31-JUL-1997

LOCUS AA100680

DEFINITION z190b02.r1 Stratagene colon (#937204) Homo sapiens cDNA clone

IMAGE:511851 5' similar to gb:M24039_cds1 HLA CLASS I

HISTOCOMPATIBILITY ANTIGEN, B-18 B*1801 ALPHA (HUMAN);, mRNA

sequence.

ACCESSION AA100680

VERSION AA100680.1 GI:1646981

KEYWORDS

EST.

SOURCE

human.

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;

Eutheria; Primates; Catarrhini; Homnidae; Homo.

1 (bases 1 to 419)

Hillier, L., Lennon, G., Becker, M., Bonaldo, M.F., Chiapelli, B.,

Chisoe, S., Dietrich, N., Dubuque, T., Favello, A., Gish, W.,

Hawkins, M., Hultman, M., Kucaba, T., Lacy, M., Le, M., Le, N.,

Mardis, E., Moore, B., Morris, M., Parsons, J., Prange, C., Rifkin, L.,

Rohlfing, T., Schellenberg, K., Soares, M.B., Tan, F., Thierry-Mieg, J.,

Trevaskis, E., Underwood, K., Wohldmann, P., Waterston, R., Wilson, R.

and Maria, M.

Generation and analysis of 280,000 human expressed sequence tags

Genome Res. 6 (9), 807-828 (1996)

97044478

Contact: Wilson RK

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800

Fax: 314 286 1810

Email: est@watson.wustl.edu

This clone is available royalty-free through LLNL; contact the

IMAGE Consortium (info@image.llnl.gov) for further information.

Insert Length: 1534 Std Error: 0.00

Seq primer: -28M13 rev2 from Amersham

High quality sequence stop: 275.

Location/Qualifiers

1..419

/organism="Homo sapiens"

/db_xref="GDB:3844346"

/db_xref="taxon:9606"

/clone="IMAGE:511851"

/clone_lib="Stratagene colon (#937204)"

/lab_host="SOLR cells (kanamycin resistant)"

/note="Organ: colon; Vector: pBluescript SK-; Site:1:

ECORI; Site:2: XhoI; Cloned unidirectionally. Primer:

Oligo dr. T-82 colonic epithelial cell line. Average

insert size: 1.0 kb; Uni-ZAP XR Vector; -5' adaptor

sequence: 5' GAATTCGACGAG 3' -3' adaptor sequence: 5'

CTCAGATTTTTTTTTTTT 3"

BASE COUNT 85 a 133 c 133 g 63 t 5 others

ORIGIN

alignment_scores:

Quality: 51.00 Length: 16

Ratio: 3.643 Gaps: 1

Percent Similarity: 87.500 Percent Identity: 75.000

alignment_block:

US-08-653-294-27 x AA100680 ..

Align seg 1/1 to: AA100680 from: 1 to: 419

5 AsnArgLeuSerGluArgArgGluSerLeuArgAsnLeuArgGlyTyr 20

```

:::|||||:|||||
225 CACAGACTTACGAGAGA.....AGCCTGGGAACCTGCGGGCTAC 266
seq_name: gb_est7:W40489

seq_documentation_block:
LOCUS      W40489      427 bp      mRNA      EST      20-MAY-1996
DEFINITION zc84b01.r1 Pancreatic Islet Homo sapiens cDNA clone IMAGE:328969 5'
            similar to gb:U11265 HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-35
            B*3501 ALPHA (HUMAN);, mRNA sequence.
ACCESSION  W40489
VERSION     W40489.1 GI:1324496
KEYWORDS    EST.
SOURCE      human.
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 427)
AUTHORS     Hillier,L., Lennon,G., Becker,M., Bonaldo,M.F., Chiapelli,B.,
            Chisoe,S., Dietrich,N., DuBuque,T., Favello,A., Gish,W.,
            Hawkins,M., Hultman,M., Kucaba,T., Lacy,M., Le,M., Le,N.,
            Wards,E., Moore,B., Morris,M., Parsons,J., Prange,C., Rifkin,L.,
            Rohlfing,T., Schellenberg,K., Soares,M.B., Tan,F., Thierry-Mieg,J.,
            Trevasakis,E., Underwood,K., Wohlmann,P., Waterston,R., Wilson,R.
            and Marita,M.
TITLE       Generation and analysis of 280,000 human expressed sequence tags
JOURNAL     Genome Res. 6 (9), 807-828 (1996)
MEDLINE     97044478
COMMENT     On Jan 25, 1995 this sequence version replaced gi:637865.
            Contact: Wilson RK
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: est@watson.wustl.edu
            This clone is available royalty-free through LLNL; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            Seq primer: mob.REGA+T
            High quality sequence stop: 397.

FEATURES             Location/Qualifiers
     source           1..427
                     /organism="Homo sapiens"
                     /db_xref="GDB:1263173"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:328969"
                     /clone_lib="Pancreatic Islet"
                     /tissue_type="pancreatic islet"
                     /lab_host="SOLR cells (kanamycin resistant)"
                     /note="Organ: pancreas; Vector: pBluescript SK-; Site_1:
                     EcoRI; Site_2: XhoI; Reference: Hum Mol Gen 2, 1795 (1993)
                     Takeda et al. Cloned unidirectionally. Primer: Oligo dT.
                     -5' adaptor sequence: 5' GAATTCGACGAG 3' -3' adaptor
                     sequence: 5' CTCGAGTTTTTTTTTTTTTTT 3"
BASE COUNT      87 a 141 c 134 g 62 t 3 others
ORIGIN
alignment_scores:
  Quality: 51.00      Length: 10
  Ratio: 5.100      Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
US-08-653-294-27 x W40489 ..
Align seg 1/1 to: W40489 from: 1 to: 427
11 ArgGluSerLeuArgAsnLeuArgGlyTyr 20
|||||
279 CGAGAGACCTTCGGAACCTGCGGGCTAC 308
seq_name: gb_est12:AA310808

```

```

seq_documentation_block:
LOCUS      AA310808      443 bp      mRNA      EST      19-APR-1997
DEFINITION EST181593 Jurkat T-cells V Homo sapiens cDNA 5' end similar to
            similar to major histocompatibility complex, class I, B0704, mRNA
            sequence.
ACCESSION  AA310808
VERSION     AA310808.1 GI:1963136
KEYWORDS    EST.
SOURCE      human.
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 443)
AUTHORS     Adams,M.D., Kerlavage,A.R., Fleischmann,R.D., Fuldner,R.A.,
            Bult,C.J., Lee,N.H., Kirkness,E.F., Weinstock,K.G., Gocayne,J.D.,
            White,O., Sutton,G., Blake,J.A., Brandon,R.C., Man'wal,C.,
            Clayton,R.A., Cline,T.R., Cotton,M.D., Earle-Hughes,J., Fine,L.D.,
            Fitzgerald,L.M., Fitzhugh,W.M., Fritchman,J.L., Geoghagen,N.S.,
            Glodek,A., Gnehm,C.L., Hanna,M.C., Hedblom,E., Hinkle,P.S., Jr.,
            Kelley,J.M., Kelley,J.C., Liu,L.-I., Margaron,S.M., Merrick,J.M.,
            Moreno-Palauques,R.F., McDonald,L.A., Nguyen,D.T., Pelligrino,S.M.,
            Phillips,C.A., Ryder,S.E., Scott,J.L., Saudek,D.M., Shirley,R.,
            Small,K.V., Spriggs,T.A., Utterback,T.R., Weidman,J.F., Li,Y.,
            Bednarek,D.P., Cao,L., Cepeda,M.A., Coleman,T.A., Collins,E.J.,
            Dimke,D., Feng,D.-F., Ferrie,A., Fischer,C., Hastings,G.A.,
            He,W.W., Hu,J.-S., Greene,J.M., Gruber,J., Hudson,P., Kim,A.K.,
            Kozak,D.L., Kunsch,C., Hungjun,J., Li,H., Meissner,P.S., Olsen,H.,
            Raymond,L., Wei,Y.F., Wing,J., Xu,C., Yu,G.L., Ruben,S.M.,
            Dillion,P.J., Fannon,M.R., Rosen,C.A., Haseltine,W.A., Fields,C.,
            Fraser,C.M. and Venter,J.C.
TITLE       Initial assessment of human gene diversity and expression patterns
            based upon 83 million nucleotides of cDNA sequence
JOURNAL     Nature 377 (6547 Suppl), 3-174 (1995)
MEDLINE     12140200
COMMENT     On Sep 12, 1996 this sequence version replaced gi:1397854.
            Other ESTs: TNC180721
            Contact: Kerlavage, AR
            Bioinformatics
            The Institute for Genomic Research
            9712 Medical Center Drive, Rockville, MD 20850 USA
            Tel: 3018699056
            Fax: 3018699423
            Email: arkerlavet@tigr.org
            For clone availability, additional sequence and expression
            information related to this EST, please check the TIGR Human Gene
            Index (http://www.tigr.org/tldb/hgi/hgi.html)
            Seq primer: M13 Reverse.
            Location/Qualifiers
     source           1..443
                     /organism="Homo sapiens"
                     /db_xref="ATCC (inhost):156811"
                     /db_xref="taxon:9606"
                     /clone_lib="Jurkat T-cells"
                     /cell_type="T-lymphocyte"
                     /note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2:
                     XhoI"
BASE COUNT      86 a 144 c 143 g 64 t 6 others
ORIGIN
alignment_scores:
  Quality: 51.00      Length: 10
  Ratio: 5.100      Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
US-08-653-294-27 x AA310808 ..
Align seg 1/1 to: AA310808 from: 1 to: 443
11 ArgGluSerLeuArgAsnLeuArgGlyTyr 20
|||||
292 CGAGAGACCTTCGGAACCTGCGGGCTAC 321

```

```

seq_name: gb_est9:C18310
seq_documentation_block: 475 bp mRNA EST 02-OCT-1996
LOCUS C18310 Homo sapiens cDNA (TFujiwara) Homo sapiens cDNA clone
DEFINITION GEN:560D07 5', mRNA sequence.
ACCESSION C18310
VERSION C18310.1 GI:1579912
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominoidea; Homo.
REFERENCE 1 (bases 1 to 475)
AUTHORS Fujiwara,T., Hirano,H., Hishigaki,H., Horie,M., Kawai,A., Kuga,Y.,
Kyushiki,H., Nagata,M., Okuno,S., Ozaki,K., Shimizu,F., Shimada,Y.,
Shinomiya,H., Suzuki,M., Takaichi,A., Takeda,S., Watanabe,T.,
Maekawa,H., Nakamura,Y. and Takahashi,E.
TITLE Otsuka cDNA project
JOURNAL Unpublished (1996)
COMMENT On Sep 12, 1996 this sequence version replaced gi:1393837.
Contact: Tsutomu Fujiwara
Otsuka GEN Research Institute
Otsuka Pharmaceutical Co.,Ltd
463-10 Kagasuno Kawauchi-cho, Tokushima, Tokushima, 771-01 Japan
Tel: 0886-65-2888
Fax: 0886-37-1035.
FEATURES
Location/Qualifiers
source
1..475
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="GEN-560D07"
/clone_lib="Human placenta cDNA (TFujiwara)"
/tissue_type="Placenta" 68 t 3 others
BASE COUNT 89 a 161 c 154 g 68 t
ORIGIN

alignment_scores:
Quality: 51.00 Length: 10
Ratio: 5.100 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
US-08-653-294-27 x C18310 ..
Align seg 1/1 to: C18310 from: 1 to: 475
11 ArgGluSerLeuArgAsnLeuArgGlyTyr 20
|||||
299 CGAGAGAGCTGCGGAACTGCGGCGCTAC 328

seq_name: gb_est17:AA663896
seq_documentation_block: 479 bp mRNA EST 15-DEC-1997
LOCUS AA663896
DEFINITION ae74d01.s1 Stratagene schizo brain S11 Homo sapiens cDNA clone
IMAGE:969889 3', similar to gb:M28203 HLA CLASS I HISTOCOMPATIBILITY
ANTIGEN, B-62 B*1504 ALPHA (HUMAN);, mRNA sequence.
ACCESSION AA663896
VERSION AA663896.1 GI:2617887
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominoidea; Homo.
REFERENCE 1 (bases 1 to 479)
AUTHORS Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S.,
Krizman,D., Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M.,
Martin,J., Moore,B., Schellenberg,K., Steptoe,M., Tan,F.,
Theising,B., White,Y., Wylie,T., Waterston,R. and Wilson,R.
..
TITLE WashU-NCI human EST project

```

```

JOURNAL Unpublished (1997)
COMMENT On Sep 12, 1996 this sequence version replaced gi:1394858.
Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through LNL : contact the
IMAGE Consortium (info@image.lnl.gov) for further information.
Possible reversed clone: polyt not found
Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 430.
FEATURES
Location/Qualifiers
source
1..479
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:969889"
/clone_lib="Stratagene schizo brain S11"
/sex="male"
/tissue_type="schizophrenic brain S-11 frontal lobe"
/dev_stage="34 years old"
/lab_host="SOLR (kanamycin resistant)"
/note="vector: Bluescript SK-; Site_1: EcoRI; Library
constructed from S-11 frontal lobe, male, 34 years old,
50% caucasian, 50% Aleutian. Schizophrenic suicide.
Random primed into EcoRI site of ZAP II Vector. Mass
excised. Custom library. Avg insert length 1.4kb.
Material obtained by Johnston N., Torrey, E.F., Yolken R.,
and the Stanley Neuropathology Consortium - Analysis of
RNAs from the Brains of Individuals with Psychiatric
Diseases (Unpublished) Stanley Neurovirology Laboratory,
Johns Hopkins School of Medicine, Baltimore MD."
BASE COUNT 91 a 165 c 158 g 64 t 1 Others
ORIGIN

alignment_scores:
Quality: 51.00 Length: 10
Ratio: 5.100 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
US-08-653-294-27 x AA663896 ..
Align seg 1/1 to: AA663896 from: 1 to: 479
11 ArgGluSerLeuArgAsnLeuArgGlyTyr 20
|||||
283 CGAGAGAGCTGCGGAACTGCGGCGCTAC 312

seq_name: gb_est35:AL039796
seq_documentation_block: 503 bp mRNA EST 29-SEP-1999
LOCUS AL039796
DEFINITION DKZPD434B1912 r1 434 (synonym: htes3) Homo sapiens cDNA clone
IMAGE:969889 3', similar to gb:M28203 HLA CLASS I HISTOCOMPATIBILITY
ANTIGEN, B-62 B*1504 ALPHA (HUMAN);, mRNA sequence.
ACCESSION AL039796
VERSION AL039796.1 GI:5408804
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominoidea; Homo.
REFERENCE 1 (bases 1 to 503)
AUTHORS Duesterhoef,A., Lauber,J., Mewes,H.W., Gassenhuber,J. and
Wiemann,S.
TITLE EST (Duesterhoeft, et al.)
JOURNAL Unpublished (1999)
COMMENT On Jun 2, 1999 this sequence version replaced gi:4967270.
Contact: Duesterhoeft A
MIPS
Am Klopferspitz 18a D-82152 Martinsried, Germany

```

This is the 5' sequence of the clone insert
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
sequenced by Qiagen within the cDNA sequencing consortium of the
German Genome Project.

FEATURES
source

```

/tissue_type="test1"
/dev_stage="adult"
/lab_host="DH10B"
/note~vector: pspopt1: Site1: NotI: Site2: SalI"
96 a 172 c 165 g 68 t 2 others
BASE COUNT

```

Quality:	51.00	Length:	10
Ratio:	5.100	Gaps:	0
Percent Similarity:	100.000	Percent Identity:	100.000

Align seg 1/1 to: AL039796 from: 1 to: 503

300 CGAGAGCCTGCGGAACCTGCGGGCTAC 329

seq_documentation_block: LOCUS AI524732 583 bp mRNA EST 18-MAR-1999
DEFINITION th12403.x1 NCI-CCAP-CLL1 Homo sapiens cDNA clone IMAGE:2118100.3,
similar to SW-MY16-MOUSE P17564 MYELOID DIFFERENTIATION PRIMARY
RESPONSE PROTEIN MYD116.1; mRNA sequence.

Seq primer: -40UP from Gibco	
High quality sequence stop: 422.	
Location/Qualifiers	
1. .583	
FEATURES	
source	

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: February 8, 2000, 04:05:43 ; Search time 133.56 Seconds
(without alignments)
3.547 Million cell updates/sec

Title: US-08-653-294-28

Perfect score: 99

Sequence: 1 YRLATLNERENLRALRY 20

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 188963 seqs, 23686106 residues

Total number of hits satisfying chosen parameters; 188963

Minimum DB seq length: 0

Maximum DB seq length: 1000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : A_Geneseq_36.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match	Score	Length	DB ID	Description
1	99	100.0	20	1 R32908	HLA-B2702 CTL modu
2	99	100.0	20	1 W33791	Peptide B2702.84-7
3	94	94.9	20	1 R32910	HLA-B2702 CTL modu
4	94	94.9	20	1 W33793	Peptide B2702.84-7
5	93	93.9	20	1 R32907	HLA-B2702 CTL modu
6	93	93.9	20	1 R95428	HLA-B2702 84-75-84
7	93	93.9	20	1 W33778	Immunomodulating d
8	88	88.9	20	1 R32909	HLA-B2702 CTL modu
9	88	88.9	20	1 W33792	Peptide B2702.84-7
10	80	80.8	20	1 R95430	HLA-B2702 84-75/7
11	50	50.5	25	1 R48286	Peptide fragment o
12	50	50.5	25	1 R83093	HLAB38 CTL modul
13	50	50.5	25	1 R95422	HLAB38.6084. Comps
14	50	50.5	184	1 Y06801	Peptide Seq ID No:
15	50	50.5	362	1 R03142	Sequence of HLA-Bw
16	50	50.5	362	1 R03144	Sequence of HLA-B5
17	50	50.5	362	1 R12463	HLA-Bw53 exon. HLA
18	49.5	50.0	20	1 R92911	HLA-B2702 CTL modu
19	49.5	50.0	20	1 W33779	Immunomodulating d
20	49	49.5	10	1 R41208	Peptide fragment o
21	49	49.5	10	1 R33062	HLA-B2702 CTL modu
22	49	49.5	10	1 R95413	Alphal-helix of HL
23	49	49.5	10	1 W07512	T-cell modulating
24	49	49.5	10	1 W47265	Immunomodulatory p
25	49	49.5	10	1 W33784	Peptide B2702.75-8
26	49	49.5	15	1 R92912	HLA-B2702 CTL modu
27	49	49.5	15	1 W33795	Peptide B2702.70-8
28	49	49.5	25	1 R41205	Peptide fragment o
29	49	49.5	25	1 R83090	HLA-B2702 CTL modu
30	49	49.5	25	1 R95416	HLA-B2702 60-84. C
31	49	49.5	25	1 W33794	Peptide B2702.60-8
32	44	44.4	10	1 R83094	HLA-B2702 CTL modu
33	44	44.4	10	1 R83095	HLA-B2702 CTL modu
34	44	44.4	10	1 R83096	HLA-B2702 CTL modu

35	44	44.4	10	1 R95425	HLA-B2702.75-84 (D)
36	44	44.4	10	1 R95426	HLA-B2702.75-84 (T)
37	44	44.4	10	1 W07513	T-cell modulating
38	44	44.4	10	1 W47266	Immunomodulatory p
39	44	44.4	10	1 W47267	Immunomodulatory p
40	44	44.4	10	1 W47269	Immunomodulatory p
41	44	44.4	10	1 W33788	Peptide B2702.75-8
42	44	44.4	10	1 W33787	Peptide B2702.75-8
43	44	44.4	10	1 W33789	Peptide B2702.75-8
44	42	42.4	20	1 R92913	HLA-B7 CTL modul
45	42	42.4	20	1 R95415	HLA-B7.84-75-84 Pa

ALIGNMENTS

RESULT 1

R92908 R92908 standard; peptide; 20 AA.
AC R92908;
DT 16-MAY-1996 (first entry)
DE HLA-B2702 CTL modulating peptide (B2702.84-75(T)/75-84).
KW Cytotoxic T lymphocyte; CTL; major histocompatibility complex; MHC;
KW immunosuppressant; graft versus host disorder; transplantation; therapy;
KW class I MHC; HLA-B2702.
OS Synthetic.
PN W09526979-A1.
PD 12-OCT-1995.
PF 05-APR-1995; U04349.
PR 05-APR-1994; US-222851.
PA (STRD) UNIV LELAND STANFORD JUNIOR.
PI Clayberger C, Krensky AM, Parham P;
DR WPI: 95-358582/46.
PT Extension of acceptance period of transplants from MHC unmatched
PT donor hosts - using Class I B75-84 MHC antigen of the recipient
PT host
PS Example 15; Page 36; 80pp; English.
CC R83061-R83085, R83090-R83096 and R92907-R92914 represent fragments of
CC class I major histocompatibility complex (MHC) antigens. This sequence
CC is an inverted dimer of residues 75-84 of the alpha-1 domain of the class
CC I MHC HLA-B2702. These sequences can be used to extend the period of
CC acceptance by a recipient of a transplant from an MHC unmatched donor.
CC The peptides are administered to a patient in conjunction with a
CC subtherapeutic amount of an immunosuppressant. This is administered to
CC the patient for a limited period of time (compared to the lifetime
CC administration for current treatments). The peptides particularly
CC modulate (or inhibit) the activity of the cytotoxic T lymphocytes (CTLs)
CC of the patient.
SQ Sequence 20 AA;

Query Match 100.0%; Score 99; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.1e-10; Indels 0; Gaps 0;
Matches 20; Conservative 0; Mismatches 0;

Oy 1 YRLATLNERENLRALRY 20

Db 1 YRLATLNERENLRALRY 20

RESULT 2

W33791 W33791 standard; peptide; 20 AA.
AC W33791;
DT 19-JUN-1998 (first entry)
DE Peptide B2702.84-75r/75-84 tested for immunomodulating activity.
KW Immunomodulating dimer; immunosuppressant drug; CTL activation;
KW transplantation; autoimmune disease; Class I HLA-B alpha-1 domain;
KW rejection.
OS Synthetic.
PN W09744351-A1.
PD 27-NOV-1997.

PF 22-MAY-1997; U08689.
 PR 24-MAY-1996; US-653294.
 PA (STRD) UNIV LELAND STANFORD JUNIOR.
 PI Beulow R, Clayberger C, Krensky AM;
 DR WPI: 98-086530/08.
 PT New immunomodulating dimer peptide(s) - based on a Class I HLA-B
 PT alpha-1 domain, used for preventing rejection of transplants or
 PT treating autoimmune diseases
 PS Example 1; Page 19; 41pp; English.
 CC Peptides W33784-98 and W33778-9 were assayed for their immunomodulating
 CC activity. A peptide-type compound or variant is claimed which has
 CC immunomodulating activity, including the N-terminal acylated and/or
 CC C-terminal amidated or esterified forms of up to 60 amino acids, where
 CC the peptide-type compound comprises the formula: A-B, where A, B =
 CC (R aa76-77L) (aa79-84) or (aa84-79) (Laa77-76R); aa76 = E or V; aa77 =
 CC D, S or N; aa79 = R or G; aa80 = I or N; aa81, aa84 = a hydrophobic or
 CC small amino acid; aa82 = R or L; aa83 = G or R; and aa represents amino
 CC acid. The sequence in the brackets may optionally be absent or truncated
 CC at any peptide type bond within the brackets. The compounds comprise
 CC amino acid sequences related to a Class I HLA-B alpha1 domain (positions
 CC 79-84). They can be used to inhibit cytotoxic T-lymphocytes (CTL) from
 CC undesirably attacking cells in a host or in vitro. They can also be
 CC used in combination with antigenic peptides or proteins of interest to
 CC activate CTLs. They can also inhibit the proliferation of T cells in
 CC response to anti-CD3. The peptide can be used for preventing rejection
 CC of transplants or for treating autoimmune diseases, e.g. diabetes,
 CC rheumatoid arthritis and lupus erythematosus. The products can also be
 CC used for detection and diagnosis.
 CC Sequence 20 AA;
 SQ

Query Match 100.0%; Score 99; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 4.1e-10;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 YRLATRLNERENLRALRY 20
 DB 1 YRLATRLNERENLRALRY 20
 RESULT 3
 R92910
 ID R92910 standard; peptide; 20 AA.
 AC R92910;
 DT 16-MAY-1996 (first entry)
 DE HLA-B2702 CTL modulating peptide (B2702.84-75(T)/75-84(T)).
 KW Cytotoxic T lymphocyte; CTL; major histocompatibility complex; MHC;
 KW immunosuppressant; graft versus host disorder; transplantation; therapy;
 KW Class I MHC; HLA-B2702.
 OS Synthetic.
 PN W09526979-A1.
 PD 12-OCT-1995.
 PF 05-APR-1995; U04349.
 PR 05-APR-1994; US-222851.
 PA (STRD) UNIV LELAND STANFORD JUNIOR.
 PI Clayberger C, Krensky AM, Parham P;
 DR WPI: 95-358582/46.
 PT Extension of acceptance period of transplants from MHC unmatched
 PT donor hosts - using Class I B7-5-84 MHC antigen of the recipient
 PT host
 PS Example 15; Page 36; 80pp; English.
 CC R83061-R83085, R83090-R83096 and R92907-R92913 represent fragments of
 CC Class I major histocompatibility complex (MHC) antigens. This sequence
 CC is an inverted dimer of residues 75-84 of the alpha-1 domain of the class
 CC I MHC HLA-B2702. These sequences can be used to extend the period of
 CC acceptance by a recipient of a transplant from an MHC unmatched donor.
 CC The peptides are administered to a patient in conjunction with a
 CC subtherapeutic amount of an immunosuppressant. This is administered to
 CC the patient for a limited period of time (compared to the lifetime
 CC administration for current treatments). The peptides particularly
 CC modulate (or inhibit) the activity of the cytotoxic T lymphocytes (CTLs)
 CC of the patient.
 CC Sequence 20 AA;
 SQ

Query Match 94.9%; Score 94; DB 1; Length 20;
 Best Local Similarity 95.0%; Pred. No. 2.7e-09;
 Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 YRLATRLNERENLRALRY 20
 DB 1 YRLATRLNERENLRALRY 20
 RESULT 5
 R92907
 ID R92907 standard; peptide; 20 AA.
 AC R92907;
 DT 16-MAY-1996 (first entry)
 DE HLA-B2702 CTL modulating peptide (B2702.84-75(T)/75-84(T)).
 KW Cytotoxic T lymphocyte; CTL; major histocompatibility complex; MHC;
 KW immunosuppressant; graft versus host disorder; transplantation; therapy;
 KW class I MHC; HLA-B2702.
 SQ

Query Match 94.9%; Score 94; DB 1; Length 20;
 Best Local Similarity 95.0%; Pred. No. 2.7e-09;
 Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 YRLATRLNERENLRALRY 20
 DB 1 YRLATRLNERENLRALRY 20
 RESULT 4
 W33793
 ID W33793 standard; peptide; 20 AA.
 AC W33793;
 DT 19-JUN-1998 (first entry)
 DE Peptide B2702.84-75(T)/75-84(T) tested for immunomodulating activity.
 KW immunomodulating dimer; immunosuppressant drug; CTL activation;
 KW transplantation; autoimmune disease; Class I HLA-B alpha-1 domain;
 KW rejection.
 OS Synthetic.
 OS Homo sapiens.
 PN W09744351-A1.
 PD 27-NOV-1997.
 PR 22-MAY-1997; U08689.
 PR 24-MAY-1996; US-653294.
 PA (STRD) UNIV LELAND STANFORD JUNIOR.
 PI Beulow R, Clayberger C, Krensky AM;
 DR WPI: 98-086530/08.
 PT New immunomodulating dimer peptide(s) - based on a Class I HLA-B
 PT alpha-1 domain, used for preventing rejection of transplants or
 PT treating autoimmune diseases
 PS Example 1; Page 19; 41pp; English.
 CC Peptides W33784-98 and W33778-9 were assayed for their immunomodulating
 CC activity. A peptide-type compound or variant is claimed which has
 CC immunomodulating activity, including the N-terminal acylated and/or
 CC C-terminal amidated or esterified forms of up to 60 amino acids, where
 CC the peptide-type compound comprises the formula: A-B, where A, B =
 CC (R aa76-77L) (aa79-84) or (aa84-79) (Laa77-76R); aa76 = E or V; aa77 =
 CC D, S or N; aa79 = R or G; aa80 = I or N; aa81, aa84 = a hydrophobic or
 CC small amino acid; aa82 = R or L; aa83 = G or R; and aa represents amino
 CC acid. The sequence in the brackets may optionally be absent or truncated
 CC at any peptide type bond within the brackets. The compounds comprise
 CC amino acid sequences related to a Class I HLA-B alpha1 domain (positions
 CC 79-84). They can be used to inhibit cytotoxic T-lymphocytes (CTL) from
 CC undesirably attacking cells in a host or in vitro. They can also be
 CC used in combination with antigenic peptides or proteins of interest to
 CC activate CTLs. They can also inhibit the proliferation of T cells in
 CC response to anti-CD3. The peptide can be used for preventing rejection
 CC of transplants or for treating autoimmune diseases, e.g. diabetes,
 CC rheumatoid arthritis and lupus erythematosus. The products can also be
 CC used for detection and diagnosis.
 CC Sequence 20 AA;
 SQ

OS Synthetic.
PN WO9526979-A1.
PD 12-OCT-1995.
PF 05-APR-1995; U04349.
PR 05-APR-1994; US-222851.
PA (STRD) UNIV LELAND STANFORD JUNIOR.
PI Clayberger C, Krensky AM, Parham P;
DR WPI: 95-358582/46.
PT Extension of acceptance period of transplants from MHC unmatched
PI donor hosts - using Class I B75-84 MHC antigen of the recipient
PI host
PS Example 15; Page 36; 80pp; English.
CC R83061-R83085, R83090-R83096 and R92907-R92914 represent fragments of
CC class I major histocompatibility complex (MHC) antigens. This sequence
CC is an inverted dimer of residues 75-84 of the alpha-1 domain of the class
CC I MHC HLA-B*2702. These sequences can be used to extend the period of
CC acceptance by a recipient of a transplant from an MHC unmatched donor.
CC The peptides are administered to a patient in conjunction with a
CC subtherapeutic amount of an immunosuppressant. This is administered to
CC the patient for a limited period of time (compared to the lifetime
CC administration for current treatments). The peptides particularly
CC modulate (or inhibit) the activity of the cytotoxic T lymphocytes (CTLs)
CC of the patient.
CC Sequence 20 AA;

Query Match 93.9%; Score 93; DB 1; Length 20;
Best Local Similarity 95.0%; Pred. No. 3.9e-09;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 YRLATRLNERENLRALRY 20
DB 1 YRLAIRLNERENLRALRY 20

RESULT 6
ID R95428 standard; peptide; 20 AA.
AC R95428;
AT 12-NOV-1996 (first entry)
DE HLA-B*2702 84-75-84 palindromic.
KW HLA: p74; alpha1-nelix; human-leucocyte-associated antigen; inhibitor;
KW T-cell lysate; membrane protein; mammal; heat shock protein; Hsc70; APC;
KW B cell; calcium influx; cytotoxic T lymphocyte; CTL; differentiation;
KW cytolysis; antigen presenting cell.
OS Synthetic.
PN WO9513288-A1.
PD 18-MAY-1995.
PF 10-NOV-1994; U12985.
PR 10-NOV-1993; US-150493.
PA (STRD) UNIV LELAND STANFORD JUNIOR.
PI Clayberger C, Krensky AM;
DR WPI: 95-194027/25.
PT Compsns. comprising lymphoid surface membrane proteins - which may
PT inhibit cytolytic activity and differentiation of CTLs.
PS Example; Page 12; 29pp; English.
CC R95413, and R95415-R95431 represent palindromes and fragments of
CC human-leucocyte-associated antigens. This sequence represents the
CC HLA-B*2702 84-75-84 palindromic. These sequences can be used to isolate
CC the protein p74 from a T-cell lysate. p74 is a T-cell surface membrane
CC protein associated with T-cell activation in mammalian T-cells, and is
CC also immunologically cross reactive with the heat shock protein Hsc70.
CC p74 is found in a limited number of cell types, but is particularly
CC expressed on B and T cells. p74 can be isolated by lysis of a suitable
CC cell with an amphoteric detergent, and then passed through an affinity
CC column containing a covalently bound HLA-B*2702 palindromic peptide.
CC Compositions comprising the extracellular fragment of p74 combined with
CC HLA-B*2702-60-84 (see R95416), induces calcium influx, and inhibits
CC cytotoxic T lymphocyte (CTL) differentiation or cytolysis. Candidate
CC compounds can be screened for their effect on the cytolytic activity of
CC T-cells, by combining them with the extracellular portion of p74 and
CC determining the amount of binding between the candidate compound and p74.
CC Modulation of CTL activity can be inhibited in a cellular composition

CC containing T-cells and antigen presenting cells (APCs), by adding to the
CC mix the extracellular portion of p74, in an amount sufficient to compete
CC with p74 for the binding of the p74 ligand.
SQ Sequence 20 AA;

Query Match 93.9%; Score 93; DB 1; Length 20;
Best Local Similarity 95.0%; Pred. No. 3.9e-09;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 YRLATRLNERENLRALRY 20
DB 1 YRLAIRLNERENLRALRY 20

RESULT 7
ID W33778 standard; peptide; 20 AA.
AC W33778;
AT 19-JUN-1998 (first entry)
DE Immunomodulating dimer peptide #1.
KW Immunomodulating dimer; immunosuppressant drug; CTL activation;
KW transplantation; autoimmune disease; Class I HLA-B alpha-1 domain;
KW rejection.
OS Synthetic.
PN WO9744351-A1.
PD 27-NOV-1997.
PF 22-MAY-1997; U08689.
PR 24-MAY-1996; US-653294.
PA (STRD) UNIV LELAND STANFORD JUNIOR.
PI Beulow R, Clayberger C, Krensky AM;
DR WPI: 98-086530/08.
PT New immunomodulating dimer peptide(s) - based on a Class I HLA-B
PT alpha-1 domain, used for preventing rejection of transplants or
PT treating autoimmune diseases
PS Claim 16; Page 35; 41pp; English.
CC This sequence represents a specifically claimed immunomodulating
CC dimer peptide of the invention. A peptide-type compound or variant is
CC claimed which has immunomodulating activity, including the N-terminal
CC acylated and/or C-terminal amidated or esterified forms of up to 60
CC amino acids, where the peptide-type compound comprises the formula: A-B,
CC where A, B = (R aa76-77L) (aa79-84) or (aa84-79) (Laa77-76R); aa76 = E or
CC V; aa77 = D, S or N; aa79 = R or G; aa80 = I or N; aa81, aa84 = a
CC hydrophobic or small amino acid; aa82 = R or L; aa83 = G or R; and aa
CC represents amino acid. The sequence in the brackets may optionally be
CC absent or truncated at any peptide type bond within the brackets. The
CC compounds comprise amino acid sequences related to a Class I HLA-B
CC alphas domain (positions 79-84). They can be used to inhibit cytotoxic
CC T-lymphocytes (CTL) from undesirably attacking cells in a host or in
CC vitro. They can also be used in combination with antigenic peptides or
CC proteins of interest to activate CTLs. They can also inhibit the
CC proliferation of T cells in response to anti-CD3. The peptide can be
CC used for preventing rejection of transplants or for treating autoimmune
CC diseases, e.g. diabetes, rheumatoid arthritis and lupus erythematosus.
CC The products can also be used for detection and diagnosis.
CC Sequence 20 AA;

Query Match 93.9%; Score 93; DB 1; Length 20;
Best Local Similarity 95.0%; Pred. No. 3.9e-09;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 YRLATRLNERENLRALRY 20
DB 1 YRLAIRLNERENLRALRY 20

RESULT 8
ID R92909 standard; peptide; 20 AA.
AC R92909;
DR 16-MAY-1996 (first entry)

DE HLA-B2702 CTL modulating peptide (B2702.84-75/75-84(T)).
 KW Cytotoxic T lymphocyte; CTL; major histocompatibility complex; MHC;
 KW immunosuppressant; graft versus host disorder; transplantation; therapy;
 KW class I MHC; HLA-B2702.
 OS Synthetic.
 PN W09526979-A1.
 PD 12-OCT-1995.
 PF 05-APR-1995; U04349.
 PR 05-APR-1994; US-222851.
 PA (STRD) UNIV LELAND STANFORD JUNIOR.
 PI Clayberger C, Krensky AM, Parham P;
 DR WPI: 95-358562/46.
 PT Extension of acceptance period of transplants from MHC unmatched
 PT donor hosts - using Class I B75-84 MHC antigen of the recipient
 PT host
 PS Example 15; Page 36; 80pp; English.
 CC R83061-R83085, R83090-R83096 and R92907-R92913 represent fragments of
 CC class I major histocompatibility complex (MHC) antigens. This sequence
 CC is an inverted dimer of residues 75-84 of the alpha-1 domain of the class
 CC I MHC HLA-B2702. These sequences can be used to extend the period of
 CC acceptance by a recipient of a transplant from an MHC unmatched donor.
 CC The peptides are administered to a patient in conjunction with a
 CC subtherapeutic amount of an immunosuppressant. This is administered to
 CC the patient for a limited period of time (compared to the lifetime
 CC administration for current treatments). The peptides particularly
 CC modulate (or inhibit) the activity of the cytotoxic T lymphocytes (CTLs)
 CC of the patient.
 SQ Sequence 20 AA;

Query Match 88.9%; Score 88; DB 1; Length 20;
 Best Local Similarity 90.0%; Pred. No. 2.6e-08;
 Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 YRLATRLNERENLRALRY 20
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 Db 1 YRLAIRLNERENLRALRY 20

RESULT 9

ID W33792 standard; peptide; 20 AA.
 AC W33792;
 DT 19-JUN-1998 (first entry)
 DE Peptide B2702.84-75/75-84T tested for immunomodulating activity.
 KW Immunomodulating dimer; immunosuppressant drug; CTL activation;
 KW transplantation; autoimmune disease; Class I HLA-B alpha-1 domain;
 KW rejection.
 OS Synthetic.
 OS Homo sapiens.
 PN W09744351-A1.
 PD 27-NOV-1997; U08689.
 PF 22-MAY-1997; US-653294.
 PR (STRD) UNIV LELAND STANFORD JUNIOR.
 PA Beulow R, Clayberger C, Krensky AM;
 PI WPI: 98-086530/08
 DR New immunomodulating dimer peptide(s) - based on a Class I HLA-B
 PT alpha-1 domain, used for preventing rejection of transplants or
 PT treating autoimmune diseases
 PS Example 1; Page 19; 41pp; English.
 CC Peptides W33784-98 and W33778-9 were assayed for their immunomodulating
 CC activity. A peptide-type compound or variant is claimed which has
 CC immunomodulating activity, including the N-terminal acylated and/or
 CC C-terminal amidated or esterified forms of up to 60 amino acids, where
 CC the peptide-type compound comprises the formula: A-B, where A, B =
 CC (R aa76-77L) (aa79-84) or (aa84-79) (Laa77-76R); aa76 = E or V; aa77 =
 CC D, S or N; aa79 = R or G; aa80 = I or N; aa81, aa84 = a hydrophobic or
 CC small amino acid; aa82 = R or L; aa83 = G or R; and aa represents amino
 CC acid. The sequence in the brackets may optionally be absent or truncated
 CC at any peptide type bond within the brackets. The compounds comprise
 CC amino acid sequences related to a Class I HLA-B alpha domain (positions
 CC 79-84). They can be used to inhibit cytotoxic T-lymphocytes (CTL) from

CC undesirably attacking cells in a host or in vitro. They can also be
 CC used in combination with antigenic peptides or proteins of interest to
 CC activate CTLs. They can also inhibit the proliferation of T cells in
 CC response to anti-CD3. The peptide can be used for preventing rejection
 CC of transplants or for treating autoimmune diseases, e.g. diabetes,
 CC rheumatoid arthritis and lupus erythematosus. The products can also be
 CC used for detection and diagnosis.
 SQ Sequence 20 AA;

Query Match 88.9%; Score 88; DB 1; Length 20;
 Best Local Similarity 90.0%; Pred. No. 2.6e-08;
 Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 YRLATRLNERENLRALRY 20
 ||||| ||||| ||||| |||||
 Db 1 YRLAIRLNERENLRALRY 20

RESULT 10

ID R95430 standard; peptide; 20 AA.
 AC R95430;
 DT 12-NOV-1996 (first entry)
 DE HLA-B2702 84-75T/75-84T palindromic.
 KW HLA; p74; alpha1-helix; human-leucocyte-associated antigen; inhibitor;
 KW T-cell lysate; membrane protein; mammal; heat shock protein; Hsc70; APC;
 KW B cell; calcium influx; cytotoxic T lymphocyte; CTL; differentiation;
 KW cytolysis; antigen presenting cell.
 OS Synthetic.
 PN W09513288-A1.
 PD 18-MAY-1995.
 PF 10-NOV-1994; U12985.
 PR 10-NOV-1993; US-150493.
 PA (STRD) UNIV LELAND STANFORD JUNIOR.
 PI Clayberger C, Krensky AM;
 DR WPI: 95-194027/25.
 PT Compns. comprising lymphoid surface membrane proteins - which may
 PT inhibit cytolytic activity and differentiation of CTLs.
 PS Example; Page 12; 29pp; English.
 CC R95413, and R95415-R95431 represent palindromes and fragments of
 CC human-leucocyte-associated antigens. This sequence represents the
 CC HLA-B2702 84-75T/75-84T palindromic. These sequences can be used to
 CC isolate the protein p74 from a T-cell lysate. p74 is a T-cell surface
 CC membrane protein associated with T-cell activation in mammalian T-cells,
 CC and is also immunologically cross reactive with the heat shock protein
 CC Hsc70. p74 is found in a limited number of cell types, but is
 CC particularly expressed on B and T cells. p74 can be isolated by lysis of
 CC a suitable cell with an amphoteric detergent, and then passed through an
 CC affinity column containing a covalently bound HLA-B2702 palindromic
 CC peptide. Compositions comprising the extracellular fragment of p74
 CC combined with HLA-B2702.60-84 (see R95416), induces calcium influx, and
 CC inhibits cytotoxic T lymphocyte (CTL) differentiation or cytolysis.
 CC Candidate compounds can be screened for their effect on the cytolytic
 CC activity of T-cells, by combining them with the extracellular portion of
 CC p74 and determining the amount of binding between the candidate compound
 CC and p74. Modulation of CTL activity can be inhibited in a cellular
 CC composition containing T-cells and antigen presenting cells (APCs), by
 CC adding to the mix the extracellular portion of p74, in an amount
 CC sufficient to compete with p74 for the binding of the p74 ligand.
 SQ Sequence 20 AA;

Query Match 80.8%; Score 80; DB 1; Length 20;
 Best Local Similarity 89.5%; Pred. No. 5.2e-07;
 Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 YRLATRLNERENLRALRY 19
 ||||| ||||| ||||| |||||
 Db 1 YRLAIRLNERENLRALRY 19

RESULT 11

R48286

ID R48286 standard; peptide: 25 AA.
 AC R48286;
 DT 15-MAR-1994 (first entry)
 DE Peptide fragment of HLA-B38 antigen.
 KW Human leukocyte antigen; HLA; peptide; transplantation; neoplasia;
 KW parasitic disease; cytotoxic T lymphocyte; modulation.
 OS Synthetic.
 PN WO9317699-A.
 PD 16-SEP-1993.
 PF 25-FEB-1993; U01758.
 PR 02-MAR-1992; US-844716.
 PA (STRD) UNIV LELAND STANFORD JUNIOR.
 PI Clayberger C, Krensky AM;
 DR WPI: 93-303134/38.
 PT New peptide(s) based on Class I HLA antigen domains - used for
 PT modulating cytotoxic T-lymphocyte activity towards targets
 PS Example 13; Page 39; 61pp; English.
 CC The peptide is used to modulate cytotoxic T-lymphocyte (CTL)
 CC activity, either by inhibition or stimulation. It can be used for
 CC inhibiting CTL toxicity in transplantations, for inducing CTL
 CC activity in parasitic diseases and neoplasia and in studies on viral
 CC infection. The peptide can also be used for identifying CTLs which
 CC bind to it and removing subsets of CTLs from a T-cell composition.
 CC This peptide is derived from the HLA-B38 antigen and corresponds
 CC to the amino acid positions 60-84 of that antigen.
 SQ Sequence 25 AA;

Query Match 50.5%; Score 50; DB 1; Length 25;

Best Local Similarity 68.8%; Pred. No. 0.051;

Matches 11; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 5 TRLNRRERENLRALRY 20

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DB 10 TNTQTYRENLRALRY 25

RESULT 12

ID R83093 standard; peptide: 25 AA.
 AC R83093;
 DT 16-MAY-1996 (first entry)
 DE HLAB38 CTL modulating peptide (B38.6084).
 KW Cytotoxic T lymphocyte; CTL; major histocompatibility complex; MHC;
 KW immunosuppressant; graft versus host disorder; transplantation; therapy;
 KW class I MHC; HLAB38.
 OS Synthetic.
 PN WO9526979-A1.
 PD 12-OCT-1995.
 PF 05-APR-1995; U04349.
 PR 05-APR-1994; US-222851.
 PA (STRD) UNIV LELAND STANFORD JUNIOR.
 PI Clayberger C, Krensky AM, Parham P;
 DR WPI: 95-358582/46.
 PT Extension of acceptance period of transplants from MHC unmatched
 PT donor hosts - using Class I B75-84 MHC antigen of the recipient
 PT host
 PS Example 13; Page 32; 80pp; English.
 CC R83061-R83085, R83090-R83096 and R92907-R92913 represent fragments of
 CC class I major histocompatibility complex (MHC) antigens. This sequence
 CC corresponds to residues 60-84 of the alpha-1 domain of the class I MHC
 CC HLAB38. These sequences can be used to extend the period of acceptance
 CC by a recipient of a transplant from an MHC unmatched donor. The peptides
 CC are administered to a patient in conjunction with a subtherapeutic amount
 CC of an immunosuppressant. This is administered to the patient for a
 CC limited period of time (compared to the lifetime administration for
 CC current treatments). The peptides particularly modulate (or inhibit) the
 CC activity of the cytotoxic T lymphocytes (CTLs) of the patient.
 SQ Sequence 25 AA;

Query Match

50.5%; Score 50; DB 1; Length 25;

Best Local Similarity 68.8%; Pred. No. 0.051;

Matches 11; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 5 TRLNRRERENLRALRY 20

| | | | | | | | | |

DB 10 TNTQTYRENLRALRY 25

RESULT 13

R95422
 ID R95422 standard; peptide: 25 AA.
 AC R95422;
 DT 12-NOV-1996 (first entry)
 DE HLAB38.6084.
 KW HLA; p74; alpha-helix; human-leucocyte-associated antigen; inhibitor;
 KW T-cell lysate; membrane protein; mammal; heat shock protein; Hsc70; APC;
 KW B cell; calcium influx; cytotoxic T lymphocyte; CTL; differentiation;
 KW cytolysis; antigen presenting cell.
 OS Synthetic.
 PN WO9513288-A1.
 PD 18-MAY-1995.
 PF 10-NOV-1994; U12985.
 PR 10-NOV-1993; US-150493.
 PA (STRD) UNIV LELAND STANFORD JUNIOR.
 PI Clayberger C, Krensky AM;
 DR WPI: 95-194027/25.
 PT Compsns. comprising lymphoid surface membrane proteins - which may
 PT inhibit cytolytic activity and differentiation of CTLs.
 PS Example; Page 9; 29pp; English.
 CC R95413, and R95415-R95431 represent palindromes and fragments of
 CC human-leucocyte-associated antigens. This sequence represents the
 CC HLAB38.6084. These sequences can be used to isolate the protein p74 from
 CC a T-cell lysate. p74 is a T-cell surface membrane protein associated
 CC with T-cell activation in mammalian T-cells, and is also immunologically
 CC cross reactive with the heat shock protein Hsc70. p74 is found in a
 CC limited number of cell types, but is particularly expressed on B and T
 CC cells. p74 can be isolated by lysis of a suitable cell with an
 CC amphoteric detergent, and then passed through an affinity column
 CC containing a covalently bound HLA-B2702 palindromic peptide.
 CC Compositions comprising the extracellular fragment of p74 combined with
 CC HLA-B2702.60-84 (see R95416), induces calcium influx, and inhibits
 CC cytotoxic T lymphocyte (CTL) differentiation or cytolysis. Candidate
 CC compounds can be screened for their effect on the cytolytic activity of
 CC T-cells, by combining them with the extracellular portion of p74 and
 CC determining the amount of binding between the candidate compound and p74.
 CC Modulation of CTL activity can be inhibited in a cellular composition
 CC containing T-cells and antigen presenting cells (APCs), by adding to the
 CC mix the extracellular portion of p74, in an amount sufficient to compete
 CC with p74 for the binding of the p74 ligand.
 SQ Sequence 25 AA;

Query Match 50.5%; Score 50; DB 1; Length 25;

Best Local Similarity 68.8%; Pred. No. 0.051;

Matches 11; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 5 TRLNRRERENLRALRY 20

| | | | | | | | | |

DB 10 TNTQTYRENLRALRY 25

RESULT 14

Y06801
 ID Y06801 standard; Protein: 184 AA.
 AC Y06801;
 DT 23-JUN-1999 (first entry)
 DE Peptide Seq ID No: 21.
 KW Major histocompatibility complex; MHC; antigen binding clef; allergy;
 KW antigen-specific T-cell; transplant rejection; autoimmune disease;
 KW multiple sclerosis; rheumatoid arthritis; systemic lupus erythematosus;
 KW insulin-dependent diabetes mellitus; immune response; cancer.
 OS Homo sapiens.
 PN WO9914236-A1.

PD 25-MAR-1999.
 PF 15-SEP-1998; U18244.
 PR 10-OCT-1997; US-064555.
 PR 16-SEP-1997; US-064552.
 PA (BURR/) BURROWS G G.
 PA (VAND/) VANDENBARK A A.
 PI Burrows GG, Vandenbark AA;
 DR WPI: 99-229498/19.
 PT Recombinant 2-domain major histocompatibility complex molecules used
 PT to manipulate antigen specific T-cells
 PS Example 1; Page 67-68; 73pp; English.
 CC The invention relates to recombinant polypeptides comprising only those
 CC domains of major histocompatibility complex (MHC) molecules that define
 CC the antigen binding cleft. These polypeptides can be used to mimic the
 CC function of mammalian MHC. The recombinant polypeptide comprises
 CC covalently linked first and second domains, where the first domain is a
 CC mammalian MHC class II beta1 domain and the second domain is a mammalian
 CC class I alpha1 domain, or where the first domain is a mammalian MHC
 CC alpha2 domain, and wherein the polypeptide is not a whole MHC class I
 CC alpha chain. The amino terminus of the second domain is covalently linked
 CC to the carboxy terminus of the first domain in both cases, optionally
 CC with a peptide linker sequence. The recombinant MHC polypeptides are
 CC useful for a wide range of in vitro and in vivo applications, and may be
 CC used in place of either intact, purified MHC molecules or antigen
 CC presenting cells that express MHC molecules. The polypeptides can be used
 CC for the detection, quantification and purification of antigen-specific
 CC T-cells in biological samples. They can also be used to activate or
 CC inactivate T-cells and to induce anergy in T-cells. The polypeptides may
 CC be used for the amelioration of conditions mediated by antigen-specific
 CC T-cells, e.g. allergies, transplant rejection and autoimmune diseases
 CC including multiple sclerosis, rheumatoid arthritis, systemic lupus
 CC erythematosus and insulin-dependent diabetes mellitus. The polypeptides
 CC may also be used to boost immune responses in certain conditions such as
 CC cancer and infectious diseases. If a toxic molecule is attached to the
 CC polypeptides, then they can also be used to kill specific T-cells.
 SQ Sequence 184 AA;

Query Match 50.5%; Score 50; DB 1; Length 184;
 Best Local Similarity 68.8%; Pred. No. 0.46;
 Matches 11; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 5 TRLNERRENRLALRY 20
 | | | | | | | | | |
 Db 69 TNTQTYRENRLALRY 84

RESULT 15
 R03142
 ID R03142 standard; protein; 362 AA.
 AC R03142, 1991 (first entry)
 DT 19-MAR-1991
 DE Sequence of HLA-B*52 antigen.
 KW Probe: HLA class I DNA; immunogen.
 OS Homo sapiens.
 PN EP-354580-A.
 PD 14-FEB-1990.
 PF 10-AUG-1989.
 PR 11-AUG-1988; JP-200758.
 PA (OLYU) Olympus Optical Co., Ltd.
 PI Kano K, Takiguchi;
 DR WPI: 90-046289/07.
 PT New DNA for class I human leucocyte antigens and derived probes and
 PT transformed cells, useful for DNA typing, as immunogens etc.
 PS Disclosure; Page 13; 23pp; English.
 CC The HLA class I DNA can be used as a source of probes for use in DNA
 CC typing. Transformed cells, which are useful as immunogens, can be
 CC obtained by introducing these DNAs into eucaryotic cells.
 SQ Sequence 362 AA;

Query Match 50.5%; Score 50; DB 1; Length 362;

Best Local Similarity 68.8%; Pred. No. 0.98;
 Matches 11; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 5 TRLNERRENRLALRY 20
 | | | | | | | | | |
 Db 93 TNTQTYRENRLALRY 108

Search completed: February 8, 2000, 04:05:43
 Job time: 9360 sec



GenCore version 4.5
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OM protein - protein search, using sw model

Run on: February 7, 2000, 18:04:38 ; Search time 111.22 Seconds
(without alignments)
8.482 Million cell updates/sec

Title: US-08-653-294-28
Perfect score: 99
Sequence: 1 YRLATPLNRRERLRY 20

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 142080 seqs, 47169319 residues

Total number of hits satisfying chosen parameters: 142080

Minimum DB seq length: 0
Maximum DB seq length: 1000000

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database : PIR_62.*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	50	50.5	273	2 I38509	MHC class I histoc
2	50	50.5	274	2 I54463	MHC HLA-B38 chain
3	50	50.5	362	2 B30345	MHC class I histoc
4	50	50.5	362	2 A45834	MHC class I histoc
5	50	50.5	362	2 I84486	transmembrane glyco
6	50	50.5	362	2 A30345	MHC class I histoc
7	50	50.5	362	2 I59633	MHC HLA-B transmem
8	50	50.5	362	2 S24434	class I histocoma
9	50	50.5	362	2 I37120	MHC class I histoc
10	49	49.5	354	2 I59308	class I histocoma
11	49	49.5	354	2 I80168	class I histocoma
12	49	49.5	354	2 I80167	class I histocoma
13	49	49.5	355	2 I80169	class I histocoma
14	49	49.5	355	2 I80171	class I histocoma
15	49	49.5	359	1 HLH012	MHC class I histoc
16	49	49.5	362	1 HLH028	MHC class I histoc
17	49	49.5	362	2 JH0541	class I histocoma
18	49	49.5	362	2 JH0539	class I histocoma
19	49	49.5	362	2 JH0540	class I histocoma
20	49	49.5	362	2 I62045	gene HLA B-1517 pr
21	49	49.5	362	2 I84490	lymphocyte antigen
22	49	49.5	362	2 I37521	HLA-Bw57.2 antigen
23	49	49.5	363	2 S07113	class I histocoma
24	49	49.5	363	2 S03537	class I histocoma
25	49	49.5	364	2 D35997	MHC class I histoc
26	49	49.5	365	2 S77963	MHC class I histoc
27	49	49.5	365	2 I54416	HLA-AW24 protein -
28	49	49.5	365	2 I54493	MHC class I histoc
29	45	45.5	355	2 I37516	HLA-B alpha-chain
30	45	45.5	362	2 S25415	class I histocoma

31	45	45.5	362	2 A45850	MHC class I histoc
32	45	45.5	362	2 I61861	MHC HLA-B44.2 chai
33	45	45.5	362	2 I54442	MHC class I histoc
34	44	44.4	274	1 HLH032	MHC class I histoc
35	44	44.4	364	2 A35997	MHC class I histoc
36	44	44.4	445	2 S67147	hypothetical prote
37	43	43.4	455	2 F64617	hypothetical prote
38	43	43.4	2013	2 C71610	probable membrane
39	42	42.4	137	2 I80174	class I histocoma
40	42	42.4	425	1 FOMVGC	gag polyprotein -
41	42	42.4	536	1 FOMVMD	gag polyprotein -
42	42	42.4	790	1 FOMVHZ	gag-kit polyprotei
43	42	42.4	912	2 F71433	probable growth re
44	42	42.4	1110	1 A70652	probable serine/th
45	42	42.4	1228	2 I40468	surface layer prot

ALIGNMENTS

RESULT 1
I38509
MHC class I histocompatibility antigen - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 06-Sep-1996 #sequence_revision 06-Sep-1996 #text_change 23-Jul-1999
C:Accession: I38509
R:Cereb, N.; Choi, J.W.; Riu, K.Z.; Yang, S.Y.
Tissue Antigens 44, 271-273, 1994.
A:Title: HLA-B*5105, a newly identified B51 IEF variant.
A:Reference number: I38509; MUID:95176331
A:Accession: I38509
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-273 <RES>
A:Cross-references: EMBL:U06697; NID:g469544; PIDN:AAA92997.1; PID:g469545
C:Genetics:
A:Gene: GDB:HLA-B
A:Cross-references: GDB:I20048; OMIM:142830
A:Map position: 6p21.3-6p21.3
C:Superfamily: class I histocompatibility antigen; immunoglobulin homology

Query Match 50.5%; Score 50; DB 2; Length 273;
Best Local Similarity 68.8%; Pred. No. 1;
Matches 11; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 5 TRLNRRERLRY 20
I | | | | | | | | | |
Db 68 TTTQTYRENLRY 83

RESULT 2
I54463
MHC HLA-B38 chain - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 07-Jun-1996 #sequence_revision 07-Jun-1996 #text_change 23-Jul-1999
C:Accession: I54463
R:Mueller, C.A.; Engler-Blum, G.; Gekeler, V.; Steiert, I.; Weiss, E.; Schmidt, H.
Immunogenetics 30, 200-207, 1989
A:Title: Genetic and serological heterogeneity of the supertypic HLA-B locus specific
A:Reference number: I54463; MUID:89379286
A:Accession: I54463
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-274 <RES>
A:Cross-references: GB:M29864; NID:g187674; PIDN:AAA36222.1; PID:g187675
C:Superfamily: class I histocompatibility antigen; immunoglobulin homology

Query Match 50.5%; Score 50; DB 2; Length 274;
Best Local Similarity 68.8%; Pred. No. 1.1;
Matches 11; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 5 TRLNERENLRALRY 20
| | | | | | | | | |
Db 69 TNTQTYRENLRALRY 84

RESULT 3

MHC class I histocompatibility antigen HLA-Bw52 precursor - human
C:Species: Homo sapiens (man)
C:Date: 29-Jan-1990 #sequence_revision 29-Jan-1990 #text_change 16-Feb-1997
C:Accession: B30345
R:Hayashi, H.; Ennis, P.D.; Ariga, H.; Salter, R.D.; Parham, P.; Kano, K.; Takiguchi, M.
J. Immunol. 142, 306-311, 1989
A:Title: HLA-B51 and HLA-Bw52 differ by only two amino acids which are in the helical re
A:Reference number: A30345; MUID:89080265
A:Accession: B30345
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-362 <HAY>
C:Superfamily: class I histocompatibility antigen; immunoglobulin homology
C:Keywords: transmembrane protein
F:220-285/Domain: immunoglobulin homology <IMM>

Query Match 50.5%; Score 50; DB 2; Length 362;
Best Local Similarity 68.8%; Pred. No. 1.4;
Matches 11; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 5 TRLNERENLRALRY 20
| | | | | | | | | |
Db 93 TNTQTYRENLRALRY 108

RESULT 4

MHC class I histocompatibility antigen HLA-B53 alpha chain precursor - human
C:Species: Homo sapiens (man)
C:Date: 03-Jun-1993 #sequence_revision 03-Jun-1993 #text_change 23-Jul-1999
C:Accession: A45834
R:Hayashi, H.; Ooba, T.; Nakayama, S.; Sekimata, M.; Kano, K.; Takiguchi, M.
Immunogenetics 32, 195-199, 1990
A:Title: Allospecificities between HLA-Bw53 and HLA-B35 are generated by substitution of
A:Reference number: A45834; MUID:91033941
A:Accession: A45834
A:Molecule type: DNA
A:Residues: 1-362 <HAY>
A:Cross-references: GB:M58636; NID:g187756; PIDN:AAA36228.1; PID:g187757; GB:M33574
A:Note: this allele is designated B*5301
C:Genetics:
A:Gene: GDB:HLA-B
A:Cross-references: GDB:120048; OMIM:142830
A:Map position: 6p21.3-6p21.3
C:Superfamily: class I histocompatibility antigen; immunoglobulin homology
C:Keywords: glycoprotein; heterodimer; transmembrane protein
F:1-24/Domain: signal sequence #status predicted <SIG>
F:220-285/Domain: immunoglobulin homology <IMM>
F:110/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 50.5%; Score 50; DB 2; Length 362;
Best Local Similarity 68.8%; Pred. No. 1.4;
Matches 11; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 5 TRLNERENLRALRY 20
| | | | | | | | | |
Db 93 TNTQTYRENLRALRY 108

RESULT 5

MHC class I histocompatibility antigen HLA-B51 precursor - human
C:Species: Homo sapiens (man)
C:Date: 29-Jan-1990 #sequence_revision 29-Jan-1990 #text_change 16-Feb-1997
C:Accession: B30345
R:Hayashi, H.; Ennis, P.D.; Ariga, H.; Salter, R.D.; Parham, P.; Kano, K.; Takiguchi, M.
J. Immunol. 142, 306-311, 1989
A:Title: HLA-B51 and HLA-Bw52 differ by only two amino acids which are in the helical re
A:Reference number: A30345; MUID:89080265
A:Accession: B30345
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-362 <HAY>
C:Superfamily: class I histocompatibility antigen; immunoglobulin homology
C:Keywords: transmembrane protein
F:220-285/Domain: immunoglobulin homology <IMM>

Query Match 50.5%; Score 50; DB 2; Length 362;
Best Local Similarity 68.8%; Pred. No. 1.4;
Matches 11; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

C:Accession: I84486
R:Hildebrand, W.H.; Domena, J.D.; Shen, S.Y.; Lau, M.; Terasaki, P.I.; Bunce, M.; Mar
Tissue Antigens 43, 209-218, 1994
A:Title: HLA-B15: a widespread and diverse family of HLA-B alleles.
A:Reference number: I38421; MUID:94367483
A:Accession: I84486
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-362 <RES>
A:Cross-references: GB:LI5005; NID:g493154; PIDN:AAA56832.1; PID:g493155
C:Genetics:
A:Gene: HLA-B*1513
C:Superfamily: class I histocompatibility antigen; immunoglobulin homology
C:Keywords: glycoprotein

Query Match 50.5%; Score 50; DB 2; Length 362;
Best Local Similarity 68.8%; Pred. No. 1.4;
Matches 11; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 5 TRLNERENLRALRY 20
| | | | | | | | | |
Db 93 TNTQTYRENLRALRY 108

RESULT 6

MHC class I histocompatibility antigen HLA-B51 precursor - human
C:Species: Homo sapiens (man)
C:Date: 29-Jan-1990 #sequence_revision 29-Jan-1990 #text_change 23-Jul-1999
C:Accession: A30345; I68746; I37499
R:Hayashi, H.; Ennis, P.D.; Ariga, H.; Salter, R.D.; Parham, P.; Kano, K.; Takiguchi, M.
J. Immunol. 142, 306-311, 1989
A:Title: HLA-B51 and HLA-Bw52 differ by only two amino acids which are in the helical
A:Reference number: A30345; MUID:89080265
A:Accession: A30345
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-362 <HAY>
R:Pohla, H.; Kuon, W.; Tabaczewski, P.; Doerner, C.; Weiss, E.H.
Immunogenetics 29, 297-307, 1989
A:Title: Allelic variation in HLA-B and HLA-C sequences and the evolution of the HLA-
A:Reference number: I54457; MUID:89233295
A:Accession: I68746
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-362 <RES>
A:Cross-references: GB:L41087; NID:g735900; PIDN:AAA64513.1; PID:g735902
R:Steinle, A.; Schendel, D.J.
Tissue Antigens 44, 268-270, 1994
A:Title: HLA class I alleles of LCL 721 and 174 x CEM.T2 (T2).
A:Reference number: I37499; MUID:95176330
A:Accession: I37499
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-206 <RE2>
A:Cross-references: EMBL:Z46808; NID:g599783; PIDN:CAA86838.1; PID:g599784
C:Genetics:
A:Gene: GDB:HLA-B
A:Cross-references: GDB:120048; OMIM:142830
A:Map position: 6p21.3-6p21.3
A:Introns: 25/1; 115/1; 207/1; 299/1; 338/1; 349/1
C:Superfamily: class I histocompatibility antigen; immunoglobulin homology
C:Keywords: transmembrane protein
F:220-285/Domain: immunoglobulin homology <IMM>

Qy 5 TRLNERENLRALRY 20
| | | | | | | | | |
Db 93 TNTQTYRENLRALRY 108

RESULT 7

MHC class I histocompatibility antigen HLA-B51 precursor - human
C:Species: Homo sapiens (man)
C:Date: 29-Jan-1990 #sequence_revision 29-Jan-1990 #text_change 23-Jul-1999
C:Accession: A30345; I68746; I37499
R:Hayashi, H.; Ennis, P.D.; Ariga, H.; Salter, R.D.; Parham, P.; Kano, K.; Takiguchi, M.
J. Immunol. 142, 306-311, 1989
A:Title: HLA-B51 and HLA-Bw52 differ by only two amino acids which are in the helical
A:Reference number: A30345; MUID:89080265
A:Accession: A30345
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-362 <HAY>
R:Pohla, H.; Kuon, W.; Tabaczewski, P.; Doerner, C.; Weiss, E.H.
Immunogenetics 29, 297-307, 1989
A:Title: Allelic variation in HLA-B and HLA-C sequences and the evolution of the HLA-
A:Reference number: I54457; MUID:89233295
A:Accession: I68746
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-362 <RES>
A:Cross-references: GB:L41087; NID:g735900; PIDN:AAA64513.1; PID:g735902
R:Steinle, A.; Schendel, D.J.
Tissue Antigens 44, 268-270, 1994
A:Title: HLA class I alleles of LCL 721 and 174 x CEM.T2 (T2).
A:Reference number: I37499; MUID:95176330
A:Accession: I37499
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-206 <RE2>
A:Cross-references: EMBL:Z46808; NID:g599783; PIDN:CAA86838.1; PID:g599784
C:Genetics:
A:Gene: GDB:HLA-B
A:Cross-references: GDB:120048; OMIM:142830
A:Map position: 6p21.3-6p21.3
A:Introns: 25/1; 115/1; 207/1; 299/1; 338/1; 349/1
C:Superfamily: class I histocompatibility antigen; immunoglobulin homology
C:Keywords: transmembrane protein
F:220-285/Domain: immunoglobulin homology <IMM>

Qy 5 TRLNERENLRALRY 20
| | | | | | | | | |
Db 93 TNTQTYRENLRALRY 108

RESULT 8

MHC class I histocompatibility antigen HLA-B51 precursor - human
C:Species: Homo sapiens (man)
C:Date: 29-Jan-1990 #sequence_revision 29-Jan-1990 #text_change 23-Jul-1999
C:Accession: A30345; I68746; I37499
R:Hayashi, H.; Ennis, P.D.; Ariga, H.; Salter, R.D.; Parham, P.; Kano, K.; Takiguchi, M.
J. Immunol. 142, 306-311, 1989
A:Title: HLA-B51 and HLA-Bw52 differ by only two amino acids which are in the helical
A:Reference number: A30345; MUID:89080265
A:Accession: A30345
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-362 <HAY>
R:Pohla, H.; Kuon, W.; Tabaczewski, P.; Doerner, C.; Weiss, E.H.
Immunogenetics 29, 297-307, 1989
A:Title: Allelic variation in HLA-B and HLA-C sequences and the evolution of the HLA-
A:Reference number: I54457; MUID:89233295
A:Accession: I68746
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-362 <RES>
A:Cross-references: GB:L41087; NID:g735900; PIDN:AAA64513.1; PID:g735902
R:Steinle, A.; Schendel, D.J.
Tissue Antigens 44, 268-270, 1994
A:Title: HLA class I alleles of LCL 721 and 174 x CEM.T2 (T2).
A:Reference number: I37499; MUID:95176330
A:Accession: I37499
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-206 <RE2>
A:Cross-references: EMBL:Z46808; NID:g599783; PIDN:CAA86838.1; PID:g599784
C:Genetics:
A:Gene: GDB:HLA-B
A:Cross-references: GDB:120048; OMIM:142830
A:Map position: 6p21.3-6p21.3
A:Introns: 25/1; 115/1; 207/1; 299/1; 338/1; 349/1
C:Superfamily: class I histocompatibility antigen; immunoglobulin homology
C:Keywords: transmembrane protein
F:220-285/Domain: immunoglobulin homology <IMM>

Db 93 TNTQTYRENRLRY 108

RESULT 7

I59633 MHC HLA-B transmembrane glycoprotein - human

C:Species: Homo sapiens (man)

C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 23-Jul-1999

C:Accession: I59633

R:Mildebrand, W.H.; Domene, J.D.; Parham, P.

Tissue Antigens 41, 190-195, 1993

A:Title: Primary structure shows HLA-B59 to be a hybrid of HLA-B55 and HLA-B51, and not

A:Reference number: I59633; MUID:93369833

A:Accession: I59633

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-362 <RES>

A:Cross-references: GB:I07743; NID:G388314; PIDN:AAA59621.1; PID:G388315

C:Genetics:

A:Gene: GDB:HLA-B

A:Cross-references: GDB:I20048; OMIM:142830

A:Map position: 6p21.3-6p21.3

C:Superfamily: class I histocompatibility antigen; immunoglobulin homology

C:Keywords: glycoprotein

Query Match 50.5%; Score 50; DB 2; Length 362;

Best Local Similarity 68.8%; Pred. No. 1.4;

Matches 11; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 5 TRLNERENRLRY 20

I 1111111111

Db 93 TNTQTYRENRLRY 108

RESULT 8

S24434

class I histocompatibility antigen HLA-B-52012 precursor - human

C:Species: Homo sapiens (man)

C:Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 07-Nov-1997

C:Accession: S24434

R:Watkins, D.I.; McAdam, S.N.; Liu, X.; Strang, C.R.; Milford, E.L.; Levine, C.G.; Garbe

Nature 357, 329-333, 1992

A:Title: New recombinant HLA-B alleles in a tribe of South American Amerindians indicate

A:Reference number: S24027; MUID:92269956

A:Accession: S24434

A:Molecule type: mRNA

A:Residues: 1-362 <WAT>

C:Genetics:

A:Gene: HLA-B-52012

C:Superfamily: class I histocompatibility antigen; immunoglobulin homology

C:Keywords: glycoprotein; transmembrane protein

F:1-24/Domain: signal sequence #status predicted <SIG>

F:25-362/Product: class I histocompatibility antigen HLA-B-52012 #status predicted <MAT>

F:25-307/Domain: extracellular #status predicted <EXT>

F:115-206/Domain: alpha-2 #status predicted <EX2>

F:220-285/Domain: immunoglobulin homology <IMM>

F:308-331/Domain: transmembrane #status predicted <TMW>

F:332-362/Domain: intracellular #status predicted <INT>

F:110/Binding site: carbohydrate (Asn) (covalent) #status predicted

F:125-188,227-283/disulfide bonds: #status predicted

Query Match

Best Local Similarity 50.5%; Score 50; DB 2; Length 362;

Matches 11; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 5 TRLNERENRLRY 20

I 1111111111

Db 93 TNTQTYRENRLRY 108

RESULT 9

I37120

MHC class I histocompatibility antigen HLA-B51 alpha chain precursor - human (isolate

C:Species: Homo sapiens (man)

A:Variety: isolate B*5104

C:Date: 12-Aug-1996 #sequence_revision 12-Aug-1996 #text_change 23-Jul-1999

C:Accession: I37120

R:Belich, M.P.; Madrigal, J.A.; Hildebrand, W.H.; Zemmour, J.; Williams, R.C.; Luz, R

Nature 357, 326-329, 1992

A:Title: Unusual HLA-B alleles in two tribes of Brazilian Indians.

A:Reference number: I37120; MUID:92269955

A:Accession: I37120

A:Status: translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-362 <RES>

A:Cross-references: EMBL:215143; NID:G28234; PIDN:CAA78849.1; PID:G28235

A:Experimental source: cell line KRC 005; isolate B*5104

C:Superfamily: class I histocompatibility antigen; immunoglobulin homology

C:Keywords: transmembrane protein

F:1-24/Domain: signal sequence #status predicted <SIG>

F:25-362/Product: MHC class I histocompatibility antigen HLA-B51 #status predicted <M

F:220-285/Domain: immunoglobulin homology <IMM>

Query Match

Best Local Similarity 50.5%; Score 50; DB 2; Length 362;

Matches 11; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 5 TRLNERENRLRY 20

I 1111111111

Db 93 TNTQTYRENRLRY 108

RESULT 10

I59308

class I histocompatibility antigen - pygmy chimpanzee (fragment)

C:Species: Pan paniscus (Pygmy chimpanzee, bonobo)

C:Date: 31-May-1996 #sequence_revision 31-May-1996 #text_change 23-Jul-1999

C:Accession: I59308

R:McAdam, S.N.; Boyson, J.E.; Liu, X.; Garber, T.L.; Hughes, A.L.; Bontrorp, R.E.; Wat

Proc. Natl. Acad. Sci. U.S.A. 91, 5893-5897, 1994

A:Title: A uniquely high level of recombination at the HLA-B locus.

A:Reference number: I59308; MUID:94286544

A:Accession: I59308

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-354 <RES>

A:Cross-references: EMBL:U05575; NID:G454767; PIDN:AAA50178.1; PID:G454768

C:Superfamily: class I histocompatibility antigen; immunoglobulin homology

Query Match

Best Local Similarity 49.5%; Score 49; DB 2; Length 354;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 RENRLRY 20

I 1111111111

Db 91 RENRLRY 100

RESULT 11

I80168

class I histocompatibility antigen - chimpanzee (fragment)

C:Species: Pan troglodytes (chimpanzee)

C:Date: 24-May-1996 #sequence_revision 24-May-1996 #text_change 23-Jul-1999

C:Accession: I80168

R:McAdam, S.N.; Boyson, J.E.; Liu, X.; Garber, T.L.; Hughes, A.L.; Bontrorp, R.E.; Wat

Proc. Natl. Acad. Sci. U.S.A. 91, 5893-5897, 1994

A:Title: A uniquely high level of recombination at the HLA-B locus.

A:Reference number: I59308; MUID:94286544

A:Accession: I80168

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-354 <RES>

A:Cross-references: EMBL:U05579; NID:g454775; PIDN:AAA50182.1; PID:g454776
C:Superfamily: class I histocompatibility antigen; immunoglobulin homology

Query Match 49.5%; Score 49; DB 2; Length 354;
Best Local Similarity 100.0%; Pred. No. 2;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 RENLIRALRY 20
| | | | | | | | | |
Db 91 RENLIRALRY 100

RESULT 12

Class I histocompatibility antigen - pygmy chimpanzee (fragment)

C:Species: Pan paniscus (pygmy chimpanzee, bonobo)
C:Date: 24-May-1996 #sequence_revision 24-May-1996 #text_change 23-Jul-1999
C:Accession: I80167

R:McAdam, S.N.; Boyson, J.E.; Liu, X.; Garber, T.L.; Hughes, A.L.; Bontrop, R.E.; Watkins
Proc. Natl. Acad. Sci. U.S.A. 91, 5893-5897, 1994

A:Title: A uniquely high level of recombination at the HLA-B locus.

A:Reference number: I59308; MUID:94286544

A:Accession: I80167

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-354 <RES>

A:Cross-references: EMBL:U05578; NID:g454773; PIDN:AAA50181.1; PID:g454774
C:Superfamily: class I histocompatibility antigen; immunoglobulin homology

Query Match 49.5%; Score 49; DB 2; Length 354;
Best Local Similarity 100.0%; Pred. No. 2;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 RENLIRALRY 20
| | | | | | | | | |
Db 91 RENLIRALRY 100

RESULT 13

Class I histocompatibility antigen - chimpanzee (fragment)

C:Species: Pan troglodytes (chimpanzee)

C:Date: 24-May-1996 #sequence_revision 24-May-1996 #text_change 23-Jul-1999

C:Accession: I80169

R:McAdam, S.N.; Boyson, J.E.; Liu, X.; Garber, T.L.; Hughes, A.L.; Bontrop, R.E.; Watkins
Proc. Natl. Acad. Sci. U.S.A. 91, 5893-5897, 1994

A:Title: A uniquely high level of recombination at the HLA-B locus.

A:Reference number: I59308; MUID:94286544

A:Accession: I80169

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-355 <RES>

A:Cross-references: EMBL:U05580; NID:g454777; PIDN:AAA50183.1; PID:g454778
C:Superfamily: class I histocompatibility antigen; immunoglobulin homology

Query Match 49.5%; Score 49; DB 2; Length 355;
Best Local Similarity 100.0%; Pred. No. 2;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 RENLIRALRY 20
| | | | | | | | | |
Db 91 RENLIRALRY 100

RESULT 14

Class I histocompatibility antigen - chimpanzee (fragment)

C:Species: Pan troglodytes (chimpanzee)

C:Date: 24-May-1996 #sequence_revision 24-May-1996 #text_change 23-Jul-1999

C:Accession: I80171

R:McAdam, S.N.; Boyson, J.E.; Liu, X.; Garber, T.L.; Hughes, A.L.; Bontrop, R.E.; Wat
Proc. Natl. Acad. Sci. U.S.A. 91, 5893-5897, 1994

A:Title: A uniquely high level of recombination at the HLA-B locus.

A:Reference number: I59308; MUID:94286544

A:Accession: I80171

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-355 <RES>

A:Cross-references: EMBL:U05582; NID:g454781; PIDN:AAA50185.1; PID:g454782

C:Superfamily: class I histocompatibility antigen; immunoglobulin homology

Query Match 49.5%; Score 49; DB 2; Length 355;
Best Local Similarity 100.0%; Pred. No. 2;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 RENLIRALRY 20
| | | | | | | | | |
Db 91 RENLIRALRY 100

RESULT 15

HLH012

MHC class I histocompatibility antigen HLA alpha chain precursor (clone PHLA 12.4) -

C:Species: Homo sapiens (man)

C:Date: 05-Apr-1983 #sequence_revision 05-Apr-1983 #text_change 22-Jun-1999

C:Accession: A02189

R:Malissen, M.; Malissen, B.; Jordan, B.R.

Proc. Natl. Acad. Sci. U.S.A. 79, 893-897, 1982

A:Title: Exon/intron organization and complete nucleotide sequence of an HLA gene.

A:Reference number: A02189; MUID:82151002

A:Accession: A02189

A:Molecule type: DNA

A:Residues: 1-359 <MAL>

A:Cross-references: GB:J00191; GB:V00526; NID:gl87600; PIDN:AAA36218.1; PID:g386873
C:Comment: The seven exons correspond approximately to the domain structure of this c

C:Genetics:

A:Map position: 6p21.3

A:Introns: 22/1; 112/1; 204/1; 296/1; 335/1; 345/1

C:Superfamily: class I histocompatibility antigen; immunoglobulin homology

C:Keywords: duplication; glycoprotein; heterodimer; transmembrane protein; transplant

F:1-21/Domain: signal sequence #status predicted <SIG>

F:22-359/Product: class I histocompatibility antigen HLA alpha chain #status predicted

F:22-304/Domain: extracellular #status predicted <EXT>

F:22-111/Domain: alpha-1 <EX1>

F:112-203/Domain: alpha-2 <EX2>

F:117-282/Domain: immunoglobulin homology <IMM>

F:305-329/Domain: transmembrane #status predicted <TM>

F:335-359/Domain: intracellular #status predicted <INT>

F:107/Binding site: carbohydrate (Asn) (covalent) #status predicted

F:224-280/Disulfide bonds: #status predicted

Query Match 49.5%; Score 49; DB 1; Length 359;
Best Local Similarity 100.0%; Pred. No. 2;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 RENLIRALRY 20
| | | | | | | | | |
Db 96 RENLIRALRY 105

Search completed: February 7, 2000, 18:04:38
Job time: 22204 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: February 8, 2000, 01:25:59 ; Search time 68.63 seconds
(without alignments)
8.703 Million cell updates/sec

Title: US-08-653-294-28

Perfect score: 99

Sequence: 1 YRLATRLNERENLRALRY 20

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 82229 seqs, 29864866 residues

Total number of hits satisfying chosen parameters: 82229

Minimum DB seq length: 0

Maximum DB seq length: 1000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : SwissProt_38.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	50	50.5	362	1	1B47_HUMAN	P30487 homo sapien
2	50	50.5	362	1	1B49_HUMAN	P18464 homo sapien
3	50	50.5	362	1	1B52_HUMAN	P30489 homo sapien
4	50	50.5	362	1	1B53_HUMAN	P30490 homo sapien
5	50	50.5	362	1	1B54_HUMAN	P30491 homo sapien
6	49	49.5	359	1	1B01_PANTR	P13750 pan troglod
7	49	49.5	362	1	1B01_PANTR	P30379 gorilla gor
8	49	49.5	362	1	1B02_GORGO	P30380 gorilla gor
9	49	49.5	362	1	1B03_GORGO	P30381 gorilla gor
10	49	49.5	362	1	1B15_HUMAN	P10317 homo sapien
11	49	49.5	362	1	1B60_HUMAN	P18465 homo sapien
12	49	49.5	362	1	1B61_HUMAN	P30497 homo sapien
13	49	49.5	362	1	1B62_HUMAN	P10319 homo sapien
14	49	49.5	362	1	1B62_HUMAN	P01893 homo sapien
15	49	49.5	365	1	1A23_HUMAN	P30447 homo sapien
16	49	49.5	365	1	1A24_HUMAN	P05534 homo sapien
17	45	45.5	362	1	1B05_HUMAN	P30461 homo sapien
18	45	45.5	362	1	1B41_HUMAN	P30481 homo sapien
19	45	45.5	362	1	1B42_HUMAN	P30482 homo sapien
20	44	44.4	365	1	1A25_HUMAN	P18462 homo sapien
21	44	44.4	365	1	1A32_HUMAN	P10314 homo sapien
22	42	42.4	414	1	GAG_FSVHZ	P04322 feline sarc
23	42	42.4	425	1	GAG_FSVGA	P03337 feline sarc
24	42	42.4	536	1	GAG_FSVMD	P03340 feline sarc
25	42	42.4	580	1	GAG_FLV	P10262 feline leuk
26	42	42.4	1228	1	SLAP_BACST	P35825 bacillus st
27	42	42.4	1807	1	TSC2_HUMAN	P49815 homo sapien
28	42	42.4	1809	1	TSC2_RAT	P49816 rattus norv
29	41	41.4	162	1	PUR6_BACSU	P12044 bacillus su
30	41	41.4	2077	1	TEGU_HSV6G	P30002 herpes simp
31	41	41.4	2077	1	TEGU_HSV6U	P52340 herpes simp
32	40.5	40.9	837	1	YLE5_CAEEL	P46941 caenorhabdi
33	40	40.4	277	1	YDIA_ECOLI	P03822 escherichia
34	40	40.4	359	1	1B40_HUMAN	P10320 homo sapien

RESULT 1

ID	1B47_HUMAN	STANDARD;	PRT;	362 AA.
AC	P30487;			
DT	01-APR-1993 (Rel. 25, Created)			
DT	01-FEB-1996 (Rel. 33, Last sequence update)			
DT	01-FEB-1996 (Rel. 33, Last annotation update)			
DE	HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-49(B-21) B*4901 ALPHA CHAIN PRECURSOR.			
GN	HLA-B OR HLAB.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE; 89235215.			
RA	PARHAM P., LAWLER D.A., LOMEN C.E., ENNIS P.D.;			
RT	"Diversity and diversification of HLA-A,B,C alleles.";			
RL	J. Immunol. 142:3937-3950(1989).			
RN	[2]			
RP	REVISION TO 78.			
RX	MEDLINE; 93056529.			
RA	HILDEBRAND W.H., MADRIGAL J.A., BELICH M.P., ZEMMOUR J., WARD F.E., WILLIAMS R.C., PARHAM P.;			
RT	"Serologic cross-reactivities poorly reflect allelic relationships in the HLA-B*2 and HLA-B*21 groups. Dominant epitopes of the alpha 2 helix.";			
RL	J. Immunol. 149:3563-3568(1992).			
CC	- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO THE IMMUNE SYSTEM.			
CC	- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-MICROGLOBULIN).			
CC	-----			
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CC	-----			
DR	EMBL; M24037; AAA02950.1; ..			
DR	HSP; P30491; 1A1M.			
DR	MIM; 142830; ..			
DR	PROSITE; PS00290; IG_MHC; 1.			
DR	PFAM; PF00047; Ig; 1.			
DR	PFAM; PF00129; MHC.I; 1.			
KW	MHC I; Transmembrane; Glycoprotein; Signal.			
FT	SIGNAL 1 24			
FT	CHAIN 25 362			
FT	-----			
FT	HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-49(B-21) B*4901 ALPHA CHAIN.			
FT	EXTRACELLULAR ALPHA-1.			
FT	DOMAIN 25 114			
FT	EXTRACELLULAR ALPHA-2.			
FT	DOMAIN 115 206			
FT	EXTRACELLULAR ALPHA-3.			
FT	DOMAIN 207 298			
FT	CONNECTING PEPTIDE.			
FT	DOMAIN 299 309			
FT	TRANSMEM 310 333			
FT	DOMAIN 334 362			
FT	CYTOPLASMIC TAIL.			

ALIGNMENTS

35	40	40.4	924	1	ORC1_DROME	O16810 drosophila
36	39	39.4	234	1	YGS_ECOLI	P52054 escherichia
37	39	39.4	354	1	GRA3_USTHO	O14438 ustilago ho
38	39	39.4	365	1	1A04_GORGO	P03078 gorilla gor
39	39	39.4	400	1	NUCM_PROWI	Q37619 protocheca
40	39	39.4	432	1	MDHD_SORVU	P37229 sorghum vul
41	39	39.4	454	1	BLH1_YEAST	Q01532 saccharomyc
42	39	39.4	506	1	MKK2_YEAST	P32491 saccharomyc
43	39	39.4	518	1	G6PD_DROVA	O27638 drosophila
44	39	39.4	591	1	GLMS_AQUAE	O66648 a glucosami
45	39	39.4	856	1	PESA_AQUAE	O67899 aquifex aeo

FT CARBOHYD 110 110 BY SIMILARITY.
 FT DISULFID 125 188 BY SIMILARITY.
 FT DISULFID 227 283 BY SIMILARITY.
 SQ SEQUENCE 362 AA; 40581 MW; E995F82F CRC32;

Query Match 50.5%; Score 50; DB 1; Length 362;
 Best Local Similarity 68.8%; Pred. No. 0.46;
 Matches 11; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 5 TRLNERENLRALRY 20
 DB 93 TNTQTYRENLRALRY 108

RESULT 2
 1B49_HUMAN STANDARD; PRT; 362 AA.
 AC P18464;
 DT 01-NOV-1990 (Rel. 16, Created)
 DT 01-NOV-1990 (Rel. 16, Last sequence update)
 DT 01-FEB-1996 (Rel. 33, Last annotation update)
 DE HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-51(B-5) B*5101 ALPHA CHAIN
 DE PRECURSOR.
 GN HLA-B OR HLAB.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia;
 OC Eutheria; Primates; Catarrhini; Homnidae; Homo.
 [1]
 RN SEQUENCE FROM N.A.
 RX MEDLINE; 90207291.
 RA ENNIS P.D., ZEMMOUR J., SALTER R.D., PARHAM P.;
 RT "Rapid cloning of HLA-A,B CDNA by using the polymerase chain
 reaction: frequency and nature of errors produced in amplification.";
 RL Proc. Natl. Acad. Sci. U.S.A. 87:2833-2837(1990).
 [2]
 RN SEQUENCE FROM N.A.
 RX MEDLINE; 89080265.
 RA HAYASHI H., ENNIS P.D., ARIGA H., SALTER R.D., PARHAM P., KANO K.,
 RT TAKIGUCHI M.;
 RN "HLA-B51 and HLA-Bw52 differ by only two amino acids, which are in the
 RT helical region of the alpha 1 domain";
 RL J. Immunol. 142:306-311(1989).
 [3]
 RN SEQUENCE FROM N.A.
 RX MEDLINE; 89233295.
 RA POHLA H., KUON W., TABACZEWSKI P., DOERNER C., WEISS E.H.;
 RT "Allelic variation in HLA-B and HLA-C sequences and the evolution of
 the HLA-B alleles";
 RL Immunogenetics 29:297-307(1989).
 CC -1- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
 CC THE IMMUNE SYSTEM.
 CC -1- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
 CC MICROGLOBULIN).

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 or send an email to license@isb-sib.ch).

EMBL; M32319; AAA36232.1;
 EMBL; M22792; AAA59620.1; ALT_SEQ.
 EMBL; M22786; AAA59620.1; JOINED.
 EMBL; M22787; AAA59620.1; JOINED.
 EMBL; M22788; AAA59620.1; JOINED.
 EMBL; M22789; AAA59620.1; JOINED.
 EMBL; M22790; AAA59620.1; JOINED.
 EMBL; M22791; AAA59620.1; JOINED.
 EMBL; L41087; AAA64513.1;
 EMBL; L41086; AAA64513.1; JOINED.

DR FIR; A30345; A30345.
 DR FIR; A30548; A30548.
 DR HSP; P30491; 1A1M.
 DR MIM; 142830;
 DR PROSITE; PS00290; IG_MHC; 1.
 DR PFAM; PF00047; Ig; 1.
 DR PFAM; PF00129; MHC_I; 1.
 KW MHC I; Transmembrane; Glycoprotein; Signal.
 FT SIGNAL 1 24
 FT CHAIN 25 362 HLA CLASS I HISTOCOMPATIBILITY ANTIGEN,
 FT B-51(B-5) B*5101 ALPHA CHAIN.
 FT DOMAIN 25 114 EXTRACELLULAR ALPHA-1.
 FT DOMAIN 115 206 EXTRACELLULAR ALPHA-2.
 FT DOMAIN 207 298 EXTRACELLULAR ALPHA-3.
 FT DOMAIN 299 308 CONNECTING PEPTIDE.
 FT TRANSMEM 309 332
 FT DOMAIN 333 362 CYTOPLASMIC TAIL.
 FT CARBOHYD 110 110 BY SIMILARITY.
 FT DISULFID 125 188 BY SIMILARITY.
 FT DISULFID 227 283 BY SIMILARITY.
 SQ SEQUENCE 362 AA; 40566 MW; 4D846F30 CRC32;

Query Match 50.5%; Score 50; DB 1; Length 362;
 Best Local Similarity 68.8%; Pred. No. 0.46;
 Matches 11; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 5 TRLNERENLRALRY 20
 DB 93 TNTQTYRENLRALRY 108

RESULT 3
 1B52_HUMAN STANDARD; PRT; 362 AA.
 ID 1B52_HUMAN
 AC P30489;
 DT 01-APR-1993 (Rel. 25, Created)
 DT 01-APR-1993 (Rel. 25, Last sequence update)
 DT 01-APR-1993 (Rel. 25, Last annotation update)
 DE HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-51(B-5) B*5104 ALPHA CHAIN
 DE PRECURSOR.
 GN HLA-B OR HLAB.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Eutheria; Primates; Catarrhini; Homnidae; Homo.
 [1]
 RN SEQUENCE FROM N.A.
 RX MEDLINE; 92269955.
 RA BELICH M.P., MADRIGAL J.A., HILDEBRAND W.H., ZEMMOUR J.,
 RA WILLIAMS R.C., LUZ R., PETZL-ERLER M.L., PARHAM P.;
 RT "Unusual HLA-B alleles in two tribes of Brazilian Indians.";
 RL Nature 357:326-329(1992).
 CC -1- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
 CC THE IMMUNE SYSTEM.
 CC -1- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
 CC MICROGLOBULIN).

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 or send an email to license@isb-sib.ch).

EMBL; 215143; CAAT8849.1;
 DR HSP; P30491; 1A1M.
 DR MIM; 142830;
 DR PROSITE; PS00290; IG_MHC; 1.
 DR PFAM; PF00047; Ig; 1.
 DR PFAM; PF00129; MHC_I; 1.
 KW MHC I; Transmembrane; Glycoprotein; Signal.
 FT SIGNAL 1 24

FT CHAIN 25 362 HLA CLASS I HISTOCOMPATIBILITY ANTIGEN,
B*51(B-5) B*5104 ALPHA CHAIN.
FT DOMAIN 25 114 EXTRACELLULAR ALPHA-1.
FT DOMAIN 115 206 EXTRACELLULAR ALPHA-2.
FT DOMAIN 207 298 EXTRACELLULAR ALPHA-3.
FT DOMAIN 299 308 CONNECTING PEPTIDE.
FT TRANSMEM 309 332 CYTOPLASMIC TAIL.
FT DOMAIN 333 362 BY SIMILARITY.
FT CARBOHYD 110 110 BY SIMILARITY.
FT DISULFID 125 188 BY SIMILARITY.
FT DISULFID 227 283 BY SIMILARITY.
SQ SEQUENCE 362 AA; 40560 MW; F22F08AB CRC32;

Query Match 50.5%; Score 50; DB 1; Length 362;
Best Local Similarity 68.8%; Pred. No. 0.46;
Matches 11; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 5 TRLNERENLRALRY 20
I | | | | | | | | | |
Db 93 TNTQTYRENLRALRY 108

RESULT 4
1B53_HUMAN
ID 1B53_HUMAN STANDARD; PRT; 362 AA.
AC P30490;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 01-APR-1993 (Rel. 25, Last annotation update)
DE HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, BW-52(B-5) B*5201 ALPHA CHAIN
DE PRECURSOR.
GN HLA-B OR HLAB.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia;
OC Eutheria; Primates; Catarrhini; Homnidae; Homo.
[1]
RN SEQUENCE FROM N.A.
RX MEDLINE; 89080265.
RA HAYASHI H., ENNIS P.D., ARIGA H., SALTER R.D., PARHAM P., KANO K.,
TAKIGUCHI M.;
RT "HLA-B51 and HLA-Bw52 differ by only two amino acids which are in the
helical region of the alpha 1 domain.";
RL J. Immunol. 142:306-311(1989).
CC -!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
THE IMMUNE SYSTEM.
CC -!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
MICROGLOBULIN).
CC
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CC
CC ENBL; M22799; AAA59645.1; ALT_SEQ.
DR ENBL; M22793; AAA59645.1; JOINED.
DR ENBL; M22794; AAA59645.1; JOINED.
DR ENBL; M22795; AAA59645.1; JOINED.
DR ENBL; M22796; AAA59645.1; JOINED.
DR ENBL; M22797; AAA59645.1; JOINED.
DR ENBL; M22798; AAA59645.1; JOINED.
DR PIR; B30345; B30345.
DR PIR; B30548; B30548.
DR HSSP; P30491; IALM.
DR MIM; 142830;
DR PROSITE; PS00290; IG_MHC; 1.
DR PFAM; PF00047; ig; 1.
DR PFAM; PF00129; MHC-I; 1.
KW MHC I; Transmembrane; Glycoprotein; Signal.
FT SIGNAL 1 24

FT CHAIN 25 362 HLA CLASS I HISTOCOMPATIBILITY ANTIGEN,
BW-52(B-5) B*5201 ALPHA CHAIN.
FT DOMAIN 25 114 EXTRACELLULAR ALPHA-1.
FT DOMAIN 115 206 EXTRACELLULAR ALPHA-2.
FT DOMAIN 207 298 EXTRACELLULAR ALPHA-3.
FT DOMAIN 299 308 CONNECTING PEPTIDE.
FT TRANSMEM 309 332 CYTOPLASMIC TAIL.
FT DOMAIN 333 362 BY SIMILARITY.
FT CARBOHYD 110 110 BY SIMILARITY.
FT DISULFID 125 188 BY SIMILARITY.
FT DISULFID 227 283 BY SIMILARITY.
SQ SEQUENCE 362 AA; 40521 MW; 3B436FE8 CRC32;

Query Match 50.5%; Score 50; DB 1; Length 362;
Best Local Similarity 68.8%; Pred. No. 0.46;
Matches 11; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 5 TRLNERENLRALRY 20
I | | | | | | | | | |
Db 93 TNTQTYRENLRALRY 108

RESULT 5
1B54_HUMAN
ID 1B54_HUMAN STANDARD; PRT; 362 AA.
AC P30491;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 13-JUL-1998 (Rel. 36, Last annotation update)
DE HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, BW-53 B*5301 ALPHA CHAIN
DE PRECURSOR.
GN HLA-B OR HLAB.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia;
OC Eutheria; Primates; Catarrhini; Homnidae; Homo.
[1]
RN SEQUENCE FROM N.A.
RX MEDLINE; 91033941.
RA HAYASHI H., Ooba T., NAKAYAMA S., SEKIMATA M., KANO K.,
TAKIGUCHI M.;
RT "All specificities between HLA-Bw53 and HLA-B35 are generated by
substitution of the residues associated with HLA-Bw4/Bw6 public
epitopes.";
RL Immunogenetics 32:195-199(1990).
RN [2]
RP X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF 25-302.
RX MEDLINE; 96209672.
RA SMITH K.J., REID S.W., HARLOS K., MCMICHAEL A.J., STUART D.I.,
BELL J.I., JONES E.Y.;
RT "Bound water structure and polymorphic amino acids act together to
allow the binding of different peptides to MHC class I HLA-B53.";
RL Immunity 4:215-228(1996).
CC -!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
THE IMMUNE SYSTEM.
CC -!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
MICROGLOBULIN).
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CC
CC ENBL; M58636; AAA36228.1;
DR PIR; A45834; A45834.
DR PDB; 1ALM; 08-APR-98.
DR PDB; 1AIO; 08-APR-98.
DR MIM; 142830;
DR PROSITE; PS00290; IG_MHC; 1.
DR PFAM; PF00047; ig; 1.

DR PFAM; PF00129; MHC_I; 1.
 KW MHC I; Transmembrane; Glycoprotein; Signal; 3D-structure.
 FT SIGNAL 1 24
 FT CHAIN 25 362 HLA CLASS I HISTOCOMPATIBILITY ANTIGEN,
 FT BW-53 B*5301 ALPHA CHAIN.
 FT DOMAIN 25 114 EXTRACELLULAR ALPHA-1.
 FT DOMAIN 115 206 EXTRACELLULAR ALPHA-2.
 FT DOMAIN 207 298 EXTRACELLULAR ALPHA-3.
 FT DOMAIN 299 308 CONNECTING PEPTIDE.
 FT TRANSMEM 309 332 CYTOPLASMIC TAIL.
 FT DOMAIN 333 362 BY SIMILARITY.
 FT CARBOHYD 110 110
 FT DISULFID 125 188
 FT SEQUENCE 362 AA; 40495 MW; 2BDC746E CRC32;
 SQ

Query Match 50.5%; Score 50; DB 1; Length 362;
 Best Local Similarity 68.8%; Pred. No. 0.46;
 Matches 11; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 5 TRLNERENLRALRY 20
 DB 93 TNRQTYRENLRALRY 108

RESULT 6
 ID 1B01_PANTR STANDARD; PRT; 359 AA.
 AC P13750;
 DT 01-JAN-1990 (Rel. 13, Created)
 DT 01-JAN-1990 (Rel. 13, Last sequence update)
 DT 01-APR-1993 (Rel. 25, Last annotation update)
 DE CHLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-1 ALPHA CHAIN PRECURSOR
 DE (FRAGMENT).
 OS Pan troglodytes (Chimpanzee).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Eutheria; Primates; Catarrhini; Hominidae; Pan.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 89030641.
 RA MAYER W.E., JONKER M., KLEIN D., IVANYI P., VAN SEVENTER G.,
 RA KLEIN J.;
 RT "Nucleotide sequences of chimpanzee MHC class I alleles: evidence for
 RT trans-species mode of evolution.";
 RL EMBO J. 7:2765-2774(1988).
 RN [2]
 RP REVISIONS.
 RA MAYER W.;
 RL Submitted (FEB-1989) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
 CC THE IMMUNE SYSTEM.
 CC -!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
 CC MICROGLOBULIN).
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 CC

EMBL; X13115; CAA31507.1;
 DR PIR; S03537; S03537.
 DR HSSP; P03989; 1HSA.
 DR PROSITE; PS00290; IG_MHC; 1.
 DR PFAM; PF00047; ig; 1.
 DR PFAM; PF00129; MHC_I; 1.
 DR MHC I; Transmembrane; Glycoprotein; Signal.
 KW MHC I; Transmembrane; Glycoprotein; Signal.
 FT NON_TER 1
 FT SIGNAL <1 20
 FT CHAIN 21 359 CHLA CLASS I HISTOCOMPATIBILITY ANTIGEN,
 FT

FT DOMAIN 21 110 B-1 ALPHA CHAIN.
 FT DOMAIN 111 202 EXTRACELLULAR ALPHA-1.
 FT DOMAIN 203 294 EXTRACELLULAR ALPHA-2.
 FT DOMAIN 295 305 EXTRACELLULAR ALPHA-3.
 FT TRANSMEM 306 329 CONNECTING PEPTIDE.
 FT DOMAIN 330 359 CYTOPLASMIC TAIL.
 FT DISULFID 121 184 BY SIMILARITY.
 FT DISULFID 223 279 BY SIMILARITY.
 FT CARBOHYD 106 106
 FT SEQUENCE 359 AA; 40173 MW; 5395FFC9 CRC32;
 SQ

Query Match 49.5%; Score 49; DB 1; Length 359;
 Best Local Similarity 100.0%; Pred. No. 0.67;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 RENLRALRY 20
 DB 95 RENLRALRY 104

RESULT 7
 ID 1B01_GORGO STANDARD; PRT; 362 AA.
 AC P30379;
 DT 01-APR-1993 (Rel. 25, Created)
 DT 01-APR-1993 (Rel. 25, Last sequence update)
 DT 01-APR-1993 (Rel. 25, Last annotation update)
 DE CLASS I HISTOCOMPATIBILITY ANTIGEN, GOGO-BO101 ALPHA CHAIN PRECURSOR.
 OS Gorilla gorilla gorilla (Lowland gorilla).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Eutheria; Primates; Catarrhini; Hominidae; Gorilla.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 92078860.
 RA LAWLOR D.A., WARREN E., TAYLOR P., PARHAM P.;
 RT "Gorilla class I major histocompatibility complex alleles: comparison
 RT to human and chimpanzee class I";
 RL J. Exp. Med. 174:1491-1509(1991).
 CC -!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
 CC THE IMMUNE SYSTEM.
 CC -!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
 CC MICROGLOBULIN).
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 CC

EMBL; X60255; CAA42807.1;
 DR PIR; JH0539; JH0539.
 DR HSSP; P03989; 1HSA.
 DR PROSITE; PS00290; IG_MHC; 1.
 DR PFAM; PF00047; ig; 1.
 DR PFAM; PF00129; MHC_I; 1.
 DR MHC I; Transmembrane; Glycoprotein; Signal.
 KW MHC I; Transmembrane; Glycoprotein; Signal.
 FT SIGNAL 1 24
 FT CHAIN 25 362 CLASS I HISTOCOMPATIBILITY ANTIGEN,
 FT GOGO-BO101 ALPHA CHAIN.
 FT DOMAIN 25 114 EXTRACELLULAR ALPHA-1.
 FT DOMAIN 115 206 EXTRACELLULAR ALPHA-2.
 FT DOMAIN 207 298 EXTRACELLULAR ALPHA-3.
 FT DOMAIN 299 308 CONNECTING PEPTIDE.
 FT TRANSMEM 309 332
 FT DOMAIN 333 362 CYTOPLASMIC TAIL.
 FT DISULFID 125 188 BY SIMILARITY.
 FT DISULFID 227 283 BY SIMILARITY.
 FT CARBOHYD 110 110
 FT SEQUENCE 362 AA; 40170 MW; 2E33E2B8 CRC32;
 SQ

Query Match 49.5%; Score 49; DB 1; Length 362;
 Best Local Similarity 100.0%; Pred. No. 0.67;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 RENLIRALRY 20
 Db 99 RENLIRALRY 108

RESULT 8
 1B02_GORGO STANDARD; PRT; 362 AA.
 AC P30380;
 DT 01-APR-1993 (Rel. 25, Created)
 DT 01-APR-1993 (Rel. 25, Last sequence update)
 DE CLASS I HISTOCOMPATIBILITY ANTIGEN, GOGO-B0102 ALPHA CHAIN PRECURSOR.
 OS Gorilla gorilla gorilla (Lowland gorilla).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Eutheria; Primates; Catarrhini; Hominidae; Gorilla.
 RN [1]

SEQUENCE FROM N.A.
 RX MEDLINE: 92078860.
 RA LAWLOR D.A., WARREN E., TAYLOR P., PARHAM P.;
 RT "Gorilla class I major histocompatibility complex alleles: comparison
 to human and chimpanzee class I.";
 RL J. Exp. Med. 174:1491-1509(1991).
 CC -!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
 THE IMMUNE SYSTEM.
 CC -!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
 MICROGLOBULIN).

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EMBL: X60693; CAA43101.1; -
 DR PIR: JH0540; JH0540.
 DR HSSP: P03989; ILSA.
 DR PROSITE: PS00290; IG_MHC; 1.
 DR PFAM: PF00047; ig; 1.
 DR MHC I; Transmembrane; Glycoprotein; Signal.
 FT SIGNAL 1 24 BY SIMILARITY.
 FT CHAIN 25 362 CLASS I HISTOCOMPATIBILITY ANTIGEN,
 GOGO-B0102 ALPHA CHAIN.
 FT DOMAIN 25 114 EXTRACELLULAR ALPHA-1.
 FT DOMAIN 115 206 EXTRACELLULAR ALPHA-2.
 FT DOMAIN 207 298 EXTRACELLULAR ALPHA-3.
 FT DOMAIN 299 308 CONNECTING PEPTIDE.
 FT TRANSMEM 309 332
 FT DOMAIN 333 362 CYTOPLASMIC TAIL.
 FT DISULFID 125 188 BY SIMILARITY.
 FT DISULFID 227 283 BY SIMILARITY.
 FT CARBOHYD 110 110 BY SIMILARITY.
 SQ SEQUENCE 362 AA; 40204 MW; 3CF119AD CRC32;

Query Match 49.5%; Score 49; DB 1; Length 362;
 Best Local Similarity 100.0%; Pred. No. 0.67;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 RENLIRALRY 20
 Db 99 RENLIRALRY 108

RESULT 9
 1B03_GORGO STANDARD; PRT; 362 AA.
 AC P30381;
 DT 01-APR-1993 (Rel. 25, Created)
 DT 01-APR-1993 (Rel. 25, Last sequence update)
 DE CLASS I HISTOCOMPATIBILITY ANTIGEN, GOGO-B0103 ALPHA CHAIN PRECURSOR.
 OS Gorilla gorilla gorilla (Lowland gorilla).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Eutheria; Primates; Catarrhini; Hominidae; Gorilla.
 RN [1]

SEQUENCE FROM N.A.
 RX MEDLINE: 92078860.
 RA LAWLOR D.A., WARREN E., TAYLOR P., PARHAM P.;
 RT "Gorilla class I major histocompatibility complex alleles: comparison
 to human and chimpanzee class I.";
 RL J. Exp. Med. 174:1491-1509(1991).
 CC -!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
 THE IMMUNE SYSTEM.
 CC -!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
 MICROGLOBULIN).

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EMBL: X60254; CAA42806.1; -
 DR PIR: JH0541; JH0541.
 DR HSSP: P03989; ILSA.
 DR PROSITE: PS00290; IG_MHC; 1.
 DR PFAM: PF00047; ig; 1.
 DR MHC I; Transmembrane; Glycoprotein; Signal.
 FT SIGNAL 1 24 BY SIMILARITY.
 FT CHAIN 25 362 CLASS I HISTOCOMPATIBILITY ANTIGEN,
 GOGO-B0103 ALPHA CHAIN.
 FT DOMAIN 25 114 EXTRACELLULAR ALPHA-1.
 FT DOMAIN 115 206 EXTRACELLULAR ALPHA-2.
 FT DOMAIN 207 298 EXTRACELLULAR ALPHA-3.
 FT DOMAIN 299 308 CONNECTING PEPTIDE.
 FT TRANSMEM 309 332
 FT DOMAIN 333 362 CYTOPLASMIC TAIL.
 FT DISULFID 125 188 BY SIMILARITY.
 FT DISULFID 227 283 BY SIMILARITY.
 FT CARBOHYD 110 110 BY SIMILARITY.
 SQ SEQUENCE 362 AA; 40248 MW; FEA6A941 CRC32;

Query Match 49.5%; Score 49; DB 1; Length 362;
 Best Local Similarity 100.0%; Pred. No. 0.67;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 RENLIRALRY 20
 Db 99 RENLIRALRY 108

RESULT 10
 1B15_HUMAN STANDARD; PRT; 362 AA.
 AC P10317;
 DT 01-MAR-1989 (Rel. 10, Created)
 DT 01-MAR-1989 (Rel. 10, Last sequence update)
 DE CLASS I HISTOCOMPATIBILITY ANTIGEN, B-27 B*2702 ALPHA CHAIN
 PRECURSOR (B-27K) (B27.2).
 GN HLA-B OR HLAB.
 OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Euthera; Primates; Catarrhini; Hominidae; Homo.
 RN [1]
 RN SEQUENCE FROM N.A.
 RX MEDLINE: 86220133.
 RA SEEMANN G.H.A., REIN R.S., BROWN C.S., PLOEGH H.L.;
 RT "Gene conversion-like mechanisms may generate polymorphism in human
 RT class I genes.";
 RL EMBO J. 5:547-552(1986).
 RN [2]
 RN SEQUENCE FROM N.A.
 RP PARHAM P., ARNETT K.L., ADAMS E.J.;
 RA Submitted (JUL-1995) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RX MEDLINE: 86042671.
 RA VEGA M.A., EZQUERRA A., ROJO S., APARTICIO P., BRAGADO R.,
 RA LOPEZ DE CASTRO J.A.;
 RT "Structural analysis of an HLA-B*27 functional variant: identification
 RT of residues that contribute to the specificity of recognition by
 RT cytolytic T lymphocytes.";
 RL Proc. Natl. Acad. Sci. U.S.A. 82:7394-7398(1985).
 CC -!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
 CC THE IMMUNE SYSTEM.
 CC -!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
 CC MICROGLOBULIN).
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 CC -----
 DR EMBL: X03664; CAA27301.1; -;
 DR EMBL: X03667; CAA27301.1; JOINED.
 DR EMBL: L38504; AAA69724.1; -;
 DR PIR: B25092; HLHUBK.
 DR HSP: P03989; LHSA.
 DR MIM: 142830; -;
 DR PROSITE: PS00290; IG_MHC; 1.
 DR PFAM: PF00047; ig; 1.
 DR PFAM: PF00129; MHC_I; 1.
 KW MHC I; Transmembrane; Glycoprotein; Signal.
 FT SIGNAL 1 24
 FT CHAIN 25 362 HLA CLASS I HISTOCOMPATIBILITY ANTIGEN,
 FT B-27 B*2702 ALPHA CHAIN.
 FT DOMAIN 25 114
 FT DOMAIN 115 206 EXTRACELLULAR ALPHA-1.
 FT DOMAIN 207 298 EXTRACELLULAR ALPHA-2.
 FT DOMAIN 299 308 EXTRACELLULAR ALPHA-3.
 FT DOMAIN 309 332 CONNECTING PEPTIDE.
 FT TRANSMEM 309 332
 FT DOMAIN 333 362 CYTOPLASMIC TAIL.
 FT CARBOHYD 110 110 BY SIMILARITY.
 FT DISULFID 125 188 BY SIMILARITY.
 FT DISULFID 227 283 BY SIMILARITY.
 SQ SEQUENCE 362 AA; 40397 MW; 9798F0BB CRC32;

Query Match 49.5%; Score 49; DB 1; Length 362;
 Best Local Similarity 100.0%; Pred. No. 0.67;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 11 RENLRLALRY 20
 DB 99 RENLRLALRY 108

RESULT 11
 1B60_HUMAN STANDARD; PRT; 362 AA.
 ID 1B60_HUMAN
 AC P18465;

DT 01-NOV-1990 (Rel. 16, Created)
 DT 01-NOV-1990 (Rel. 16, Last sequence update)
 DT 01-APR-1993 (Rel. 25, Last annotation update)
 DE HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-57(B-17) B*5701 ALPHA
 DE CHAIN PRECURSOR (BWS7.1).
 GN HLA-B OR HLAB.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Euthera; Primates; Catarrhini; Hominidae; Homo.
 RN [1]
 RN SEQUENCE FROM N.A.
 RP MEDLINE: 90207291.
 RX ENNIS P.D., ZEMMOUR J., SALTER R.D., PARHAM P.;
 RA "Rapid cloning of HLA-A,B CDNA by using the polymerase chain
 RT reaction: frequency and nature of errors produced in amplification.";
 RT Proc. Natl. Acad. Sci. U.S.A. 87:2833-2837(1990).
 RN [2]
 RN SEQUENCE FROM N.A.
 RP MEDLINE: 91067476.
 RX ISAMAT M., GIRDLESTONE J., MILSTEIN C.;
 RA "Nucleotide sequence of an HLA-Bw57 gene.";
 RT Nucleic Acids Res. 18:6702-6702(1990).
 RL Nucleic Acids Res. 18:6702-6702(1990).
 CC -!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
 CC THE IMMUNE SYSTEM.
 CC -!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
 CC MICROGLOBULIN).
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 CC -----
 DR EMBL: M32318; AAA36231.1; -;
 DR EMBL: X55711; CAA39244.1; -;
 DR PIR: S12622; S12622.
 DR PIR: D35997; D35997.
 DR HSP: P30491; IALM.
 DR MIM: 142830; -;
 DR PROSITE: PS00290; IG_MHC; 1.
 DR PFAM: PF00047; ig; 1.
 DR PFAM: PF00129; MHC_I; 1.
 KW MHC I; Transmembrane; Glycoprotein; Signal.
 FT SIGNAL 1 24
 FT CHAIN 25 362 HLA CLASS I HISTOCOMPATIBILITY ANTIGEN,
 FT B-57(B-17) B*5701 ALPHA CHAIN.
 FT DOMAIN 25 114
 FT DOMAIN 115 206 EXTRACELLULAR ALPHA-1.
 FT DOMAIN 207 298 EXTRACELLULAR ALPHA-2.
 FT DOMAIN 299 308 EXTRACELLULAR ALPHA-3.
 FT DOMAIN 309 332 CONNECTING PEPTIDE.
 FT TRANSMEM 309 332
 FT DOMAIN 333 362 CYTOPLASMIC TAIL.
 FT CARBOHYD 110 110 BY SIMILARITY.
 FT DISULFID 125 188 BY SIMILARITY.
 FT DISULFID 227 283 BY SIMILARITY.
 SQ SEQUENCE 362 AA; 40224 MW; D91DF8DD CRC32;

Query Match 49.5%; Score 49; DB 1; Length 362;
 Best Local Similarity 100.0%; Pred. No. 0.67;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 11 RENLRLALRY 20
 DB 99 RENLRLALRY 108

RESULT 12
 1B61_HUMAN STANDARD; PRT; 362 AA.
 ID 1B61_HUMAN
 AC P30497;

DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 01-APR-1993 (Rel. 25, Last annotation update)
DE HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B*57(B-17) B*5702 ALPHA CHAIN
DE PRECURSOR (BW57.2).
GN HLA-B OR HLAB.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia;
OC Eutheria; Primates; Catarrhini; Hominidae; Homo.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 93056508.
RA MADRIGAL J.A., BELICH M.P., HILDEBRAND W.H., BENJAMIN R.J.,
RA LITTLE A.-M., ZEMMOUR J., ENNIS P.D., WARD F.E., PETZL-ERLER M.L.,
RA MATELL R.W., DU TOIT E.D., PARHAM P.;
RT "Distinctive HLA-A,B antigens of black populations formed by
RT interallelic conversion.";1992).
RL J. Immunol. 149:3411-3415(1992).
CC -1- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
CC THE IMMUNE SYSTEM.
CC -1- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
CC MICROGLOBULIN).
CC -----
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CC -----
DR EMBL; X61707; CAA43876.1; -
DR PIR; S16774; S16774.
DR HSSP; P30491; 1ALM.
DR MIM; 142830; -
DR PROSITE; PS00290; IG_MHC; 1.
DR PFAM; PF00047; ig; 1.
DR PFAM; PF00129; MHC_I; 1.
KW MHC I; Transmembrane; Glycoprotein; Signal.
FT SIGNAL 1 24
FT CHAIN 25 362 HLA CLASS I HISTOCOMPATIBILITY ANTIGEN,
FT DOMAIN 25 114 B*57(B-17) B*5702 ALPHA CHAIN.
FT DOMAIN 115 206 EXTRACELLULAR ALPHA-1.
FT DOMAIN 207 298 EXTRACELLULAR ALPHA-2.
FT DOMAIN 299 308 EXTRACELLULAR ALPHA-3.
FT TRANSMEM 309 332 CONNECTING PEPTIDE.
FT DOMAIN 333 362 CYTOPLASMIC TAIL.
FT CARBOHYD 110 110 BY SIMILARITY.
FT DISULFID 125 188 BY SIMILARITY.
FT DISULFID 227 283 BY SIMILARITY.
SQ SEQUENCE 362 AA; 40342 MW; 628C2156 CRC32;

Query Match 49.5%; Score 49; DB 1; Length 362;
Best Local Similarity 100.0%; Pred. No. 0.67;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 11 RENRLALRY 20
DB 99 RENRLALRY 108
|||||
RESULT 13
1B62_HUMAN STANDARD; PRT; 362 AA.
ID 1B62_HUMAN
AC P10319;
DT 01-MAR-1989 (Rel. 10, Created)
DT 01-MAR-1989 (Rel. 10, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, BW-56(B-17) B*5801 ALPHA
DE CHAIN PRECURSOR.
GN HLA-B OR HLAB.

OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Primates; Catarrhini; Hominidae; Homo.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 86008247.
RA WAYS J.P., COPPIN H.L., PARHAM P.;
RT "The complete primary structure of HLA-B*58.";
RL J. Biol. Chem. 260:11924-11933(1985).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE; 86008247.
RA INOUE T., OGAWA A.;
RL Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
CC THE IMMUNE SYSTEM.
CC -1- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
CC MICROGLOBULIN).
CC -----
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CC -----
DR EMBL; M11799; AAA59628.1; -
DR EMBL; AB008102; BAA22916.1; -
DR PIR; A23895; HLHUB8.
DR HSSP; P30491; 1ALM.
DR MIM; 142830; -
DR PROSITE; PS00290; IG_MHC; 1.
DR PFAM; PF00047; ig; 1.
DR PFAM; PF00129; MHC_I; 1.
KW MHC I; Transmembrane; Glycoprotein; Signal.
FT SIGNAL 1 24
FT CHAIN 25 362 HLA CLASS I HISTOCOMPATIBILITY ANTIGEN,
FT DOMAIN 25 114 B*58(B-17) B*5801 ALPHA CHAIN.
FT DOMAIN 115 206 EXTRACELLULAR ALPHA-1.
FT DOMAIN 207 298 EXTRACELLULAR ALPHA-2.
FT DOMAIN 299 308 EXTRACELLULAR ALPHA-3.
FT TRANSMEM 309 332 CONNECTING PEPTIDE.
FT DOMAIN 333 362 CYTOPLASMIC TAIL.
FT CARBOHYD 110 110 BY SIMILARITY.
FT DISULFID 125 188 BY SIMILARITY.
FT DISULFID 227 283 BY SIMILARITY.
SQ SEQUENCE 362 AA; 40337 MW; 3E5E7534 CRC32;

Query Match 49.5%; Score 49; DB 1; Length 362;
Best Local Similarity 100.0%; Pred. No. 0.67;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 RENRLALRY 20
DB 99 RENRLALRY 108
|||||

RESULT 14
HLAH_HUMAN STANDARD; PRT; 362 AA.
ID HLAH_HUMAN
AC P01893;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 15-DEC-1999 (Rel. 39, Last annotation update)
DE HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, ALPHA CHAIN H PRECURSOR
DE (HLA-AR) (HLA-12.4).
GN HLA-H OR HLAH.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Primates; Catarrhini; Hominidae; Homo.

```

RN RP SEQUENCE FROM N.A.
RX MEDLINE; 82151002.
RA MALISSEN M., MALISSEN B., JORDAN B.R.;
RT "Exon/intron organization and complete nucleotide sequence of an HLA
RL gene.";
RL Proc. Natl. Acad. Sci. U.S.A. 79:893-897(1982).
CC -1- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
CC THE IMMUNE SYSTEM. COULD BE THE PRODUCT OF A PSEUDOGENE.
CC -1- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
CC MICROGLOBULIN).
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; J00191; AAA36218.1; ALT_INIT.
DR PIR; A02189; HLH12.
DR HSP; P03989; IHSA.
DR MIN; 142800.
DR PROSITE; PS00290; IG_MHC; 1.
DR PFAM; PF00047; Ig; 1.
DR PFAM; PF00129; MHC_I; 1.
DR MHC_I; Transmembrane; Glycoprotein; Signal.
KW SIGNAL 1 24
FT CHAIN 25 362 HLA CLASS I HISTOCOMPATIBILITY ANTIGEN,
FT FT ALPHA CHAIN H.
FT DOMAIN 25 114 EXTRACELLULAR ALPHA-1.
FT DOMAIN 115 206 EXTRACELLULAR ALPHA-2.
FT DOMAIN 207 298 EXTRACELLULAR ALPHA-3.
FT DOMAIN 299 308 CONNECTING PEPTIDE.
FT TRANSMEM 309 332
FT DOMAIN 333 362 CYTOPLASMIC TAIL.
FT CARBOHYD 110 110 BY SIMILARITY.
FT DISULFID 227 283 BY SIMILARITY.
SQ SEQUENCE 362 AA; 40850 MW; 5E610F63 CRC32;

Query Match 49.5%; Score 49; DB 1; Length 362;
Best Local Similarity 100.0%; Pred. No. 0.67;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 RNLRIALRY 20
Db 99 RNLRIALRY 108

RESULT 15
1A23_HUMAN
ID 1A23_HUMAN STANDARD; PRT; 365 AA.
AC P30447;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, A-23(A-9) ALPHA CHAIN
DE PRECURSOR.
GN HLA-A OR HLA-A.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Primates; Catarrhini; Hominidae; Homo.
[1]
RN RP SEQUENCE FROM N.A. (A*2301).
RX MEDLINE; 92104637.
RA LITTLE A.-M., MADRIGAL J.A., PARHAM P.;
RT "Molecular definition of an elusive third HLA-A9 molecule: HLA-A9.3.";
RL Immunogenetics 35:41-45(1992).
CC -1- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
CC THE IMMUNE SYSTEM.
CC -1- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
CC MICROGLOBULIN).
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; M64742; AAA03662.1; -.
DR HSP; P01892; IAQD.
DR MIN; 142800.
DR PROSITE; PS00290; IG_MHC; 1.
DR PFAM; PF00047; Ig; 1.
DR PFAM; PF00129; MHC_I; 1.
DR MHC_I; Transmembrane; Glycoprotein; Signal.
KW SIGNAL 1 24
FT CHAIN 25 365 HLA CLASS I HISTOCOMPATIBILITY ANTIGEN,
FT FT A-23(A-9) ALPHA CHAIN.
FT DOMAIN 25 114 EXTRACELLULAR ALPHA-1.
FT DOMAIN 115 206 EXTRACELLULAR ALPHA-2.
FT DOMAIN 207 298 EXTRACELLULAR ALPHA-3.
FT DOMAIN 299 308 CONNECTING PEPTIDE.
FT TRANSMEM 309 332
FT DOMAIN 333 365 CYTOPLASMIC TAIL.
FT CARBOHYD 110 110 BY SIMILARITY.
FT DISULFID 227 283 BY SIMILARITY.
SQ SEQUENCE 365 AA; 40732 MW; B1C21094 CRC32;

Query Match 49.5%; Score 49; DB 1; Length 365;
Best Local Similarity 100.0%; Pred. No. 0.68;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 RNLRIALRY 20
Db 99 RNLRIALRY 108

Search completed: February 8, 2000, 01:25:59
Job time: 1559 sec
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Result No.	Score	Query %		DB	ID	Description
		Match	Length			
1	50	50.5	89	7	019569	019569 homo sapien
2	50	50.5	172	7	019770	019770 homo sapien
3	50	50.5	172	7	019774	019774 homo sapien
4	50	50.5	172	7	019775	019775 homo sapien
5	50	50.5	172	7	019780	019780 homo sapien
6	50	50.5	172	7	095364	095364 homo sapien
7	50	50.5	172	7	019771	019771 homo sapien
8	50	50.5	172	7	019772	019772 homo sapien
9	50	50.5	172	7	019773	019773 homo sapien
10	50	50.5	175	7	029694	029694 homo sapien
11	50	50.5	181	7	046703	046703 homo sapien
12	50	50.5	181	7	062899	062899 homo sapien
13	50	50.5	181	7	062922	062922 homo sapien
14	50	50.5	181	7	019623	019623 homo sapien
15	50	50.5	181	7	019747	019747 homo sapien
16	50	50.5	181	7	029667	029667 homo sapien
17	50	50.5	181	7	030198	030198 homo sapien
18	50	50.5	181	7	029708	029708 homo sapien
19	50	50.5	181	7	079559	079559 homo sapien
20	50	50.5	181	7	019597	019597 homo sapien

OC Eutheria; Primates; Catarrhini; Hominidae; Homo.

RN [1]
RP SEQUENCE FROM N.A.
RA CHANDANAYINGYONG D., SIRIKONG M., LONGTA K., SRINAK D., RUNGROUNG E.,
RA BEJCHANDRA S., JUJI T., TOKUNAGA K.;
RL Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; U90421; AAB50144.1; -.
DR EMBL; U90420; AAB50144.1; JOINED.
DR PFAM; PF00129; MHC_I; 1.
KW MHC.
FT NON_TER 1
FT NON_TER 172 172
SQ SEQUENCE 172 AA; 19909 MW; CAAE5641 CRC32;

Query Match 50.5%; Score 50; DB 7; Length 172;
Best Local Similarity 68.8%; Pred. No. 1.3;
Matches 11; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 5 TRLNERENLRALRY 20
DB 62 TNTQTYENLRALRY 77

RESULT 3

ID O19774 PRELIMINARY; PRT; 172 AA.
AC O19774;
DT 01-JAN-1998 (TREMBlrel. 05, Created)
DT 01-JAN-1998 (TREMBlrel. 05, Last sequence update)
DT 01-NOV-1998 (TREMBlrel. 08, Last annotation update)
DE MHC CLASS I HLA-B (FRAGMENT).
GN HLA-B.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Primates; Catarrhini; Hominidae; Homo.
RN [1]
RP SEQUENCE FROM N.A.
RA CHANDANAYINGYONG D., SIRIKONG M., LONGTA K., SRINAK D., RUNGROUNG E.,
RA BEJCHANDRA S., BLASZYK R., GROSE-WILDE H.;
RL Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; U90423; AAB50145.1; -.
DR EMBL; U90422; AAB50145.1; JOINED.
DR PFAM; PF00129; MHC_I; 1.
KW MHC.
FT NON_TER 1
FT NON_TER 172 172
SQ SEQUENCE 172 AA; 19909 MW; CAAE5641 CRC32;

Query Match 50.5%; Score 50; DB 7; Length 172;
Best Local Similarity 68.8%; Pred. No. 1.3;
Matches 11; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 5 TRLNERENLRALRY 20
DB 62 TNTQTYENLRALRY 77

RESULT 4

ID O19775 PRELIMINARY; PRT; 172 AA.
AC O19775;
DT 01-JAN-1998 (TREMBlrel. 05, Created)
DT 01-JAN-1998 (TREMBlrel. 05, Last sequence update)
DT 01-NOV-1998 (TREMBlrel. 08, Last annotation update)
DE MHC CLASS I HLA-B (FRAGMENT).
GN HLA-B.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Primates; Catarrhini; Hominidae; Homo.
RN [1]
RP SEQUENCE FROM N.A.

RA CHANDANAYINGYONG D., SIRIKONG M., LONGTA K., SRINAK D., RUNGROUNG E.,
RA BEJCHANDRA S.;
RL Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; U90425; AAB50146.1; -.
DR EMBL; U90424; AAB50146.1; JOINED.
DR PFAM; PF00129; MHC_I; 1.
KW MHC.
FT NON_TER 1
FT NON_TER 172 172
SQ SEQUENCE 172 AA; 19909 MW; CAAE5641 CRC32;

Query Match 50.5%; Score 50; DB 7; Length 172;
Best Local Similarity 68.8%; Pred. No. 1.3;
Matches 11; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 5 TRLNERENLRALRY 20
DB 62 TNTQTYENLRALRY 77

RESULT 5

ID O19780 PRELIMINARY; PRT; 172 AA.
AC O19780;
DT 01-JAN-1998 (TREMBlrel. 05, Created)
DT 01-JAN-1998 (TREMBlrel. 05, Last sequence update)
DT 01-NOV-1998 (TREMBlrel. 08, Last annotation update)
DE MHC CLASS I HLA-B (FRAGMENT).
GN HLA-B.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Primates; Catarrhini; Hominidae; Homo.
RN [1]
RP SEQUENCE FROM N.A.
RA CHANDANAYINGYONG D., SIRIKONG M., LONGTA K., SRINAK D., RUNGROUNG E.,
RA BEJCHANDRA S., JUJI T., TOKUNAGA K.;
RL Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; U90419; AAB50143.1; -.
DR EMBL; U90418; AAB50143.1; JOINED.
DR PFAM; PF00129; MHC_I; 1.
KW MHC.
FT NON_TER 1
FT NON_TER 172 172
SQ SEQUENCE 172 AA; 19909 MW; CAAE5641 CRC32;

Query Match 50.5%; Score 50; DB 7; Length 172;
Best Local Similarity 68.8%; Pred. No. 1.3;
Matches 11; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 5 TRLNERENLRALRY 20
DB 62 TNTQTYENLRALRY 77

RESULT 6

ID Q95364 PRELIMINARY; PRT; 172 AA.
AC Q95364;
DT 01-FEB-1997 (TREMBlrel. 02, Created)
DT 01-FEB-1997 (TREMBlrel. 02, Last sequence update)
DT 01-NOV-1998 (TREMBlrel. 08, Last annotation update)
DE MHC HLA-B*51 PROTEIN (FRAGMENT).
GN HLA-B*51FA.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Primates; Catarrhini; Hominidae; Homo.
RN [1]
RP SEQUENCE FROM N.A.
RA BLASZYK R.;
RL Submitted (MAR-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; X96473; CAA65327.1; -.

DR PFAM: PF00129; MHC_I; 1.
KW MHC.
FT NON_TER 1
FT NON_TER 172
SQ SEQUENCE 172 AA; 19942 MW; 1A73E47D CRC32;

Query Match 50.5%; Score 50; DB 7; Length 172;
Best Local Similarity 68.8%; Pred. No. 1.3;
Matches 11; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 5 TRLNERRENLRALRY 20
| | | | | | | | | |
Db 59 TNTQTYRENLRALRY 74

RESULT 7
O19771 PRELIMINARY; PRT; 172 AA.
ID O19771;
AC O19771;
DT 01-JAN-1998 (TREMELrel. 05, Created)
DT 01-JAN-1998 (TREMELrel. 05, Last sequence update)
DT 01-NOV-1998 (TREMELrel. 08, Last annotation update)
DE MHC CLASS I HLA-B (FRAGMENT).
GN HLA-B.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Primates; Catarrhini; Hominidae; Homo.
RN [1]
RA CHANDANAYONG D., SIRIKONG M., LONGTA K., SRINAK D.,
RA SIRIBOONRIT U., RUNGROUNG E., BEJCHANDRA S.;
RL Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL: U90612; AAB50151.1;
DR EMBL: U90611; AAB50151.1; JOINED.
DR PFAM: PF00129; MHC_I; 1.
KW MHC.
FT NON_TER 1
FT NON_TER 172
SQ SEQUENCE 172 AA; 20026 MW; 4D9A1043 CRC32;

Query Match 50.5%; Score 50; DB 7; Length 172;
Best Local Similarity 68.8%; Pred. No. 1.3;
Matches 11; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 5 TRLNERRENLRALRY 20
| | | | | | | | | |
Db 62 TNTQTYRENLRALRY 77

RESULT 8
O19772 PRELIMINARY; PRT; 172 AA.
ID O19772;
AC O19772;
DT 01-JAN-1998 (TREMELrel. 05, Created)
DT 01-JAN-1998 (TREMELrel. 05, Last sequence update)
DT 01-NOV-1998 (TREMELrel. 08, Last annotation update)
DE MHC CLASS I HLA-B (FRAGMENT).
GN HLA-B.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Primates; Catarrhini; Hominidae; Homo.
RN [1]
RA CHANDANAYONG D., SIRIKONG M., LONGTA K., SRINAK D.,
RA SIRIBOONRIT U., RUNGROUNG E., BEJCHANDRA S.;
RL Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL: U90614; AAB50244.1;
DR EMBL: U90613; AAB50244.1; JOINED.
DR PFAM: PF00129; MHC_I; 1.
KW MHC.
FT NON_TER 1

FT NON_TER 172
SQ SEQUENCE 172 AA; 20026 MW; 4D9A1043 CRC32;

Query Match 50.5%; Score 50; DB 7; Length 172;
Best Local Similarity 68.8%; Pred. No. 1.3;
Matches 11; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 5 TRLNERRENLRALRY 20
| | | | | | | | | |
Db 62 TNTQTYRENLRALRY 77

RESULT 9
O19773 PRELIMINARY; PRT; 172 AA.
ID O19773;
AC O19773;
DT 01-JAN-1998 (TREMELrel. 05, Created)
DT 01-JAN-1998 (TREMELrel. 05, Last sequence update)
DT 01-NOV-1998 (TREMELrel. 08, Last annotation update)
DE MHC CLASS I HLA-B (FRAGMENT).
GN HLA-B.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Primates; Catarrhini; Hominidae; Homo.
RN [1]
RA CHANDANAYONG D., SIRIKONG M., LONGTA K., SRINAK D.,
RA SIRIBOONRIT U., RUNGROUNG E., BEJCHANDRA S.;
RL Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL: U90616; AAB50245.1;
DR EMBL: U90615; AAB50245.1; JOINED.
DR PFAM: PF00129; MHC_I; 1.
KW MHC.
FT NON_TER 1
FT NON_TER 172
SQ SEQUENCE 172 AA; 20052 MW; F6214671 CRC32;

Query Match 50.5%; Score 50; DB 7; Length 172;
Best Local Similarity 68.8%; Pred. No. 1.3;
Matches 11; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 5 TRLNERRENLRALRY 20
| | | | | | | | | |
Db 62 TNTQTYRENLRALRY 77

RESULT 10
O29694 PRELIMINARY; PRT; 175 AA.
ID O29694;
AC O29694;
DT 01-NOV-1996 (TREMELrel. 01, Created)
DT 01-NOV-1996 (TREMELrel. 01, Last sequence update)
DT 01-NOV-1999 (TREMELrel. 12, Last annotation update)
DE MHC CLASS I HLA-B ANTIGEN (FRAGMENT).
GN HLA-B.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Primates; Catarrhini; Hominidae; Homo.
RN [1]
RA PETERSDORF E.;
RL Submitted (JUN-1995) to the EMBL/GenBank/DBJ databases.
DR EMBL: U28759; AAB60367.1;
DR HSSP: P10318; 1ROG.
DR PFAM: PF00129; MHC_I; 1.
KW MHC.
FT NON_TER 1
FT NON_TER 67
FT VARIANT 73
FT VARIANT 73
FT NON_TER 175

SQ SEQUENCE 175 AA; 20332 MW; 83A0C5C3 CRC32;

Query Match 50.5%; Score 50; DB 7; Length 175;
Best Local Similarity 68.8%; Pred. No. 1.3;
Matches 11; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 5 TRLNERRENRLALRY 20
| | | | | | | | | |
DB 62 TNTQTYRENRLALRY 77

RESULT 11

046703 PRELIMINARY; PRT; 181 AA.
ID 046703
AC 046703;
DT 01-JUN-1998 (TREMBLrel. 06, Created)
DT 01-JUN-1998 (TREMBLrel. 06, Last sequence update)
DT 01-NOV-1999 (TREMBLrel. 12, Last annotation update)
DE HLA-B*51IM (FRAGMENT).
GN HLA-B*51IM.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Primates; Catarrhini; Hominidae; Homo.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-BLOOD;
RA GAO X., MATHESON B.;
RL Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; U58320; AAB87725.1; -.
DR EMBL; U58319; AAB87725.1; JOINED.
DR HSSP; P10318; IROG.
DR PFAM; PF00129; MHC_I; 1.
KW MHC.
FT NON_TER 1
FT NON_TER 181
SQ SEQUENCE 181 AA; 21113 MW; 61FB4281 CRC32;

Query Match 50.5%; Score 50; DB 7; Length 181;
Best Local Similarity 68.8%; Pred. No. 1.3;
Matches 11; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 5 TRLNERRENRLALRY 20
| | | | | | | | | |
DB 68 TNTQTYRENRLALRY 83

RESULT 12

062899 PRELIMINARY; PRT; 181 AA.
ID 062899
AC 062899;
DT 01-AUG-1998 (TREMBLrel. 07, Created)
DT 01-AUG-1998 (TREMBLrel. 07, Last sequence update)
DT 01-NOV-1999 (TREMBLrel. 12, Last annotation update)
DE MHC CLASS I ANTIGEN (FRAGMENT).
GN HLA-B.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Primates; Catarrhini; Hominidae; Homo.
RN [1]
RP SEQUENCE FROM N.A.
RA MARCOS C.Y., LAZARO A.M., STASTNY P.;
RL Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF056480; AAC14122.1; -.
DR EMBL; AF056479; AAC14122.1; JOINED.
DR HSSP; P10318; IROG.
DR PFAM; PF00129; MHC_I; 1.
KW MHC.
FT NON_TER 1
FT NON_TER 181
SQ SEQUENCE 181 AA; 21224 MW; 6736F2EB CRC32;

Query Match 50.5%; Score 50; DB 7; Length 181;
Best Local Similarity 68.8%; Pred. No. 1.3;
Matches 11; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 5 TRLNERRENRLALRY 20
| | | | | | | | | |
DB 68 TNTQTYRENRLALRY 83

RESULT 13

062922 PRELIMINARY; PRT; 181 AA.
ID 062922
AC 062922;
DT 01-AUG-1998 (TREMBLrel. 07, Created)
DT 01-AUG-1998 (TREMBLrel. 07, Last sequence update)
DT 01-NOV-1999 (TREMBLrel. 12, Last annotation update)
DE MHC CLASS I ANTIGEN (FRAGMENT).
GN HLA-B.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Primates; Catarrhini; Hominidae; Homo.
RN [1]
RP SEQUENCE FROM N.A.
RA STEINER N.K., HURLEY C.K., KOESTER R.P.;
RL Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF065645; AAC18389.1; -.
DR EMBL; AF065644; AAC18389.1; JOINED.
DR HSSP; P10318; IROG.
DR PFAM; PF00129; MHC_I; 1.
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FT NON_TER 181
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Query Match 50.5%; Score 50; DB 7; Length 181;
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Matches 11; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 5 TRLNERRENRLALRY 20
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DB 68 TNTQTYRENRLALRY 83

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AC 019623;
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DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
DT 01-NOV-1999 (TREMBLrel. 12, Last annotation update)
DE MHC CLASS I ANTIGEN B*5108 (FRAGMENT).
GN HLA-B.
OS Homo sapiens (Human).
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OC Eutheria; Primates; Catarrhini; Hominidae; Homo.
RN [1]
RP SEQUENCE FROM N.A.
RA STEINER N.K., NG J., BUSH J., HARTZMAN R.J., JOHNSON-DOW L.,
HURLEY C.K.;
RL Hum. Immunol. 56:0-0(1997).
DR EMBL; U52816; AAB80619.1; -.
DR EMBL; U52815; AAB80619.1; JOINED.
DR HSSP; P10318; IROG.
DR PFAM; PF00129; MHC_I; 1.
KW MHC.
FT NON_TER 1
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Db 68 TNOTYRENLRALRY 83

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DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
DT 01-NOV-1999 (TREMBLrel. 12, Last annotation update)
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OC Eutheria; Primates; Catarrhini; Hominidae; Homo.
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RA STEINER N.K., NG J., BUSH J., HARTZMAN R.J., JOHNSON-DOW L.,
RA HURLEY C.K.;
RL Hum. Immunol. 56:0-0(1997).
DR EMBL; U52170; AAB82331.1; -.
DR EMBL; U52169; AAB82331.1; JOINED.
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KW MHC.
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Db 68 TNOTYRENLRALRY 83

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1. The Role of the State in the Development of the Economy	Journal of Economic Surveys	See also 2. The Role of the State in the Development of the Economy
2. The Role of the State in the Development of the Economy	Journal of Economic Surveys	See also 1. The Role of the State in the Development of the Economy
3. The Role of the State in the Development of the Economy	Journal of Economic Surveys	See also 1. The Role of the State in the Development of the Economy
4. The Role of the State in the Development of the Economy	Journal of Economic Surveys	See also 1. The Role of the State in the Development of the Economy
5. The Role of the State in the Development of the Economy	Journal of Economic Surveys	See also 1. The Role of the State in the Development of the Economy
6. The Role of the State in the Development of the Economy	Journal of Economic Surveys	See also 1. The Role of the State in the Development of the Economy
7. The Role of the State in the Development of the Economy	Journal of Economic Surveys	See also 1. The Role of the State in the Development of the Economy
8. The Role of the State in the Development of the Economy	Journal of Economic Surveys	See also 1. The Role of the State in the Development of the Economy
9. The Role of the State in the Development of the Economy	Journal of Economic Surveys	See also 1. The Role of the State in the Development of the Economy
10. The Role of the State in the Development of the Economy	Journal of Economic Surveys	See also 1. The Role of the State in the Development of the Economy

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*		contig of 17974 bp in length
*		gap of unknown length
*	139036	181036:
*		contig of 42001 bp in length
*		gap of unknown length

2

AUTHORS Poli, F.
 TITLE Direct Submission
 JOURNAL Submitted (11-DEC-1995) F. Poli, Centro Trasfusionale e di Immunologie del Trapianti, Ospedale Maggiore Policlinico, Via Francesco Sforza 35, 20122 Milan, ITALY
 REMARK revised by [3]
 REFERENCE 3 (bases 1 to 270)
 AUTHORS Poli, F.
 JOURNAL Direct Submission
 TITLE Submitted (03-APR-1997) F. Poli, Centro Trasfusionale e di Immunologie del Trapianti, Ospedale Maggiore Policlinico, Via Francesco Sforza 35, 20122 Milan, ITALY
 COMMENT On Apr 7, 1997 this sequence version replaced gi:1841917.
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 DEFINITION Human MHC class I HLA-B51 (alpha-1 domain) gene, exon 2.
 ACCESSION M22787 M21035
 VERSION M22787.1 GI:187683
 KEYWORDS HLA-B51 protein; cell surface antigen; cell surface glycoprotein; class I gene; integral membrane protein; major histocompatibility complex.
 SEGMENT 2 of 7
 SOURCE Human EBV transformed B lymphoblastoid (LXT-2, Toto cell line) DNA, clone LXT.18, Toto B4.
 ORGANISM Homo sapiens
 Eukaryota; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 270)
 AUTHORS Hayashi, H., Ennis, P. D., Ariga, H., Salter, R. D., Parham, P., Kano, K. and Takiguchi, M.
 TITLE HLA-B51 and HLA-Bw52 differ by only two amino acids which are in the helical region of the alpha 1 domain
 JOURNAL J. Immunol. 142 (1), 306-311 (1989)
 MEDLINE 85080265
 COMMENT Draft entry and computer-readable sequence [1] kindly submitted by P. Ennis, 14-OCT-1988.
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 204 ACCAACACACAGACTTACCGAGAGAACTCGGATCGGCTCCGCTAC 251

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N_Genesed_36:Q018322	+	50.00	141.46	2.80	1086	Sequence encoding HLA-B*52 anti
N_Genesed_36:Q005693	+	50.00	141.43	2.81	1089	HLA-B*51 gene for production of
N_Genesed_36:Q005701	+	50.00	141.43	2.81	1089	HLA-B*52 gene for production of
N_Genesed_36:Q012114	+	50.00	141.43	2.81	1089	HLA-B*53 exon. HLA-B*53 gene.
N_Genesed_36:1T42608	+	49.00	150.97	0.8283	285	Synthetic gene, Lqhiv encoding
N_Genesed_36:1T60544	+	44.50	134.62	6.74	345	(Pro23-Lys37)delAsn37-ile-134
N_Genesed_36:1T60542	+	44.50	132.81	8.50	417	MetGDNF Degenerate DNA sequence
N_Genesed_36:1T82476	+	43.00	106.51	248.08	3973	T. niveum alanine-racemase. Ne
N_Genesed_36:1T82481	+	43.00	106.51	248.08	3973	T. niveum alanine-racemase. Ne
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N_Genesed_36:Q054386	+	43.00	83.00	5.1e+03	46899	Mechanococcus jannaschii FEN-1
N_Genesed_36:1V63837	+	42.00	116.60	68.01	981	FEV-B gag/pol gene. Multi-val
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N_Genesed_36:Q029114	+	42.00	104.02	341.14	3674	DNA for Bacillus stearothermo
N_Genesed_36:1T75487	+	42.00	103.99	342.61	3687	sbsA gene encoding s-layer pro
N_Genesed_36:1T83695	+	42.00	103.62	359.14	3832	Tuberculosis sclerosis 2 TSC2 ge
N_Genesed_36:Q090251	+	42.00	100.23	555.13	5474	Streptococcus pneumoniae geno
N_Genesed_36:1V52236	+	42.00	100.08	565.55	5558	FEV F6A provirus clone 61E g
N_Genesed_36:1T13265	+	42.00	96.10	941.95	8440	Immunogen DNA from n-(ABCDP) he
N_Genesed_36:Q070008	+	41.00	135.21	6.25	99	PHULI core sequence from Lact
N_Genesed_36:Q028344	+	41.00	110.37	151.15	1344	Encodes acid alpha-amylase enz
N_Genesed_36:Q031009	+	41.00	99.66	597.17	4140	Human canalicular multispecifi
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N_Genesed_36:1T14180	+	41.00	91.53	1.7e+03	9718	Streptococcus pneumoniae g
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N_Genesed_36:1T84918	+	40.00	107.08	230.56	1333	Burkholderia cepacia ET12 stra
N_Genesed_36:1T30417	+	40.00	106.97	233.69	1368	H. pylori outer membrane prote
N_Genesed_36:1T67839	+	40.00	106.37	252.60	1458	H. pylori cytoplasmic protein
N_Genesed_36:Q03536	+	40.00	106.10	261.30	1499	Subtilisin gene. Mutant prokar
N_Genesed_36:N71241	-	40.00	106.10	261.51	1500	Subtilisin gene from Bacillus
N_Genesed_36:N090058	-	40.00	106.10	261.51	1500	Bacillus subtilis subtilisin g
N_Genesed_36:Q090042	-	40.00	106.10	261.51	1500	B. subtilis subtilisin gene. Re
N_Genesed_36:1T60306	+	40.00	106.10	261.51	1500	Caenorhabditis elegans SBL-12
N_Genesed_36:N60475	-	40.00	105.94	266.63	1524	Sequence of thapsi [Bsu] gene

DRP New DNA class 1 human leucocyte antigens and derived probes and
PT transformed cells, useful for DNA typing, as immunogens etc.
PT Claim 1; Page 11; 23pp; English.
CC The HLA class I DNA can be used as a source of probes for use in DNA
CC typing. Transformed cells, which are useful as immunogens, can be
CC obtained by introducing these DNAs into eucaryotic cells.
SQ sequence 1086 Bp; 224 A; 334 C; 356 G; 172 T;
SQ Wnt: 90-G06265/07.

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AC Q01822;
DT 19-MAY-1991 (first entry)
DE Sequence encoding HLA-Bw52 antigen.
KW Probe: HLA class I DNA; immunogen; ss.
OS Homo sapiens.
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FT cds 1..1086
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PN EP-354580-A.
PD 14-FEB-1990.
PF 10-AUG-1989.
PR 11-AUG-1988; JP-200758.
PA (OLYU) Olympus Optical Co., Ltd.
PI Kano K. Takiguchi;
DR WPI; 90-046289/07.
DR P-PSDB; R03142.
PT New DNA for class I human leucocyte antigens and derived probes and
PT transformed cells, useful for DNA typing, as immunogens etc.
PS Claim 2: pp11-12; 23pp; English.
CC The HLA class I DNA can be used as a source of probes for use in DNA
CC typing. Transformed cells, which are useful as immunogens, can be
CC obtained by introducing these DNAs into eucaryotic cells.
SQ Sequence 1086 BP; 223 A; 335 C; 358 G; 170 T;

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AC Q05693;
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KW Allotype specific monoclonal anti-HLA antibodies; hybridomas;
KW transgenic animals; HLA-B51 gene; ss.
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PD 22-AUG-1990.
PF 07-FEB-1990; 102424.
PR 08-FEB-1989; JP-029313.
PA (OLYU) OLYMPUS OPTICAL KK.
PI Takiguchi M;
DR WPI; 90-255479/34.
PT Allotype specific monoclonal anti- HLA antibodies prodn. - using
PT hybridomas derived from transgenic animals carrying HLA gene and
PT immunised with HLA antigen of different allotype
PS Disclosure; Fig 1 A-G; 20pp; English.
CC The human HLA-B51 gene was injected into fertilised mouse eggs and
CC then these introduced into the uterus of a pseudo pregnant mouse.
CC The young were tested to ensure incorporation of the gene into the
CC chromosome, and one of them mated 3 times with a normal male to
CC produce 16 young, seven of which carried the HLA-B51 gene.
CC The transgenic offspring were immunised with HLA antigen.
CC The spleen lymphocytes were fused with myeloma cells. Hybridomas
CC producing antibodies were selected.
CC See also Q05701.
SQ Sequence 1089 BP; 224 A; 335 C; 357 G; 173 T;

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AC Q05701;
DT 03-JAN-1991 (first entry)
DE HLA-Bw52 gene for production of monoclonal antibodies.
KW Allotype specific monoclonal anti-HLA antibodies; hybridomas;
KW transgenic animals; HLA-Bw52 gene; ss.
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FT 22-AUG-1990.
FT 07-FEB-1990; 102424.
FT 08-FEB-1989; JP-029313.
FT (OLYU ) OLYMPUS OPTICAL KK.
FT Takiguchi M;
FT WPI; 90-255479/34.
FT Allotype specific monoclonal anti- HLA antibodies prodn. - using
FT hybridomas derived from transgenic animals carrying HLA gene and
FT immunised with HLA antigen of different allotype
FT Disclosure; Fig 1 A-G; 20pp; English.
FT The human HLA-Bw52 gene was introduced into mouse L cells and
FT then these cells used to immunise one of the transgenic mice
FT (See Q05693).
FT The spleen lymphocytes were fused with myeloma cells (P3x63-Ag8.653).
FT Hybridomas producing antibodies were selected.
FT Sequence 1089 BP; 223 A; 336 C; 359 G; 171 T;

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Ratio: 3.846 Gaps: 0
Percent Similarity: 81.250 Percent Identity: 68.750

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AC T42608:
DT 07-AUG-1991 (first entry)
DE Synthetic gene, LqhIV encoding scorpion neurotoxin.
KW neurotoxin; pest control; insect; acarid; nematode; LqhIV; LqhVI;
KW venom; Leirus quinquatratus hebraeus; scorpion; lepidoptera;
KW baculovirus; arthropod; ds.
OS Synthetic.
FH Key Location/Qualifiers
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FT /note= "no start codon given"
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FT W09636221-A2.
FT 21-NOV-1996.
FT 30-APR-1996; U06076.
FT 08-MAY-1995; US-435040.
FT (REGC ) UNIV CALIFORNIA.
FT Hammock BD, Herrmann R, Moskowitz H;
FT WPI; 97-011744/01.
FT P-PSDB; W06339.
FT Control of insects, acarids and nematodes - using novel scorpion
FT toxins or a combination of 2 or more insect toxins
FT
FT Claim 1; Fig 1; 35pp; English.
FT A novel method for controlling pests selected from insects, acarids, and
FT nematodes, comprises treating the pests or their loci with at least two
FT different insect toxins, the source of the toxins being at least one
FT recombinant microbe, the toxins having non-overlapping binding sites at
FT an insect cellular membrane channel. The present sequence is a synthetic
FT gene for LqhIV toxin, derived from the venom of Leirus quinquatratus
FT hebraeus (Scorpion). LqhIV is the most potent lepidopterous toxin
FT isolated from scorpion venom to date, whilst LqhVI (W06340) has weak
FT mammal toxicity. In particular the insect toxin genes are expressed
FT by baculovirus vectors, as the baculoviruses infect only arthropods,
FT therefore pose little or no risk to humans, plants or the environment.
FT Sequence 285 BP; 67 A; 92 C; 70 G; 56 T;

alignment_scores:
Quality: 49.00 Length: 19
Ratio: 3.062 Gaps: 0
Percent Similarity: 84.211 Percent Identity: 52.632

alignment_block:
US-08-653-294-28 x T42608 ..
Align seg 1/1 to: T42608 from: 1 to: 285

1 TyrArgLeuAlaThrArgLeuAsnGluArgGluAsnLeuArgIleAl 17

```

```

PS Claim 1; Page 1; lipp; Japanese.
CC Probes comprising part of the sequence can be used to identify
CC Class I genes. The DNA can be expressed for immunisation of
CC animals and prodn. of monoclonal antibodies specific for the
CC HLA-Bw53 antigen. See also J03112485 and J03112486. 174 T;
SQ Sequence 1089 BP; 222 A; 337 C; 356 G; 174 T;

alignment_scores:
Quality: 50.00 Length: 16
Ratio: 3.846 Gaps: 0
Percent Similarity: 81.250 Percent Identity: 68.750

alignment_block:
US-08-653-294-28 x Q12114 ..
Align seg 1/1 to: Q12114 from: 1 to: 1089

5 ThrArgLeuAsnGluArgGluAsnLeuArgIleAlaLeuArgTyr 20
277 ACCAACACACAGACTTACCGAGAGAACCTGCGGATCGCGCTCCGCTAC 324

seq_name: N_Geneseq_36:T42608

seq_documentation_block:
ID T42608 standard; DNA; 285 BP.
AC T42608:
DT 07-AUG-1997 (first entry)
DE Synthetic gene, LqhIV encoding scorpion neurotoxin.
KW neurotoxin; pest control; insect; acarid; nematode; LqhIV; LqhVI;
KW venom; Leirus quinquatratus hebraeus; scorpion; lepidoptera;
KW baculovirus; arthropod; ds.
OS Synthetic.
FH Key Location/Qualifiers
FT cds 70..267
FT /*tag= a
FT /note= "no start codon given"
FT
FT W09636221-A2.
FT 21-NOV-1996.
FT 30-APR-1996; U06076.
FT 08-MAY-1995; US-435040.
FT (REGC ) UNIV CALIFORNIA.
FT Hammock BD, Herrmann R, Moskowitz H;
FT WPI; 97-011744/01.
FT P-PSDB; W06339.
FT Control of insects, acarids and nematodes - using novel scorpion
FT toxins or a combination of 2 or more insect toxins
FT
FT Claim 1; Fig 1; 35pp; English.
FT A novel method for controlling pests selected from insects, acarids, and
FT nematodes, comprises treating the pests or their loci with at least two
FT different insect toxins, the source of the toxins being at least one
FT recombinant microbe, the toxins having non-overlapping binding sites at
FT an insect cellular membrane channel. The present sequence is a synthetic
FT gene for LqhIV toxin, derived from the venom of Leirus quinquatratus
FT hebraeus (Scorpion). LqhIV is the most potent lepidopterous toxin
FT isolated from scorpion venom to date, whilst LqhVI (W06340) has weak
FT mammal toxicity. In particular the insect toxin genes are expressed
FT by baculovirus vectors, as the baculoviruses infect only arthropods,
FT therefore pose little or no risk to humans, plants or the environment.
FT Sequence 285 BP; 67 A; 92 C; 70 G; 56 T;

alignment_scores:
Quality: 49.00 Length: 19
Ratio: 3.062 Gaps: 0
Percent Similarity: 84.211 Percent Identity: 52.632

alignment_block:
US-08-653-294-28 x T42608 ..
Align seg 1/1 to: T42608 from: 1 to: 285

1 TyrArgLeuAlaThrArgLeuAsnGluArgGluAsnLeuArgIleAl 17

```


Percent Similarity: 73.684

Percent Similarity: 73.684

Align seg 1/1 to: Q54386 from

Align seg 1/1 to: Q54386 from

2 ArgLeuAlaThrArgLeuAsnGluArgGluAsnLeuArgIleAlaLeu 18
 ||| ||||||| ::||| ||||||| ::||| |||||||
 1117 CGCAGCGCCAGGAGCTCCGAGCGCTTCAAGGACGAGGATGCGTG 1166
 18 uArgTyr 20
 |||
 1167 GCGGTAC 1173

seq_name: N_Geneseq_36:V65837

seq_documentation_block:

ID V65837 standard; DNA; 981 BP.
 AC V65837;
 DT 02-FEB-1999 (first entry)
 DE Methanococcus jannaschii FEN-1 endonuclease gene ORF.
 KW Nucleic acid detection; multiple sequential invasive cleavage;
 OS FEN-1; endonuclease; nuclease; ds.
 PS Methanococcus jannaschii.
 PN WO9842873-A1.
 PD 01-OCT-1998.
 PF 24-MAR-1998; U05809.
 PR 24-MAR-1997; US-823516.
 PA (THIR-) THIRD WAVE TECHNOLOGIES INC.
 PI Brow MAD, Hall JG, Kwiatkowski RW, Lyamichev VI,
 PI Mast AL, Vavra SH;
 DR WPI: 98-557036/47.
 DR P-PSDB: W79969.
 DT Detecting target nucleic acid by sequence-specific cleavage of
 PT complex with two specific oligonucleotides - used to detect
 PT cyomegalovirus DNA
 PS Example 28a; Page 313-314; 524pp; English.
 CC This is the nucleotide sequence of the open reading frame encoding
 CC the FEN-1 endonuclease (see W79969) of Methanococcus jannaschii
 CC (Mja). It was obtained from genomic DNA by PCR amplification (see
 CC also V65835-36). The PCR product has been ligated into vector
 CC pirc99a, and FEN-1 was expressed in E. coli cells. The invention
 CC relates to means for the detection and characterisation of nucleic
 CC acid sequences, and variations in nucleic acid sequences. It also
 CC relates to methods for forming a nucleic acid cleavage structure on
 CC a target sequence and cleaving this structure in a site-specific
 CC manner, preferably using a thermostable structure-specific nuclease
 CC such as FEN-1. Cleavage of the cleavage structure by the
 CC nuclease indicates the presence of specific nucleic acid sequences
 CC or specific variants. The invention further relates to methods for
 CC the separation of nucleic acid molecules based on charge, methods
 CC for the detection of non-target cleavage products via the formation
 CC of a complete and activated protein binding region, and methods for
 CC the detection of nucleic acid from various viruses (e.g. human
 CC cytomegalovirus) in a sample. The method amplifies the detection
 CC molecule rather than the target itself, is less subject to
 CC contamination than exponential amplification processes, and allows
 CC many targets to be analysed in a single reaction.
 SQ Sequence 981 BP; 370 A; 105 C; 225 G; 281 T;

alignment_scores:
 Quality: 42.00 Length: 12
 Ratio: 3.818 Gaps: 0
 Percent Similarity: 91.667 Percent Identity: 75.000

alignment_block:

US-08-653-294-28 x V65837 ..

Align seg 1/1 to: V65837 from: 1 to: 981

7 LeuAsnGluArgGluAsnLeuArgIleAlaLeu 18
 ||||||| ||| ::||| ||||||| ::||| |||||||
 598 TTAATGACGCTTTAGAGGATTTAAGATTCCTTG 633

seq_name: N_Geneseq_36:V49262

seq_documentation_block:

ID V49262 standard; DNA; 3023 BP.

AC V49262;
 DT 28-OCT-1998 (first entry)
 DE FELV-B gag/pol gene.
 KW Multivalent vaccine; cat; pathogen; respiratory disease; FELV; FPV; FCV;
 KW digestive disease; feline leukaemia virus; feline panleukopaemia virus;
 KW feline calicivirus; feline immunodeficiency virus; FIV; rabies virus;
 KW vector; envelope glycoprotein; ss.
 OS Feline leukemia virus.
 FH Key
 FT Location/Qualifiers
 CDS 1..1743
 FT /*tag- a
 FT /product= "gag protein"
 CDS 1736..3023
 FT /*tag- b
 FT /product= "pol protein"
 FT /note= "the coding sequence for this protein does
 FT not contain a start codon at the 5' end of
 FT the sequence; the pol protein is generated
 FT by a translational frameshift at the 3' end
 FT of the gag gene; also the 3' end of the gene
 FT contains no stop codon"
 PN FR2751223-A1.
 PD 23-JAN-1998.
 PF 19-JUL-1996; 009337.
 PR 19-JUL-1996; FR-009337.
 PA (INMR) RHONE MERIEUX SA.
 PI Audonnet JCF, Baudu P, Bouchardon A, Riviere MEA;
 DR WPI: 98-112823/11.
 DR P-PSDB: W68402, W68403.
 DT Multi-valent polynucleotide vaccines against feline pathogens -
 PT consist of at least 3 plasmids able to express protective antigens
 PT from specified viruses
 PS Example 9; Fig 5; 42pp; French.
 CC The invention relates to a multivalent vaccine for protecting cats
 CC against several pathogens, especially pathogens associated with
 CC respiratory and digestive diseases. The pathogens are especially
 CC selected from feline leukaemia virus (FELV), feline panleukopaemia
 CC virus (FPV), feline calicivirus (FCV), feline immunodeficiency virus
 CC (FIV), or rabies virus. The vaccines are preferably composed of
 CC polynucleotide sequences encoding 3 antigens, all as part of vectors.
 CC This sequence represents the coding region for the gag/pol proteins
 CC (gag/pol) from the feline leukaemia virus (FELV) sub-type A strain
 CC Glasgow-1. The sequence was sub-cloned into the plasmid pVR1012 to
 CC generate plasmid pPB181 for use in the vaccine.
 SQ Sequence 3023 BP; 824 A; 831 C; 714 G; 654 T;

alignment_scores:

Quality: 42.00 Length: 11
 Ratio: 3.818 Gaps: 0
 Percent Similarity: 100.000 Percent Identity: 72.727

alignment_block:

US-08-653-294-28 x V49262 ..

Align seg 1/1 to: V49262 from: 1 to: 3023

3 LeuAlaThrArgLeuAsnGluArgGluAsn 13
 ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::|||
 757 ATTCAAGCGCGCTTAGGGAACGACGAGAAAC 789

seq_name: N_Geneseq_36:Q29114

seq_documentation_block:

ID Q29114 standard; DNA; 3674 BP.

AC Q29114;
 DT 24-FEB-1993 (first entry)
 DE FELV-A gag/pol fragment.
 KW ALVAC; feline leukemia virus; FELV-A; gag; pol; pFGA-2 gag; PCR;
 KW polymerase chain reaction; vaccinia virus; H6 promoter; PC3FGAG;
 KW PC3FGAGVQ; expression cassette; PC3DOFGAGVQ; VCP83; VCP87; ATI;
 KW rescue virus; VCP97; immunosuppressive region; VCP93; polylinker;
 KW A type inclusion body region; PSD341; ss.

OS Synthetic.
 FH Key Location/Qualifiers
 FT misc_feature 652..654
 FT /*tag= a
 FT /label= Initiation_codon
 PN WO9215672-A.
 PD 17-SEP-1992.
 PF 09-MAR-1992; U01906.
 PR 07-MAR-1991; US-666056.
 PR 11-JUN-1991; US-713967.
 PR 06-MAR-1992; US-847951.
 PA (VIR-) VIROGENETICS CORP.
 PI Cox WI, De Taisne C, Francis J, Gettig RR, Johnson GP,
 PI Limbach KJ, Norton EK, Paoletti E, Perkins ME, Pincus SE,
 PI Riviere M, Tartaglia J, Taylor J;
 DR WPI: 92-331718/40.
 PT Vaccine comprises recombinant, attenuated pox-virus - use for
 PT vaccinating against viral infections such as rabies, hepatitis B,
 PT HIV, HSV, EBV, CMV, mumps etc.
 PS Disclosure: Fig 27; 456pp; English.
 CC The sequence given encodes the feline leukemia virus (FeLV-A) gag
 CC gene. This sequence was used in the construction of an ALVAC-based
 CC recombinant containing the FeLV-A gag gene. The gag/pol sequence was
 CC derived from plasmid pFGA-2 gag. The gag gene was liberated on a 2.5
 CC kb fragment and was amplified by polymerase chain reaction (PCR).
 CC This sequence was aligned with the vaccinia virus H6 promoter. The
 CC FeLV-A pol gene was also included in this construction to yield a
 CC plasmid designated pc3FCGAG. Termination codons were included to form
 CC the plasmid pc3FCGAGVQ. The FeLV gag/pol expression cassette was
 CC excised from this plasmid and designated pc3DORAGVQ. pc3DORAGVQ
 CC was used in standard in vitro recombination assays with vCP83 and
 CC vCP87 as rescue viruses. Recombinants containing the entire FeLV-A
 CC gag/pol sequences and the entire FeLV-A env gene were designated
 CC vCP97, while recombinants containing the same gag/pol sequences and
 CC the entire FeLV-A env lacking the immuno-suppressive region were
 CC designated vCP93. The FeLV-A gag can be inserted into a vaccinia
 CC virus background by including a polylinker sequence flanking the
 CC coding region and using these sequences to insert the gag region into
 CC the A type inclusion body region (ATI) of the plasmid-PSB541. See
 CC also Q35501-864.
 SQ Sequence 3674 BP; 970 A; 1018 C; 883 G; 803 T;

alignment_scores:
 Quality: 42.00 Length: 11
 Ratio: 3.818 Gaps: 0
 Percent Similarity: 100.000 Percent Identity: 72.727

alignment_block:
 US-08-653-294-28 x Q29114 ..
 Align seg 1/1 to: Q29114 from: 1 to: 3674
 3 LeuAlaThrArgLeuAsnGluArgGluAsn 13
 :::::::::::::::::::::::::::::::
 1408 ATTGCAAGCGCGCTAAGGGAACGACGAGAAAC 1440

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[illegible]

Rhabditina; Rhabditoidea; Rhabditiidae; Peloderinae; Caenorhabditis
1 (bases 1 to 360)
Kohara,Y., Mitsuki.H., Nishigaki,A., Motohashi,T., Sugimoto,A. and
Tabata,H.
Title Toward an expression map of the C.elegans genome
JOURNAL Unpublished (1994)
COMMENT Contact: Yuji Kohara
Gene Library Lab
National Institute of Genetics
Yata 1111, Mishima, Shizuoka 411, Japan
Tel: 81-559-81-6854
Fax: 81-559-81-6855
Email: ykohara@lab.nig.ac.jp.

FEATURES
source
1..360
/organism="Caenorhabditis elegans"
/strain="CB1489 him-8(e1489)"
/db_xref="taxon:6239"
/clone="yk19g6"
/sex="hermaphrodite, male"
/tissue_type="whole animal"
/dev_stage="varied"

BASE COUNT 116 a 85 c 79 g 80 t
ORIGIN

alignment_scores:
Quality: 52.00 Length: 17
Ratio: 3.714 Gaps: 0
Percent Similarity: 82.353 Percent Identity: 70.588

alignment_block:
US-08-653-294-28 x D35321 ..

Align seg 1/1 to: D35321 from: 1 to: 360

```

2 ArgLeuAlaThrArgLeuAsnGluArgArgGluAsnLeuArgileAlaLe 18
|||||:::|||||:::|||||:::|||||:::|||||:::||
79 AGATCCGGTGAAGGTTCACCGAAGAAGATCCTCATCTGAGGATTATTCT 128

18 u 18
   |
129 G 129
```

seq_name: gb_estl:D35579

seq_documentation_block:
LOCUS D35579 360 bp mRNA EST 08-AUG-1994
DEFINITION CELK02269F Yuji Kohara unpublished cdNA Caenorhabditis elegans cdNA
clone yk22g 5', mRNA sequence.

ACCESSION D35579
VERSION D35579.1 GI:527030
KEYWORDS EST.
SOURCE Caenorhabditis elegans.
ORGANISM Caenorhabditis elegans
Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditiidae;
Rhabditiina; Rhabditoidea; Rhabditiidae; Peloderinae; Caenorhabditis.
1 (bases 1 to 360)
Kohara,Y., Mitsuki.H., Nishigaki,A., Motohashi,T., Sugimoto,A. and
Tabata,H.
Title Toward an expression map of the C.elegans genome
JOURNAL Unpublished (1994)
COMMENT Contact: Yuji Kohara
Gene Library Lab
National Institute of Genetics
Yata 1111, Mishima, Shizuoka 411, Japan
Tel: 81-559-81-6854
Fax: 81-559-81-6855
Email: ykohara@lab.nig.ac.jp.

FEATURES
source
1..360
/organism="Caenorhabditis elegans"

seq_name: gb_est17:C69958

EST.
human.
Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 748)
NCI-CCAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
On Mar 16, 1998 this sequence version replaced gi:2961758.
Contact: Robert Strausberg, Ph.D.

Life Technologies catalog #: 11548-013
DNA sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html

Seq primer: -40UP from Gibco
High quality sequence stop: 424.
Location/Qualifiers
1. .748
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2324421"
/clone_lib="NCI CGAP_Panl"
/tissue_type="adenocarcinoma"
/lab_host="DH10B"
/note="Organ: pancreas; Vector: pCMV-SPORT6; Site_1: SalI;
Site_2: NotI; Cloned unidirectionally. Primer: Oligo dt.
Average insert size 1.72 kb. Life Technologies catalog #:

```

ores:
  Quality: 50.00
  Ratio: 3.846
  Williarity: 81.250
  Length: 16
  Gaps: 0
  Percent Identity: 68.750

ock:
  94-28 x AR696864
  ..
  from: 1 to: 748
  /1 to: AR696864

```

AACACACAGACTTACCGAGAGAACCTGCGGATCGCGCTCGCTAC 166
_est10:AA151891
ation_block: 255 bp mRNA EST 10-DEC-1996
z001f06.r1 Strataene colon (#937204) Homo sapiens cDNA clone
IMAGE:566435 5', similar to gb:M15497.cdsl HLA CLASS I
HISTOCOMPATIBILITY ANTIGEN, A-24(A-9) A*2401 (HUMAN);, mRNA
sequence.
AA151891
AA151891.1 GI:1720754

Homio sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominiidae; Homo.
1 (bases 1 to 255)
1. Haller, L., Lennon, C., Becker, M., Bonaldo, M. F., Chiapelli, B.,
Chissio, S., Dietrich, N., DuBuque, T., Favello, A., Gish, W.,
Hawkins, M., Hultman, M., Kucab, T., Lacy, M., Le, M., Le, N.,
Mardis, E., Moore, B., Morris, M., Parsons, J., Prange, C., Rifkin, L.,
Rohlfing, T., Schellenberg, K., Soares, M. B., Tan, F., Thierry-Mieg, J.,

Trevaskis, E., Underwood, K., Wohldmann, P., Waterston, R., Wilson, R. and Marra, M.

Generation and analysis of 280,000 human expressed sequence tags
Genome Res. 6 (9), 807-828 (1996)

TITLE

JOURNAL

MEDLINE

COMMENT

97044478

On May 8, 1995 this sequence version replaced gi:800234.

Contact: Wilson RK

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800

Fax: 314 286 1810

Email: estevan@wustl.edu

This clone is available royalty-free through LLNL; contact the

IMAGE Consortium (info@image.llnl.gov) for further information.

Trace considered overall poor quality

Seq primer: -28W13 rev2 from Amersham

High quality sequence stop: 1.

FEATURES

source

1. .255

/organism="Homo sapiens"

/db_xref="CDR:4590888"

/db_xref="taxon:9606"

/clone="IMAGE:566435"

/clone_lib="Stratagene colon (#937204)"

/lab_host="SOLR cells (kanamycin resistant)"

/note="Organ: colon; vector: pBluescript SK-; Site: 1:

ECORI; Site: 2: XhoI; Cloned unidirectionally. Primer:

Oligo df. T-84 colonic epithelial cell line. Average

insert size: 1.0 kb; Uni-ZAP XR Vector; -5' adaptor

sequence: 5' GAATTCGCGCAG 3' -3' adaptor sequence: 5'

CTCGAGTTTTTTTTTTTTTTT 3'"

BASE COUNT 57 a 70 c 75 g 44 t 9 others

ORIGIN

alignment_scores:

Quality: 49.00 Length: 10

Ratio: 4.900 Gaps: 0

Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:

US-08-653-294-28 x AA151891

Align seg 1/1 to: AA151891 from: 1 to: 255

11 ArgGluAsnLeuArgIleAlaLeuArgTyr 20

|||||

77 CGAGAGAACCTCGGATCGCNCCTCGGTAC 106

seq_name: gb_est36:AV186046

seq_documentation_block:

LOCUS AV186046 360 bp mRNA EST 22-JUL-1999

DEFINITION AV186046 Yuji Kohara unpublished cDNA:Strain N2 hermaphrodite

embryo Caenorhabditis elegans cDNA clone yk494e6 5', mRNA sequence.

ACCESSION AV186046

VERSION AV186046.1 GI:5568029

KEYWORDS EST.

SOURCE Caenorhabditis elegans.

ORGANISM Caenorhabditis elegans

Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida;

Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.

1 (bases 1 to 360)

Kohara, Y., Shin-i, T., Thierry-Mieg, J., Thierry-Mieg, D., Mitsuki, H.,

Nishigaki, A., Motohashi, T., Zeng, Q., Watanabe, H., Sugimoto, A.,

Sano, M., Miyata, A., Mitani, Y., Iida, K., Uesugi, H., Sugiyama, Y. and

Nomoto, H.

Expressed genes in C. elegans

Unpublished (1999)

On Dec 20, 1995 this sequence version replaced gi:1135120.

Contact: Yuji Kohara

Gene Library Lab

National Institute of Genetics

FEATURES

source

1. .393

/organism="Lycopersicon esculentum"

/cultivar="Ril-13 (Rio Grande x Money Maker)"

/db_xref="taxon:4081"

Yata 1111, Mishima, Shizuoka 411, Japan

Tel: 81-559-81-6854

Fax: 81-559-81-6855

Email: ykohara@lab.nig.ac.jp.

FEATURES

source

1. .360

/organism="Caenorhabditis elegans"

/strain="N2"

/db_xref="taxon:6239"

/clone="yk494e6"

/clone_lib="Yuji Kohara unpublished cDNA:Strain N2

hermaphrodite embryo"

/sex="hermaphrodite"

/dev_stage="embryo"

BASE COUNT 103 a 90 c 109 g 58 t

ORIGIN

alignment_scores:

Quality: 49.00 Length: 19

Ratio: 3.062 Gaps: 0

Percent Similarity: 84.211 Percent Identity: 52.632

alignment_block:

US-08-653-294-28 x AV186046/rev

Align seg 1/1 to reverse of: AV186046 from: 1 to: 360

2 ArgLeuAlaThrArgLeuAsnGluArgGluAsnLeuArgIleAlaLe 18

174 CGTTGTGCTCAGCGCTTCGGGAGCGACGACGACGCGCTTCGCT 125

18 uArgTyr 20

|||||

124 CCGATTT 118

seq_name: gb_est33:AI777709

seq_documentation_block:

LOCUS AI777709 393 bp mRNA EST 29-JUN-1999

DEFINITION EST258504 tomato susceptible, Cornell Lycopersicon esculentum cDNA

clone CLES2H21, mRNA sequence.

ACCESSION AI777709

VERSION AI777709.1 GI:5275666

KEYWORDS EST.

SOURCE tomato.

ORGANISM Lycopersicon esculentum

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons; core

eudicots; Asteridae; euasterids I; Solanales; Solanaceae; Solanum;

Potatoe; Lycopersicon.

REFERENCE 1 (bases 1 to 393)

D' Ascenzo, M., He, X., Lyman, J., Matern, A.L., Vision, T., Holt, I.E.,

Liang, F., Upton, J., Ronning, C.M., Craven, M.B., Fujii, C.Y.,

Bowman, C.L., Nierman, W., Fraser, C.M., Venter, J.C., Tanksley, S.D.,

Giovannoni, J.J. and Martin, G.B.

Generation of ESTs from Pseudomonas susceptible tomato

Unpublished (1999)

On Jun 5, 1998 this sequence version replaced gi:3187603.

Other ESTs: TC2175

Contact: David Frisch

Clemson University Genomics Institute

Clemson University

100 Jordan Hall, Clemson, SC 29634, USA

Tel: 864 656 4366

Fax: 864 656 4293

Email: dfrisch@CLEMSON.EDU

5 prime sequence.

Location/Qualifiers

1. .393

/organism="Lycopersicon esculentum"

/cultivar="Ril-13 (Rio Grande x Money Maker)"

/db_xref="taxon:4081"

```

/clone="CLES2H21"
/clone_lib="tomato susceptible, Cornell"
/tissue_type="leaf"
/dev_stage="4-week old"
/lab_host="SOLR"
/note="Vector: pBlueScript SK(-); Site_1: EcoRI; Site_2:
XhoI; CLES - Tomato Pseudomonas Susceptible EST Library.
Directionally cloned cDNAs inserted into pBlueScript
SK(-) at 5' end with EcoRI and 3' end with XhoI site."
BASE COUNT      119 a 57 c 70 g 147 t
ORIGIN

alignment_scores:
  Quality: 49.00      Length: 20
  Ratio: 3.267       Gaps: 0
  Percent Similarity: 75.000  Percent Identity: 45.000

alignment_block:
US-08-653-294-28 x AI777709/rev ..
Align seg 1/1 to reverse of: AI777709 from: 1 to: 393

1 TyrArgLeuAlaThrArgLeuAsnGluArgArgGluAsnLeuArgIleAl 17
||||| ||| :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
365 TATATATATTATACAAAGAACAAATACAAACAGAGAAATCTAAATCTAGC 316

17 aLeuArgTyr 20
|:|:|:|:|:|
68 AATCAAAATAT 306

seq_name: gb_est33:AI774937

seq_documentation_block: 496 bp mRNA EST 29-JUN-1999
LOCUS AI774937
DEFINITION EST256037 tomato resistant, Cornell Lycopersicon esculentum cDNA
clone cLER13H12, mRNA sequence.
ACCESSION AI774937
VERSION AI774937.1 GI:5272978
KEYWORDS EST.
SOURCE tomato.
ORGANISM Lycopersicon esculentum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons; core
eudicots; Asteridae; euasterids I; Solanales; Solanaceae; Solanum;
Potatoe; Lycopersicon.
1 (bases 1 to 496)
D'Ascenzo,M., He,X., Lyman,J., Matern,A.L., Vision,T., Holt,I.E.,
Liang,F., Upton,J., Ronning,C.M., Craven,M.B., Fujii,C.Y.,
Bowman,C.L., Nierman,W., Fraser,C.M., Venter,J.C., Tanksley,S.D.,
Giovannoni,J.J. and Martin,G.B.
Generation of ESTs from Pseudomonas resistant tomato
Unpublished (1999)
On May 18, 1998 this sequence version replaced gi:3136691.
Other ESTs: TC2175
Contact: David Frisch
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 4366
Fax: 864 656 4293
Email: dfrisch@CLEMSON.EDU
5 prime sequence.
FEATURES
  Location/Qualifiers
    1..496
      /organism="Lycopersicon esculentum"
      /cultivar="R11-12 (35S::Pto in Rio Grande x Money Maker)"
      /db_xref="taxon:4081"
      /clone="CLES2H21"
      /clone_lib="tomato resistant, Cornell"
      /tissue_type="leaf"
      /dev_stage="4-week old"
      /lab_host="SOLR"

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/note="Vector: pBlueScript SK(-); Site_1: EcoRI; Site_2:
XhoI; cLER - Tomato Pseudomonas Resistant EST Library.
Directionally cloned cDNAs inserted into pBlueScript
SK(-) at 5' end with EcoRI and 3' end with XhoI site."
BASE COUNT      174 a 88 c 81 g 153 t
ORIGIN

alignment_scores:
  Quality: 49.00      Length: 20
  Ratio: 3.267       Gaps: 0
  Percent Similarity: 75.000  Percent Identity: 45.000

alignment_block:
US-08-653-294-28 x AI774937 ..
Align seg 1/1 to: AI774937 from: 1 to: 496

1 TyrArgLeuAlaThrArgLeuAsnGluArgArgGluAsnLeuArgIleAl 17
||||| ||| :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
18 TATATATATTATACAAAGAACAAATACAAACAGAGAAATCTAAATCTAGC 67

17 aLeuArgTyr 20
|:|:|:|:|:|
68 AATCAAAATAT 77

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: February 8, 2000, 04:05:43 ; Search time 133.56 seconds
(without alignments)
3.547 Million cell updates/sec

Title: US-08-653-294-29

Perfect score: 99

Sequence: 1 YRLAIRLNERENLTALRY 20

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 188963 seqs, 23686106 residues

Total number of hits satisfying chosen parameters: 188963

Minimum DB seq length: 0

Maximum DB seq length: 1000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : A_Geneseq_36.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	99	100.0	20	1	R92909	HLA-B2702 CTL modu
2	99	100.0	20	1	W33792	Peptide B2702.84-7
3	94	94.9	20	1	R92910	HLA-B2702 CTL modu
4	94	94.9	20	1	W33793	Peptide B2702.84-7
5	93	93.9	20	1	R92907	HLA-B2702 CTL modu
6	93	93.9	20	1	R95428	HLA-B2702 84-75-84
7	93	93.9	20	1	W33778	Immunomodulating d
8	88	88.9	20	1	R92908	HLA-B2702 CTL modu
9	88	88.9	20	1	W33791	Peptide B2702.84-7
10	80	80.8	20	1	R95430	HLA-B2702 84-75T/7
11	51.5	52.0	20	1	R92911	HLA-B2702 CTL modu
12	51.5	52.0	20	1	W33779	Immunomodulating d
13	50	50.5	10	1	R83095	HLA-B2702 CTL modu
14	50	50.5	10	1	R95426	HLA-B2702.75-84(f)
15	50	50.5	10	1	W33788	Peptide B2702.75-8
16	49	49.5	10	1	W47266	Immunomodulatory p
17	44	44.4	10	1	R41208	Peptide fragment o
18	44	44.4	10	1	R83062	HLA-B2702 CTL modu
19	44	44.4	10	1	R95413	Alpha1-helix of HL
20	44	44.4	10	1	W07512	T-cell modulating
21	44	44.4	10	1	W47265	Immunomodulatory p
22	44	44.4	10	1	W47268	Immunomodulatory p
23	44	44.4	10	1	W47270	Immunomodulatory p
24	44	44.4	10	1	W33784	Peptide B2702.75-8
25	44	44.4	15	1	R92912	HLA-B2702 CTL modu
26	44	44.4	15	1	W33795	Peptide B2702.70-8
27	44	44.4	25	1	R41205	Peptide fragment o
28	44	44.4	25	1	R48286	Peptide fragment o
29	44	44.4	25	1	R83090	HLA-B2702 CTL modu
30	44	44.4	25	1	R83093	HLA-B2702 CTL modul
31	44	44.4	25	1	R95416	HLA-B2702.60-84. C
32	44	44.4	25	1	R95422	HLA-B2702.60-84. C
33	44	44.4	25	1	W33794	Peptide B2702.60-8
34	44	44.4	184	1	Y06801	Peptide seq ID No:

35 44 44.4 362 1 R03142 Sequence of HLA-B*
36 44 44.4 362 1 R03144 Sequence of HLA-B*
37 44 44.4 362 1 R12463 HLA-B*53 exon. HLA
38 43 43.4 10 1 W07522 T-cell modulating
39 43 43.4 1849 1 W17900 Photolabidus lumin
40 43 43.4 1849 1 W56573 Toxin TcdAII, enco
41 43 43.4 2516 1 W17899 Photolabidus lumin
42 43 43.4 2516 1 W56572 Toxin TcdA, encode
43 42.5 42.9 373 1 Y00067 Enterococcus faeca
44 42.5 42.9 406 1 Y00066 Enterococcus faeca
45 42 42.4 20 1 R92913 HLA-B*7 CTL modul

ALIGNMENTS

RESULT 1

R92909 ID R92909 standard; peptide; 20 AA.
AC R92909;
DT 16-MAY-1996 (first entry)
DE HLA-B2702 CTL modulating peptide (B2702.84-75/75-84(T)).
KW Cytotoxic T lymphocyte; CTL; major histocompatibility complex; MHC;
KW Immunosuppressant; graft versus host disorder; transplantation; therapy;
KW class I MHC; HLA-B2702.
OS Synthetic.
PN W09526979-Al.
PD 12-OCT-1995.
PF 05-APR-1995; U04349.
PR 05-APR-1994; US-222851.
PA (STRD) UNIV LELAND STANFORD JUNIOR.
PI Clayberger C, Krensky AM, Parham P;
DR WPI: 95-359582/46.
PT Extension of acceptance period of transplants from MHC unmatched
PT donor hosts - using Class I B75-84 MHC antigen of the recipient
PT host
PS Example 15; Page 36; 80pp; English.
CC R83061-R83085, R83090-R83096 and R92907-R92913 represent fragments of
CC class I major histocompatibility complex (MHC) antigens. This sequence
CC is an inverted dimer of residues 75-84 of the alpha-1 domain of the class
CC I MHC HLA-B2702. These sequences can be used to extend the period of
CC acceptance by a recipient of a transplant from an MHC unmatched donor.
CC The peptides are administered to a patient in conjunction with a
CC subtherapeutic amount of an immunosuppressant. This is administered to
CC the patient for a limited period of time (compared to the lifetime
CC administration for current treatments). The peptides particularly
CC modulate (or inhibit) the activity of the cytotoxic T lymphocytes (CTLs)
CC of the patient.
SQ Sequence 20 AA;

Query Match 100.0%; Score 99; DB 1; Length 20;

Best Local Similarity 100.0%; Pred. No. 3e-10; Mismatches 0; Indels 0; Gaps 0;

Matches 20; Conservative 0;

QY 1 YRLAIRLNERENLTALRY 20

DB 1 YRLAIRLNERENLTALRY 20

RESULT 2

W33792

ID W33792 standard; peptide; 20 AA.

AC W33792;

DT 19-JUN-1998 (first entry)

DE Peptide B2702.84-75/75-84T tested for immunomodulating activity.

KW Immunomodulating dimer; immunosuppressant drug; CTL activation;

KW transplantation; autoimmune disease; Class I HLA-B alpha-1 domain;

KW rejection.

OS Synthetic.

OS Homo sapiens.

PN W09744351-Al.

PD 27-NOV-1997.

PF 22-MAY-1997; U08689.
 PR (STRD) UNIV LELAND STANFORD JUNIOR.
 PI Beulow R, Clayberger C, Krensky AM;
 DR WPI; 98-086530/08.
 PT New immunomodulating dimer peptide(s) - based on a Class I HLA-B
 PT alpha-1 domain, used for preventing rejection of transplants or
 PT treating autoimmune diseases
 PS Example 1; Page 19; 41pp; English.
 CC Peptides W3784-98 and W3778-9 were assayed for their immunomodulating
 CC activity. A peptide-type compound or variant is claimed which has
 CC immunomodulating activity, including the N-terminal acylated and/or
 CC C-terminal amidated or esterified forms of up to 60 amino acids, where
 CC the peptide-type compound comprises the formula: A-B, where A, B =
 CC (R aa76-77L) (aa79-84) or (aa84-79) (Laa77-76R); aa76 = E or V; aa77 =
 CC D, S or N; aa79 = R or G; aa80 = I or N; aa81, aa84 = a hydrophobic or
 CC small amino acid; aa82 = R or L; aa83 = G or R; and aa represents amino
 CC acid. The sequence in the brackets may optionally be absent or truncated
 CC at any peptide type bond within the brackets. The compounds comprise
 CC amino acid sequences related to a Class I HLA-B alpha1 domain (positions
 CC 79-84). They can be used to inhibit cytotoxic T-lymphocytes (CTL) from
 CC undesirably attacking cells in a host or in vitro. They can also be
 CC used in combination with antigenic peptides or proteins of interest to
 CC activate CTLs. They can also inhibit the proliferation of T cells in
 CC response to anti-CD3. The peptide can be used for preventing rejection
 CC of transplants or for treating autoimmune diseases, e.g. diabetes,
 CC rheumatoid arthritis and lupus erythematosus. The products can also be
 CC used for detection and diagnosis.
 SQ Sequence 20 AA;

Query Match 100.0%; Score 99; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 3e-10;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 YRLAIRLNERENLTALRY 20
 DB 1 YRLAIRLNERENLTALRY 20
 ||||| ||||| ||||| ||||| |||||

RESULT 3
 ID R92910 standard; peptide; 20 AA.
 AC R92910; (first entry)
 DE HLA-B2702 CTL modulating peptide (B2702.84-75(T)/75-84(T)).
 KW Cytotoxic T lymphocyte; CTL; major histocompatibility complex; MHC;
 KW immunosuppressant; graft versus host disorder; transplantation; therapy;
 KW class I MHC; HLA-B2702.
 OS Synthetic.
 PN W09526979-A1.
 PD 12-OCT-1995.
 PF 05-APR-1995; U04349.
 PR (STRD) UNIV LELAND STANFORD JUNIOR.
 PI Clayberger C, Krensky AM, Parham P;
 DR WPI; 95-358562/46.
 PT Extension of acceptance period of transplants from MHC unmatched
 PT donor hosts - using Class I B75-84 MHC antigen of the recipient
 PT host
 PS Example 15; Page 36; 80pp; English.
 CC R83061-R83085, R83090-R83096 and R92907-R92913 represent fragments of
 CC class I major histocompatibility complex (MHC) antigens. This sequence
 CC is an inverted dimer of residues 75-84 of the alpha-1 domain of the class
 CC I MHC HLA-B2702. These sequences can be used to extend the period of
 CC acceptance by a recipient of a transplant from an MHC unmatched donor.
 CC The peptides are administered to a patient in conjunction with a
 CC subtherapeutic amount of an immunosuppressant. This is administered to
 CC the patient for a limited period of time (compared to the lifetime
 CC administration for current treatments). The peptides particularly
 CC modulate (or inhibit) the activity of the cytotoxic T lymphocytes (CTLs)
 CC of the patient.
 SQ Sequence 20 AA;

Query Match 94.9%; Score 94; DB 1; Length 20;
 Best Local Similarity 95.0%; Pred. No. 2e-09;
 Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 OY 1 YRLAIRLNERENLTALRY 20
 DB 1 YRLAIRLNERENLTALRY 20
 ||||| ||||| ||||| ||||| |||||

RESULT 4
 ID W37793 standard; peptide; 20 AA.
 AC W37793;
 DT 19-JUN-1998 (first entry)
 DE Peptide B2702.84-75(T)/75-84(T) tested for immunomodulating activity.
 KW Immunomodulating dimer; immunosuppressant drug; CTL activation;
 KW transplantation; autoimmune disease; Class I HLA-B alpha-1 domain;
 KW rejection.
 OS Synthetic.
 OS Homo sapiens.
 PN W09744351-A1.
 PD 27-NOV-1997.
 PF 22-MAY-1997; U08689.
 PR 24-MAY-1996; US-653294.
 PA (STRD) UNIV LELAND STANFORD JUNIOR.
 PI Beulow R, Clayberger C, Krensky AM;
 DR WPI; 98-086530/08.
 PT New immunomodulating dimer peptide(s) - based on a Class I HLA-B
 PT alpha-1 domain, used for preventing rejection of transplants or
 PT treating autoimmune diseases
 PS Example 1; Page 19; 41pp; English.
 CC Peptides W3784-98 and W3778-9 were assayed for their immunomodulating
 CC activity. A peptide-type compound or variant is claimed which has
 CC immunomodulating activity, including the N-terminal acylated and/or
 CC C-terminal amidated or esterified forms of up to 60 amino acids, where
 CC the peptide-type compound comprises the formula: A-B, where A, B =
 CC (R aa76-77L) (aa79-84) or (aa84-79) (Laa77-76R); aa76 = E or V; aa77 =
 CC D, S or N; aa79 = R or G; aa80 = I or N; aa81, aa84 = a hydrophobic or
 CC small amino acid; aa82 = R or L; aa83 = G or R; and aa represents amino
 CC acid. The sequence in the brackets may optionally be absent or truncated
 CC at any peptide type bond within the brackets. The compounds comprise
 CC amino acid sequences related to a Class I HLA-B alpha1 domain (positions
 CC 79-84). They can be used to inhibit cytotoxic T-lymphocytes (CTL) from
 CC undesirably attacking cells in a host or in vitro. They can also be
 CC used in combination with antigenic peptides or proteins of interest to
 CC activate CTLs. They can also inhibit the proliferation of T cells in
 CC response to anti-CD3. The peptide can be used for preventing rejection
 CC of transplants or for treating autoimmune diseases, e.g. diabetes,
 CC rheumatoid arthritis and lupus erythematosus. The products can also be
 CC used for detection and diagnosis.
 SQ Sequence 20 AA;

Query Match 94.9%; Score 94; DB 1; Length 20;
 Best Local Similarity 95.0%; Pred. No. 2e-09;
 Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 OY 1 YRLAIRLNERENLTALRY 20
 DB 1 YRLAIRLNERENLTALRY 20
 ||||| ||||| ||||| ||||| |||||

RESULT 5
 ID R92907 standard; peptide; 20 AA.
 AC R92907;
 DT 16-MAY-1996 (first entry)
 DE HLA-B2702 CTL modulating peptide (B2702.84-75/75-84).
 KW Cytotoxic T lymphocyte; CTL; major histocompatibility complex; MHC;
 KW immunosuppressant; graft versus host disorder; transplantation; therapy;
 KW class I MHC; HLA-B2702.

OS Synthetic.
 PN W09526979-A1.
 PD 12-OCT-1995.
 PF 05-APR-1995; U04349.
 PR 05-APR-1994; US-222851.
 PA (STRD) UNIV LELAND STANFORD JUNIOR.
 PI Clayberger C, Krensky AM, Parham P;
 DR WPI: 95-358582/46.
 PT Extension of acceptance period of transplants from MHC unmatched
 PT donor hosts - using Class I B75-84 MHC antigen of the recipient
 PT host
 PS Example 15; Page 36; 80pp; English.
 CC R83061-R83085, R83090-R83096 and R92907-R92914 represent fragments of
 CC class I major histocompatibility complex (MHC) antigens. This sequence
 CC is an inverted dimer of residues 75-84 of the alpha-1 domain of the class
 CC I MHC HLA-B*2702. These sequences can be used to extend the period of
 CC acceptance by a recipient of a transplant from an MHC unmatched donor.
 CC The peptides are administered to a patient in conjunction with a
 CC subtherapeutic amount of an immunosuppressant. This is administered to
 CC the patient for a limited period of time (compared to the lifetime
 CC administration for current treatments). The peptides: particularly
 CC modulate (or inhibit) the activity of the cytotoxic T lymphocytes (CTLs)
 CC of the patient.
 SQ Sequence 20 AA;

Query Match 93.9%; Score 93; DB 1; Length 20;
 Best Local Similarity 95.0%; Pred. No. 2.9e-09;
 Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YRLAIRLNERENLRALRY 20
 |||||
 DB 1 YRLAIRLNERENLRALRY 20

RESULT 6.

ID R95428 standard; peptide; 20 AA.
 AC R95428;
 DT 12-NOV-1996 (first entry)
 DE HLA-B*2702 84-75-84 palindromic.
 KW HLA; p74; alpha1-helix; human-leucocyte-associated antigen; inhibitor;
 KW T-cell lysate; membrane protein; mammal; heat shock protein; Hsc70; APC;
 KW B cell; calcium influx; cytotoxic T lymphocyte; CTL; differentiation;
 KW cytolysis; antigen presenting cell.
 OS Synthetic.
 PN W09513288-A1.
 PD 18-MAY-1995.
 PF 10-NOV-1994; U12985.
 PR 10-NOV-1993; US-150493.
 PA (STRD) UNIV LELAND STANFORD JUNIOR.
 PI Clayberger C, Krensky AM;
 DR WPI: 95-194027/25.
 PT Compsns. comprising lymphoid surface membrane proteins - which may
 PT inhibit cytolytic activity and differentiation of CTLs.

PS Example; Page 12; 29pp; English.
 CC R95413, and R95415-R95431 represent palindromes and fragments of
 CC human-leucocyte-associated antigens. This sequence represents the
 CC HLA-B*2702 84-75-84 palindromic. These sequences can be used to isolate
 CC the protein p74 from a T-cell lysate. p74 is a T-cell surface membrane
 CC protein associated with T-cell activation in mammalian T-cells, and is
 CC also immunologically cross reactive with the heat shock protein Hsc70.
 CC p74 is found in a limited number of cell types, but is particularly
 CC expressed on B and T cells. p74 can be isolated by lysis of a suitable
 CC cell with an amphoteric detergent, and then passed through an affinity
 CC column containing a covalently bound HLA-B*2702 palindromic peptide.
 CC Compositions comprising the extracellular fragment of p74 combined with
 CC HLA-B*2702 60-84 (see R95416), induces calcium influx, and inhibits
 CC cytotoxic T lymphocyte (CTL) differentiation or cytolysis. Candidate
 CC compounds can be screened for their effect on the cytolytic activity of
 CC T-cells, by combining them with the extracellular portion of p74 and
 CC determining the amount of binding between the candidate compound and p74.
 CC Modulation of CTL activity can be inhibited in a cellular composition

CC containing T-cells and antigen presenting cells (APCs), by adding to the
 CC mix the extracellular portion of p74, in an amount sufficient to compete
 CC with p74 for the binding of the p74 ligand.
 SQ Sequence 20 AA;

Query Match 93.9%; Score 93; DB 1; Length 20;
 Best Local Similarity 95.0%; Pred. No. 2.9e-09;
 Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YRLAIRLNERENLRALRY 20
 |||||
 DB 1 YRLAIRLNERENLRALRY 20

RESULT 7

W33778
 ID W33778 standard; peptide; 20 AA.
 AC W33778;
 DT 19-JUN-1998 (first entry)
 DE Immunomodulating dimer peptide #1.
 DE Immunomodulating dimer; immunosuppressant drug; CTL activation;
 KW transplacental; autoimmune disease; Class I HLA-B alpha-1 domain;
 KW rejection.
 OS Synthetic.
 OS Homo sapiens.
 PN W09744351-A1.
 PD 27-NOV-1997.
 PF 22-MAY-1997; U08689.
 PR 24-MAY-1996; US-653294.
 PA (STRD) UNIV LELAND STANFORD JUNIOR.
 PI Beulow R, Clayberger C, Krensky AM;
 DR WPI: 98-086530/08
 PT New immunomodulating dimer peptide(s) - based on a Class I HLA-B
 PT alpha-1 domain, used for preventing rejection of transplants or
 PT treating autoimmune diseases

PS Claim 16; Page 35; 41pp; English.
 CC This sequence represents a specifically claimed immunomodulating
 CC dimer peptide of the invention. A peptide-type compound or variant is
 CC claimed which has immunomodulating activity, including the N-terminal
 CC acylated and/or C-terminal amidated or esterified forms of up to 60
 CC amino acids, where the peptide-type compound comprises the formula: A-B,
 CC where A, B = (R aa76-77L) (aa79-84) or (aa84-79) (Laa77-76R); aa76 = E or
 CC V; aa77 = D, S or N; aa79 = R or G; aa80 = I or N; aa81, aa84 = a
 CC hydrophobic or small amino acid; aa82 = R or L; aa83 = G or R; and aa
 CC represents amino acid. The sequence in the brackets may optionally be
 CC absent or truncated at any peptide type bond within the brackets. The
 CC compounds comprise amino acid sequences related to a Class I HLA-B
 CC alpha1 domain (positions 79-84). They can be used to inhibit cytotoxic
 CC T-lymphocytes (CTL) from undesirably attacking cells in a host or in
 CC vitro. They can also be used in combination with antigenic peptides or
 CC proteins of interest to activate CTLs. They can also inhibit the
 CC proliferation of T cells in response to anti-CD3. The peptide can be
 CC used for preventing rejection of transplants or for treating autoimmune
 CC diseases, e.g. diabetes, rheumatoid arthritis and lupus erythematosus.
 CC The products can also be used for detection and diagnosis.

SQ Sequence 20 AA;

Query Match 93.9%; Score 93; DB 1; Length 20;
 Best Local Similarity 95.0%; Pred. No. 2.9e-09;
 Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YRLAIRLNERENLRALRY 20
 |||||
 DB 1 YRLAIRLNERENLRALRY 20

RESULT 8

R92908
 ID R92908 standard; peptide; 20 AA.
 AC R92908;
 DT 16-MAY-1996 (first entry)

DE HLA-B2702 CTL modulating peptide (B2702.84-75(T)/75-84).
 KW Cytotoxic T lymphocyte; CTL; major histocompatibility complex; MHC;
 KW immunosuppressant; graft versus host disorder; transplantation; therapy;
 KW class I MHC; HLA-B2702.
 OS Synthetic.
 PN WO9526979-A1.
 PD 12-OCT-1995.
 PF 05-APR-1995; U04349.
 PR 05-APR-1994; US-222851.
 PA (STRD) UNIV LELAND STANFORD JUNIOR.
 PI Clayberger C, Krensky AM, Parham P;
 DR WPI; 95-358582/46.
 PT Extension of acceptance period of transplants from MHC unmatched
 PT donor hosts - using Class I B75-84 MHC antigen of the recipient
 PT host
 PS Example 15; Page 36; 80pp; English.
 CC R83061-R83085, R83090-R83096 and R92907-R92914 represent fragments of
 CC class I major histocompatibility complex (MHC) antigens. This sequence
 CC is an inverted dimer of residues 75-84 of the alpha-1 domain of the class
 CC I MHC HLA-B2702. These sequences can be used to extend the period of
 CC acceptance by a recipient of a transplant from an MHC unmatched donor.
 CC The peptides are administered to a patient in conjunction with a
 CC subtherapeutic amount of an immunosuppressant. This is administered to
 CC the patient for a limited period of time (compared to the lifetime
 CC administration for current treatments). The peptides particularly
 CC modulate (or inhibit) the activity of the cytotoxic T lymphocytes (CTLs)
 CC of the patient.
 SQ Sequence 20 AA;

Query Match 88.9%; Score 88; DB 1; Length 20;
 Best Local Similarity 90.0%; Pred. No. 2e-08;
 Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 YRLAIRLNERRENLRTALRY 20
 ||||| ||||| ||||| |||||
 Db 1 YRLATRLNERRENLRTALRY 20

RESULT 9

W33791
 ID W33791 standard; peptide; 20 AA.
 AC W33791;
 DE 19-JUN-1998 (first entry)
 DT Peptide B2702.84-75(T)/75-84 tested for immunomodulating activity.
 KW Immunomodulating dimer; immunosuppressant drug; CTL activation;
 KW transplantation; autoimmune disease; Class I HLA-B alpha-1 domain;
 KW rejection.
 OS Synthetic.
 OS Homo sapiens.
 PN WO9744351-A1.
 PD 27-NOV-1997; U08689.
 PF 22-MAY-1997; U08689.
 PR 24-MAY-1996; US-653294.
 PA (STRD) UNIV LELAND STANFORD JUNIOR.
 PI Beulow R, Clayberger C, Krensky AM;
 DR WPI; 98-086530/08.
 PT New immunomodulating dimer peptide(s) - based on a Class I HLA-B
 PT alpha-1 domain, used for preventing rejection of transplants or
 PT treating autoimmune diseases
 PS Example 1; Page 19; 41pp; English.
 CC Peptides W33784-98 and W33778-9 were assayed for their immunomodulating
 CC activity. A peptide-type compound or variant is claimed which has
 CC immunomodulating activity, including the N-terminal acylated and/or
 CC C-terminal amidated or esterified forms of up to 60 amino acids, where
 CC the peptide-type compound comprises the formula: A-B, where A, B =
 CC (R aa76-77L) (aa79-84) or (aa84-79) (Laa77-76R); aa76 - E or V; aa77 -
 CC D, S or N; aa79 = R or G; aa80 = I or N; aa81, aa84 = a hydrophobic or
 CC small amino acid; aa82 = R or L; aa83 = G or R; and aa represents amino
 CC acid. The sequence in the brackets may optionally be absent or truncated
 CC at any peptide type bond within the brackets. The compounds comprise
 CC amino acid sequences related to a Class I HLA-B alpha domain (positions
 CC 79-84). They can be used to inhibit cytotoxic T-lymphocytes (CTL) from

CC undesirably attacking cells in a host or in vitro. They can also be
 CC used in combination with antigenic peptides or proteins of interest to
 CC activate CTLs. They can also inhibit the proliferation of T cells in
 CC response to anti-CD3. The peptide can be used for preventing rejection
 CC of transplants or for treating autoimmune diseases, e.g. diabetes,
 CC rheumatoid arthritis and lupus erythematosus. The products can also be
 CC used for detection and diagnosis.
 SQ Sequence 20 AA;

Query Match 88.9%; Score 88; DB 1; Length 20;
 Best Local Similarity 90.0%; Pred. No. 2e-08;
 Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 YRLAIRLNERRENLRTALRY 20
 ||||| ||||| ||||| |||||
 Db 1 YRLATRLNERRENLRTALRY 20

RESULT 10

R95430
 ID R95430 standard; peptide; 20 AA.
 AC R95430;
 DT 12-NOV-1996 (first entry)
 DE HLA-B2702.84-75(T)/75-84T palindromic.
 KW HLA; p74; alpha1-helix; human-leucocyte-associated antigen; inhibitor;
 KW T-cell lysate; membrane protein; mammal; heat shock protein; Hsc70; APC;
 KW B cell; calcium influx; cytotoxic T lymphocyte; CTL; differentiation;
 KW cytolysis; antigen presenting cell.
 OS Synthetic.
 PN WO9513288-A1.
 PD 18-MAY-1995.
 PF 10-NOV-1994; U12985.
 PR 10-NOV-1993; US-150493.
 PA (STRD) UNIV LELAND STANFORD JUNIOR.
 PI Clayberger C, Krensky AM;
 DR WPI; 95-194027/25.
 PT Compens. comprising lymphoid surface membrane proteins - which may
 PT inhibit cytolytic activity and differentiation of CTLs.
 PS Example; Page 12; 29pp; English.
 CC R95413, and R95415-R95431 represent palindromes and fragments of
 CC human-leucocyte-associated antigens. This sequence represents the
 CC HLA-B2702.84-75(T)/75-84T palindromic. These sequences can be used to
 CC isolate the protein p74 from a T-cell lysate. p74 is a T-cell surface
 CC membrane protein associated with T-cell activation in mammalian T-cells,
 CC and is also immunologically cross reactive with the heat shock protein
 CC Hsc70. p74 is found in a limited number of cell types, but is
 CC particularly expressed on B and T cells. p74 can be isolated by lysis of
 CC a suitable cell with an amphoteric detergent, and then passed through an
 CC affinity column containing a covalently bound HLA-B2702 palindromic
 CC peptide. Compositions comprising the extracellular fragment of p74
 CC combined with HLA-B2702.60-84 (see R95416), induces calcium influx, and
 CC inhibits cytotoxic T lymphocyte (CTL) differentiation or cytolysis.
 CC Candidate compounds can be screened for their effect on the cytolytic
 CC activity of T-cells, by combining them with the extracellular portion of
 CC p74 and determining the amount of binding between the candidate compound
 CC and p74. Modulation of CTL activity can be inhibited in a cellular
 CC composition containing T-cells and antigen presenting cells (APCs), by
 CC adding to the mix the extracellular portion of p74, in an amount
 CC sufficient to compete with p74 for the binding of the p74 ligand.
 SQ Sequence 20 AA;

Query Match 80.8%; Score 80; DB 1; Length 20;
 Best Local Similarity 89.5%; Pred. No. 4e-07;
 Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 YRLAIRLNERRENLRTALR 19
 ||||| ||||| ||||| |||||
 Db 1 YRLAIRNETRENLRTALR 19

RESULT 11

CC represents amino acid. The sequence in the brackets may optionally be
 CC absent or truncated at any peptide type bond within the brackets. The
 CC compounds comprise amino acid sequences related to a Class I HLA-B
 CC alpha domain (positions 75-84). They can be used to inhibit cytotoxic
 CC T-lymphocytes (CTL) from undesirably attacking cells in a host or in
 CC vitro. They can also be used in combination with antigenic peptides or
 CC proteins of interest to activate CTLs. They can also inhibit the
 CC proliferation of T cells in response to anti-CD3. The peptide can be
 CC used for preventing rejection of transplants or for treating autoimmune
 CC diseases, e.g. diabetes, rheumatoid arthritis and lupus erythematosus.
 CC The products can also be used for detection and diagnosis.
 CC Sequence 20 AA;

Query Match 52.0%; Score 51.5; DB 1; Length 20;
 Best Local Similarity 68.4%; Pred. No. 0.02;
 Matches 13; Conservative 1; Mismatches 2; Indels 3; Gaps 0

QY 1 YRLAIRLNERENRLPTALR 19
 |||||
 DB 1 YRLAIRLNER--YRLAIR 16

RESULT 13
 R83095
 ID R83095 standard; peptide: 10 AA.
 AC R83095;
 DE 16-WAY-1996 (first entry)
 DT HLA-B*2702 CTL modulating peptide (B2702.75-84(T)).
 KW Cytotoxic T lymphocyte; CTL; major histocompatibility complex; MHC;
 KW immunosuppressant; graft versus host disorder; transplantation; therapy;
 KW class I MHC; HLA-B*2702.
 OS Synthetic.
 PN W09526979-A1.
 PD 12-OCT-1995.
 PF 05-APR-1995; U04349.
 PR 05-APR-1994; US-222851.
 PA (STRD) UNIV LELAND STANFORD JUNIOR.
 PI Clayberger C, Krensky AM, Parham P;
 DR WPI: 95-359582/46.
 PT Extension of acceptance period of transplants from MHC unmatched
 PT donor hosts - using Class I B*75-84 MHC antigen of the recipient
 PT host
 PS Example 14; Page 34; 80pp; English.
 PS R83061-R83085, R83090-R83096 and R92907-R92913 represent fragments of
 CC class I major histocompatibility complex (MHC) antigens. This sequence
 CC corresponds to residues 75-84 of the alpha-1 domain of the class I MHC
 CC HLA-B*2702. This sequence showed no inhibitory effect upon cytotoxic T
 CC lymphocytes (CTLs). These sequences can be used to extend the period of
 CC acceptance by a recipient of a transplant from an MHC unmatched donor.
 CC The peptides are administered to a patient in conjunction with
 CC a subtherapeutic amount of an immunosuppressant. This is administered
 CC the patient for a limited period of time (compared to the lifetime
 CC administration for current treatments). The peptides particularly
 CC modulate (or inhibit) the activity of the CTLs of the patient.
 CC Sequence 10 AA;

Query Match 50.5%; Score 50; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.016;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0

QY 11 RENLRTALRY 20
 |||||
 DB 1 RENLRTALRY 10

RESULT 14
 R95426
 ID R95426 standard; peptide: 10 AA.
 AC R95426;
 DE 12-NOV-1996 (first entry)
 DT HLA-B*2702.75-84(T).
 DE HLA-B*2702.75-84(T).

KW HLA; p74; alpha-helix; human-leucocyte-associated antigen; inhibitor;
 KW T-cell lysate; membrane protein; mammal; heat shock protein; Hsc70; APC;
 KW B cell; calcium influx; cytotoxic T lymphocyte; CTL; differentiation;
 KW Cytolysis; antigen presenting cell.
 OS Synthetic.
 FH Key
 FT Location/Qualifiers
 misc_difference 6 /note= "I6T mutation"
 FT
 PN W09513288-Al.
 PD 18-MAY-1995.
 PF 10-NOV-1994; U12985.
 PR 10-NOV-1993; US-150493.
 PA (STRD) UNIV LELAND STANFORD JUNIOR.
 PI Clayberger C, Krensky AM;
 DR WPI: 95-194027/25.
 PT Compens. comprising lymphoid surface membrane proteins - which may
 PT inhibit cytolytic activity and differentiation of CTLs.
 PS Example; Page 11; 29pp; English.
 CC R95413, and R95415-R95431 represent palindromes and fragments of
 CC human-leucocyte-associated antigens. This sequence represents the
 CC HLA-B2702.75-84(T). These sequences can be used to isolate the protein
 CC p74 from a T-cell lysate. p74 is a T-cell surface membrane protein
 CC associated with T-cell activation in mammalian T-cells, and is also
 CC immunologically cross reactive with the heat shock protein Hsc70. p74 is
 CC found in a limited number of cell types, but is particularly expressed on
 CC B and T cells. p74 can be isolated by lysis of a suitable cell with an
 CC amphoteric detergent, and then passed through an affinity column
 CC containing a covalently bound HLA-B2702 palindromic peptide.
 CC Compositions comprising the extracellular fragment of p74 combined with
 CC HLA-B2702.80-84 (see R95416), induces calcium influx, and inhibits
 CC cytotoxic T lymphocyte (CTL) differentiation or cytotoxicity. Candidate
 CC compounds can be screened for their effect on the cytolytic activity of
 CC T-cells, by combining them with the extracellular portion of p74 and
 CC determining the amount of binding between the candidate compound and p74.
 CC Modulation of CTL activity can be inhibited in a cellular composition
 CC containing T-cells and antigen presenting cells (APCs), by adding to the
 CC mix the extracellular portion of p74, in an amount sufficient to compete
 CC with p74 for the binding of the p74 ligand.
 SQ Sequence 10 AA;

Query Match 50.5%; Score 50; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.016;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 RENEALTRY 20
 Db 1 RENEALTRY 10

RESULT 15

W33788
 ID W33788 standard; peptide; 10 AA.
 AC W33788;
 DT 19-JUN-1998 (first entry)
 DE Peptide B2702.75-84T80 tested for immunomodulating activity.
 KW Immunomodulating dimer; immunosuppressant drug; CTL activation;
 KW transplantation; autoimmune disease; Class I HLA-B alpha-1 domain;
 KW rejection.
 OS Synthetic.
 OS Homo sapiens.
 PN W09744351-Al.
 PD 27-NOV-1997.
 PF 22-MAY-1997; U08689.
 PR 24-MAY-1996; US-653294.
 PA (STRD) UNIV LELAND STANFORD JUNIOR.
 PI Beulow R, Clayberger C, Krensky AM;
 DR WPI: 98-086530/08.
 PT New immunomodulating dimer peptide(s) - based on a Class I HLA-B
 PT alpha-1 domain, used for preventing rejection of transplants or
 PT treating autoimmune diseases
 PS Example 1; Page 19; 41pp; English.
 CC Peptides W33784-98 and W33778-9 were assayed for their immunomodulating

CC activity. A peptide-type compound or variant is claimed which has
 CC immunomodulating activity, including the N-terminal acylated and/or
 CC C-terminal amidated or esterified forms of up to 60 amino acids, where
 CC the peptide-type compound comprises the formula: A-B, where A, B =
 CC (R aa76-77L) (aa79-84) or (aa84-79) (Laa77-76R); aa76 = E or V; aa77 =
 CC D, S or N; aa79 = R or G; aa80 = I or N; aa81, aa84 = a hydrophobic or
 CC small amino acid; aa82 = R or L; aa83 = G or R; and aa represents amino
 CC acid. The sequence in the brackets may optionally be absent or truncated
 CC at any peptide type bond within the brackets. The compounds comprise
 CC amino acid sequences related to a Class I HLA-B alpha domain (positions
 CC 79-84). They can be used to inhibit cytotoxic T-lymphocytes (CTL) from
 CC undesirably attacking cells in a host or in vitro. They can also be
 CC used in combination with antigenic peptides or proteins of interest to
 CC activate CTLs. They can also inhibit the proliferation of T cells in
 CC response to anti-CD3. The peptide can be used for preventing rejection
 CC of transplants or for treating autoimmune diseases, e.g. diabetes,
 CC rheumatoid arthritis and lupus erythematosus. The products can also be
 CC used for detection and diagnosis.
 SQ Sequence 10 AA;

Query Match 50.5%; Score 50; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.016;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 RENEALTRY 20
 Db 1 RENEALTRY 10

Search completed: February 8, 2000, 04:05:43
 Job time: 9360 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: February 7, 2000, 18:04:38 ; Search time 111.22 seconds
(without alignments)
8.482 Million cell updates/sec

Title: US-08-653-294-29

Perfect score: 99

Sequence: 1 YRLAIRLNERENLRALRY 20

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 142080 seqs, 47169319 residues

Total number of hits satisfying chosen parameters: 142080

Minimum DB seq length: 0

Maximum DB seq length: 1000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

PIR_62:*

1: pir1.*

2: pir2.*

3: pir3.*

4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	50	50.5	355	2 I37516	HLA-B alpha-chain
2	50	50.5	362	2 S25415	class I histocompa
3	50	50.5	362	2 A45850	MHC class I histoc
4	50	50.5	362	2 I81861	MHC HLA-B*44.2 cha
5	50	50.5	362	2 I34442	MHC class I histoc
6	46	46.5	2077	1 W2BE24	240K tegument prot
7	46	46.5	2078	2 T09326	tegument protein -
8	45	45.5	137	2 I80174	class I histocompa
9	45	45.5	359	1 HLHUB4	MHC class I histoc
10	45	45.5	362	2 I34457	MHC class I lympho
11	44	44.4	273	2 I38509	MHC class I histoc
12	44	44.4	274	2 I54463	MHC HLA-B*38 chain
13	44	44.4	292	2 I57806	MHC H-2K-kml mRNa
14	44	44.4	354	2 I59308	class I histocompa
15	44	44.4	354	2 I80168	class I histocompa
16	44	44.4	354	2 I80167	class I histocompa
17	44	44.4	355	2 I80169	class I histocompa
18	44	44.4	355	2 I80171	class I histocompa
19	44	44.4	359	1 HLHUI2	MHC class I histoc
20	44	44.4	362	1 HLHUB8	MHC class I histoc
21	44	44.4	362	2 B45876	class I histocompa
22	44	44.4	362	2 B30345	MHC class I histoc
23	44	44.4	362	2 JH0541	class I histocompa
24	44	44.4	362	2 JH0539	class I histocompa
25	44	44.4	362	2 JH0540	class I histocompa
26	44	44.4	362	2 A45834	MHC class I histoc
27	44	44.4	362	2 I84486	transmembrane glyc
28	44	44.4	362	2 I62045	gene HLA B-1517 pr
29	44	44.4	362	2 I84490	lymphocyte antigen
30	44	44.4	362	2 I37521	HLA-B*57.2 antigen

ALIGNMENTS

RESULT 1

I37516

HLA-B alpha-chain - human (fragment)

C:Species: Homo sapiens (man)

C>Date: 04-Oct-1996 #sequence_revision 04-Oct-1996 #text_change 23-Jul-1999

C:Accession: I37516

R:Gauchat-Feiss, D.; Breur-Vriesendorp, B.S.; Rufer, N.; Jeannet, M.; Roosnek, E.; Tl

Tissue Antigens 44, 261-264, 1994

A>Title: Sequencing of a novel functional HLA-B*44 subtype differing in two residues i

A:Reference number: I37516; MUID:95176328

A:Accession: I37516

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-355 <RES>

A:Cross-references: EMBL:X75953; NID:G791007; PIDN:CAA53566.1; PID:G791008

C:Superfamily: class I histocompatibility antigen; immunoglobulin homology

Query Match 50.5%; Score 50; DB 2; Length 355;

Best Local Similarity 100.0%; Pred. No. 1.4;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 RENLRTALRY 20

|||||

Db 99 RENLRTALRY 108

RESULT 2

S25415

class I histocompatibility antigen HLA-B*4403 alpha chain - human

C:Species: Homo sapiens (man)

C>Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 23-Jul-1999

C:Accession: S25415

R:Fleischhauer, K.; Kernan, N.A.; Dupont, B.; Yang, S.Y.

A>Title: The two major subtypes of HLA-B*44 differ for a single amino acid in codon 15

A:Reference number: S25415; MUID:91335451

A:Accession: S25415

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-362 <FILE>

A:Cross-references: EMBL:X64366; NID:G32178; PIDN:CAA45718.1; PID:G32179

C:Genetics:

A:Gene: GDB:HLA-B

A:Cross-references: GDB:120048; OMIM:142830

A:Map position: 6p21.3-6p21.3

C:Superfamily: class I histocompatibility antigen; immunoglobulin homology

C:Keywords: transmembrane protein

F:220-285/Domain: immunoglobulin homology <IMM>

Query Match

Best Local Similarity 100.0%; Score 50; DB 2; Length 362;

Pred. No. 1.5;

© Ziemann, J.; Ellis, F.D.; Farnham, F.; Dupont, B.

A:Residues: 1-2078 <NIC>
A:Cross-references: EMBL:L25528; NID:q451932; PID:q451957
C:Genetics:
A:Gene: HHRF1
C:Superfamily: varicella-zoster virus 240K tegument protein

Query Match 46.5%; Score 46; DB 2; Length 2078;
Best Local Similarity 38.9%; Pred. No. 41;
Matches 7; Conservative 8; Mismatches 3; Indels 0; Gaps 0;

Qy 1 YRLAIRNERRENLTAL 18
|:|:|:|:|:|:|:
Db 496 YKVAVLLNEKRKEIQEI 513

RESULT 8

180174
class I histocompatibility antigen - chimpanzee (fragment)
C:Species: Pan troglodytes (chimpanzee)
C:Date: 24-May-1996 #sequence_revision 24-May-1996 #text_change 23-Jul-1999
C:Accession: 180174
R:McAdam, S.N.; Boyson, J.E.; Liu, X.; Garber, T.L.; Hughes, A.L.; Bontrop, R.E.; Watkins
Proc. Natl. Acad. Sci. U.S.A. 91, 5893-5897, 1994
A:Title: A uniquely high level of recombination at the HLA-B locus.
A:Reference number: 159308; MUID:94286544
A:Accession: 180174
A:Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: DNA
A:Residues: 1-137 <RES>
A:Cross-references: EMBL:U05585; NID:q454787; PIDN:AAA50188.1; PID:q454788
C:Superfamily: class I histocompatibility antigen; immunoglobulin homology

Query Match 45.5%; Score 45; DB 2; Length 137;
Best Local Similarity 90.0%; Pred. No. 3.2;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 11 RNLRLTALRY 20
|:|:|:|:|:|:
Db 40 RNLRLTLRY 49

RESULT 9

HLRUB4
MHC class I histocompatibility antigen HLA-B44 alpha chain precursor - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change 22-Jun-1999
C:Accession: A25295
R:Kottmann, A.H.; Seemann, G.H.A.; Guessow, H.D.; Roos, M.H.
Immunogenetics 23, 396-400, 1986
A:Title: DNA sequence of the coding region of the HLA-B44 gene.
A:Reference number: A25295; MUID:86249389
A:Accession: A25295
A:Molecule type: mRNA
A:Residues: 1-359 <KOT>
A:Cross-references: GB:M15470; NID:g187680; PIDN:AAA59619.1; PID:g386883
C:Genetics:
A:Gene: GDB:HLA-B
A:Cross-references: GDB:120048; OMIM:142830
A:Map position: 6p21.3-6p21.3
C:Superfamily: class I histocompatibility antigen; immunoglobulin homology
C:Keywords: duplication; glycoprotein; heterodimer; transmembrane protein; transplantati
F:1-21/Domain: signal sequence (fragment) #status predicted <SIG>
F:22-359/Product: class I histocompatibility antigen HLA-B44 alpha chain #status predict
F:22-304/Domain: extracellular alpha-1 <EX1>
F:22-111/Domain: alpha-1 <EX1>
F:112-203/Domain: alpha-2 <EX2>
F:217-282/Domain: immunoglobulin homology <IMM>
F:305-328/Domain: transmembrane #status predicted <TM>
F:329-359/Domain: intracellular #status predicted <INT>
F:107/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 45.5%; Score 45; DB 1; Length 359;
Best Local Similarity 90.0%; Pred. No. 9;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 11 RNLRLTALRY 20
|:|:|:|:|:|:
Db 96 RNLRLTALRY 105

RESULT 10

154457
MHC class I lymphocyte antigen - human
C:Species: Homo sapiens (man)
C:Date: 07-Jun-1996 #sequence_revision 07-Jun-1996 #text_change 23-Jul-1999
C:Accession: 154457
R:Pohla, H.; Kuon, W.; Tabaczewski, P.; Doerner, C.; Weiss, E.H.
Immunogenetics 29, 297-307, 1989
A:Title: Allelic variation in HLA-B and HLA-C sequences and the evolution of the HLA-
A:Reference number: 154457; MUID:89233295
A:Accession: 154457
A:Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: mRNA
A:Residues: 1-362 <RES>
A:Cross-references: GB:M28205; NID:g576470; PIDN:AAA57145.1; PID:g576471
C:Superfamily: class I histocompatibility antigen; immunoglobulin homology

Query Match 45.5%; Score 45; DB 2; Length 362;
Best Local Similarity 90.0%; Pred. No. 9.1;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 11 RNLRLTALRY 20
|:|:|:|:|:|:
Db 99 RNLRLTLRY 108

RESULT 11

138509
MHC class I histocompatibility antigen - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 06-Sep-1996 #sequence_revision 06-Sep-1996 #text_change 23-Jul-1999
C:Accession: 138509
R:Cereb, N.; Choi, J.W.; Riu, K.Z.; Yang, S.Y.
Tissue Antigens 44, 271-273, 1994
A:Title: HLA-B*5105, a newly identified B51 IEF variant.
A:Reference number: 138509; MUID:95176331
A:Accession: 138509
A:Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: mRNA
A:Residues: 1-273 <RES>
A:Cross-references: EMBL:U06697; NID:g469544; PIDN:AAA92997.1; PID:g469545
C:Genetics:
A:Gene: GDB:HLA-B
A:Cross-references: GDB:120048; OMIM:142830
A:Map position: 6p21.3-6p21.3
C:Superfamily: class I histocompatibility antigen; immunoglobulin homology

Query Match 44.4%; Score 44; DB 2; Length 273;
Best Local Similarity 90.0%; Pred. No. 9.7;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 11 RNLRLTALRY 20
|:|:|:|:|:|:
Db 74 RNLRLTALRY 83

RESULT 12

154463
MHC HLA-B*38 chain - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 07-Jun-1996 #sequence_revision 07-Jun-1996 #text_change 23-Jul-1999

C:Accession: I54463
R:Mueller, C.A.; Engler-Blum, G.; Gekeler, V.; Steiert, I.; Weiss, E.; Schmidt, H.
Immunogenetics 30, 200-207, 1989
A:Title: Genetic and serological heterogeneity of the supertypic HLA-B locus specificity
A:Reference number: I54463; MUID:89379286
A:Accession: I54463
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-274 <RES>
A:Cross-references: GB:M29864; NID:gl87674; PIDN:AAA36222.1; PID:gl87675
C:Superfamily: class I histocompatibility antigen; immunoglobulin homology

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Residues: 1-274 <RES>
A:Cross-references: GB:M29864; NID:gl87674; PIDN:AAA36222.1; PID:gl87675
C:Superfamily: class I histocompatibility antigen; immunoglobulin homology

Query Match 44.4%; Score 44; DB 2; Length 274;
Best Local Similarity 90.0%; Pred. No. 9.7;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 11 RENLRLALRY 20
||||| |||||
DB 75 RENLRLALRY 84

RESULT 13
I57806
MHC H-2K-kml mRNA - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 23-Jul-1999
C:Accession: I57806
R:Martin, J.M.; Solheim, J.C.; Gellibter, J.
Mol. Immunol. 25, 267-274, 1988
A:Title: The H-2K-kml mutation: A single nucleotide substitution is responsible for mult
A:Reference number: I57806; MUID:88232726
A:Accession: I57806
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-292 <RES>
A:Cross-references: GB:M34932; NID:gl99405; PIDN:AAA39596.1; PID:gl99406
C:Superfamily: class I histocompatibility antigen; immunoglobulin homology

Query Match 44.4%; Score 44; DB 2; Length 292;
Best Local Similarity 73.3%; Pred. No. 10;
Matches 11; Conservative 1; Mismatches 1; Indels 2; Gaps 1;

QY 8 NER--RENLRLALRY 20
||| | ||||| |||||
DB 70 NEQIFRNRLALRY 84

RESULT 14
I59308
Class I histocompatibility antigen - pygmy chimpanzee (fragment)
C:Species: Pan paniscus (pygmy chimpanzee, bonobo)
C:Date: 31-May-1996 #sequence_revision 31-May-1996 #text_change 23-Jul-1999
C:Accession: I59308
R:McAdam, S.N.; Boyson, J.E.; Liu, X.; Garber, T.L.; Hughes, A.L.; Bontrop, R.E.; Watkin
Proc. Natl. Acad. Sci. U.S.A. 91, 5893-5897, 1994
A:Title: A uniquely high level of recombination at the HLA-B locus.
A:Reference number: I59308; MUID:94286544
A:Accession: I59308
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-354 <RES>
A:Cross-references: EMBL:U05575; NID:9454767; PIDN:AAA50178.1; PID:9454768
C:Superfamily: class I histocompatibility antigen; immunoglobulin homology

Query Match 44.4%; Score 44; DB 2; Length 354;
Best Local Similarity 90.0%; Pred. No. 13;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 11 RENLRLALRY 20
||||| ||||| |||||

DB 91 RENLRLALRY 100 -
RESULT 15
I80168
Class I histocompatibility antigen - chimpanzee (fragment)
C:Species: Pan troglodytes (chimpanzee)
C:Date: 24-May-1996 #sequence_revision 24-May-1996 #text_change 23-Jul-1999
C:Accession: I80168
R:McAdam, S.N.; Boyson, J.E.; Liu, X.; Garber, T.L.; Hughes, A.L.; Bontrop, R.E.; Wat
Proc. Natl. Acad. Sci. U.S.A. 91, 5893-5897, 1994
A:Title: A uniquely high level of recombination at the HLA-B locus.
A:Reference number: I59308; MUID:94286544
A:Accession: I80168
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-354 <RES>
A:Cross-references: EMBL:U05579; NID:9454775; PIDN:AAA50182.1; PID:9454776
C:Superfamily: class I histocompatibility antigen; immunoglobulin homology

Query Match 44.4%; Score 44; DB 2; Length 354;
Best Local Similarity 90.0%; Pred. No. 13;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 11 RENLRLALRY 20
||||| ||||| |||||
DB 91 RENLRLALRY 100

Search completed: February 7, 2000, 18:04:39
Job time: 22205 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: February 8, 2000, 01:25:59 ; Search time 68.63 Seconds
(without alignments)
8.703 Million cell updates/sec

Title: US-08-653-294-29

Perfect score: 99

Sequence: 1 YRLAIRLNERENLTALRY 20

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 82229 seqs, 29864866 residues

Total number of hits satisfying chosen parameters: 82229

Minimum DB seq length: 0

Maximum DB seq length: 1000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : SwissProt_38.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	50	50.5	362	1	1B05_HUMAN
2	50	50.5	362	1	1B41_HUMAN
3	50	50.5	362	1	1B42_HUMAN
4	46	46.5	2077	1	TEGU_HSV6G
5	46	46.5	2077	1	TEGU_HSV6U
6	45	45.5	359	1	1B40_HUMAN
7	44	44.4	351	1	CBIG_SALTY
8	44	44.4	359	1	1B01_PANTR
9	44	44.4	362	1	1B01_GORGO
10	44	44.4	362	1	1B02_GORGO
11	44	44.4	362	1	1B03_GORGO
12	44	44.4	362	1	1B15_HUMAN
13	44	44.4	362	1	1B47_HUMAN
14	44	44.4	362	1	1B49_HUMAN
15	44	44.4	362	1	1B52_HUMAN
16	44	44.4	362	1	1B53_HUMAN
17	44	44.4	362	1	1B54_HUMAN
18	44	44.4	362	1	1B60_HUMAN
19	44	44.4	362	1	1B61_HUMAN
20	44	44.4	362	1	1B62_HUMAN
21	44	44.4	362	1	HLAH_HUMAN
22	44	44.4	365	1	1A23_HUMAN
23	44	44.4	365	1	1A24_HUMAN
24	44	44.4	369	1	HAJK_MOUSE
25	42	42.4	591	1	GLWS_AQUAE
26	40	40.4	338	1	1B20_HUMAN
27	40	40.4	361	1	1B14_HUMAN
28	40	40.4	362	1	1B16_HUMAN
29	40	40.4	362	1	1B18_HUMAN
30	40	40.4	362	1	1B19_HUMAN
31	40	40.4	362	1	1B29_HUMAN
32	40	40.4	362	1	1B45_HUMAN
33	40	40.4	433	1	HEN2_SPIOL
34	40	40.4	924	1	ORC1_DROME

35 40 40.4 1126 1 MEM2_DROME
36 39 39.4 162 1 PUR6_BACSU
37 39 39.4 187 1 ATPE_ANASP
38 39 39.4 281 1 APE_BRARE
39 39 39.4 298 1 HAY_MOUSE
40 39 39.4 303 1 DMA_TREPA
41 39 39.4 365 1 1A25_HUMAN
42 39 39.4 365 1 1A32_HUMAN
43 39 39.4 365 1 1A12_MOUSE
44 39 39.4 375 1 SR55_DROME
45 39 39.4 380 1 LEU3_PHACH

P55162 drosophila
P12044 bacillus su
P12407 anabaena sp
O42364 brachydanio
P01895 mus musculus
O33844 treponema p
P18462 homo sapien
P10314 homo sapien
P01900 mus musculus
P26686 drosophila
O59930 phanerochaete

ALIGNMENTS

RESULT 1
ID 1B05_HUMAN STANDARD; PRT; 362 AA.
AC P30461;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-13 B*1301 ALPHA CHAIN
DE PRECURSOR (B13.1).
GN HLA-B OR HLAB.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Primates; Catarrhini; Hominidae; Homo.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 89235215.
RA PARHAM P., LAWOR D.A., LOMEN C.E., ENNIS P.D.;
RT "Diversity and diversification of HLA-A,B,C alleles";
RL J. Immunol. 142:3937-3950(1989).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE; 88152906.
RA ZEMOUR J., ENNIS P.D., PARHAM P., DUPONT B.;
RT "Comparison of the structure of HLA-B*47 to HLA-B13 and its
RL relationship to 21-hydroxylase deficiency.";
RN Immunogenetics 27:281-287(1988).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE; 96053518.
RA LIN L., TOKUNAGA K., NAKAJIMA F., ISHIKAWA Y., KASHIWASE K.,
RA TANAKA H., KUWATA S., SDELTSEVA E., AKAZA T., TADOKORO K.,
RA SHIBATA Y., CHANDANAVONGYONG D., JUJI T.;
RT "Both HLA-B*1301 and B*1302 exist in Asian populations and are
RT associated with different haplotypes";
Hum. Immunol. 43:51-56(1995).
CC -!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
CC THE IMMUNE SYSTEM.
CC -!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
CC MICROGLOBULIN).
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CC
CC EMBL; M24041; AAA59660.1; -
DR EMBL; M19757; AAA52657.1; -
DR EMBL; P50291; BAA08822.1; -
DR HSSP; P30491; 1A1M.
DR MIM; 142830; -
DR PROSITE; PS00290; IG_MHC; 1.
DR PFAM; PF00047; Ig; 1.
DR PFAM; PF00129; MHC_I; 1.

KW MHC I; Transmembrane; Glycoprotein; Signal.
 FT SIGNAL 1 24
 FT CHAIN 25 362 HLA CLASS I HISTOCOMPATIBILITY ANTIGEN,
 FT B-13 B*1301 ALPHA CHAIN.
 FT DOMAIN 25 114 EXTRACELLULAR ALPHA-1.
 FT DOMAIN 115 206 EXTRACELLULAR ALPHA-2.
 FT DOMAIN 207 298 EXTRACELLULAR ALPHA-3.
 FT DOMAIN 299 309 CONNECTING PEPTIDE.
 FT TRANSMEM 310 333
 FT DOMAIN 334 362 CYTOPLASMIC TAIL.
 FT CARBOHYD 110 110 BY SIMILARITY.
 FT DISULFID 125 188 BY SIMILARITY.
 FT DISULFID 227 283 BY SIMILARITY.
 SQ SEQUENCE 362 AA; 40474 MW; 28867875 CRC32;

Query Match 50.5%; Score 50; DB 1; Length 362;
 Best Local Similarity 100.0%; Pred. No. 0.58;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 RENLRTALRY 20
 |||||
 Db 99 RENLRTALRY 108

RESULT 2
 1B41_HUMAN STANDARD; PRT; 362 AA.
 ID 1B41_HUMAN
 AC P30481;
 DT 01-APR-1993 (Rel. 25, Created)
 DT 01-APR-1993 (Rel. 25, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, BW-44(B-12) B*4402 ALPHA CHAIN
 DE PRECURSOR (B44.2).
 GN HLA-B OR HLAB.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Eutheria; Primates; Catarrhini; Homiidae; Homo.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 89235215.
 RA PARHAM P., LAWLER D.A., LOMEN C.E., ENNIS P.D.;
 RT "Diversity and diversification of HLA-A,B,C alleles.";
 RL J. Immunol. 142:3937-3950(1989).
 CC -!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
 THE IMMUNE SYSTEM.
 CC -!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
 MICROGLOBULIN).
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 CC
 CC EMBL; M24038; AAA59663.1;
 DR HSSP; P30491; IALM.
 DR MIM; 142830;
 DR PROSITE; PS00290; IG_MHC; 1.
 DR PFAM; PF00047; Ig; 1.
 DR PFAM; PF00129; MHC_I; 1.
 KW MHC I; Transmembrane; Glycoprotein; Signal.
 FT SIGNAL 1 24
 FT CHAIN 25 362 HLA CLASS I HISTOCOMPATIBILITY ANTIGEN,
 FT BW-44(B-12) B*4402 ALPHA CHAIN.
 FT DOMAIN 25 114 EXTRACELLULAR ALPHA-1.
 FT DOMAIN 115 206 EXTRACELLULAR ALPHA-2.
 FT DOMAIN 207 298 EXTRACELLULAR ALPHA-3.
 FT DOMAIN 299 309 CONNECTING PEPTIDE.
 FT TRANSMEM 310 333
 FT DOMAIN 334 362 CYTOPLASMIC TAIL.

FT CARBOHYD 110 110 BY SIMILARITY.
 FT DISULFID 125 188 BY SIMILARITY.
 FT DISULFID 227 283 BY SIMILARITY.
 SQ SEQUENCE 362 AA; 40481 MW; DOAE6DD5 CRC32;

Query Match 50.5%; Score 50; DB 1; Length 362;
 Best Local Similarity 100.0%; Pred. No. 0.58;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 RENLRTALRY 20
 |||||
 Db 99 RENLRTALRY 108

RESULT 3
 1B42_HUMAN STANDARD; PRT; 362 AA.
 ID 1B42_HUMAN
 AC P30482;
 DT 01-APR-1993 (Rel. 25, Created)
 DT 01-APR-1993 (Rel. 25, Last sequence update)
 DT 15-JUL-1998 (Rel. 36, Last annotation update)
 DE HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, BW-44(B-12) B*4403 ALPHA CHAIN
 DE PRECURSOR.
 GN HLA-B OR HLAB.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Eutheria; Primates; Catarrhini; Homiidae; Homo.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 91335451.
 RA FLEISCHHAUER K., KERNAN N.A., DUPONT B., YANG S.Y.;
 RT "The two major subtypes of HLA-B*44 differ for a single amino acid in
 codon 156.";
 RL Tissue Antigens 37:133-137(1991).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 96435470.
 RA ADAMS E.J., LITTLE A.M., ARNETT K.L., MCAULEY J.E., WILLIAMS R.C.,
 RA PARHAM P.;
 RT "Three new HLA-B alleles found in Mexican-Americans.";
 RL Tissue Antigens 46:414-416(1995).
 CC -!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
 THE IMMUNE SYSTEM.
 CC -!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
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 CC
 CC EMBL; X64366; CAA45718.1;
 DR EMBL; L42282; AAB51454.1;
 DR EMBL; L42283; AAB51455.1;
 DR PIR; S25415; S25415.
 DR HSSP; P30491; IALM.
 DR MIM; 142830;
 DR PROSITE; PS00290; IG_MHC; 1.
 DR PFAM; PF00047; Ig; 1.
 DR PFAM; PF00129; MHC_I; 1.
 KW MHC I; Transmembrane; Glycoprotein; Signal.
 FT SIGNAL 1 24
 FT CHAIN 25 362 HLA CLASS I HISTOCOMPATIBILITY ANTIGEN,
 FT BW-44(B-12) B*4403 ALPHA CHAIN.
 FT DOMAIN 25 114 EXTRACELLULAR ALPHA-1.
 FT DOMAIN 115 206 EXTRACELLULAR ALPHA-2.
 FT DOMAIN 207 298 EXTRACELLULAR ALPHA-3.
 FT DOMAIN 299 309 CONNECTING PEPTIDE.
 FT TRANSMEM 310 333

FT DOMAIN 334 362 CYTOPLASMIC TAIL.
 FT CARBOHYD 110 110 BY SIMILARITY.
 FT DISULFID 125 188 BY SIMILARITY.
 FT DISULFID 227 283 BY SIMILARITY.
 SQ SEQUENCE 362 AA; 40479 MW; E72CE669 CRC32;

Query Match 50.5%; Score 50; DB 1; Length 362;
 Best Local Similarity 100.0%; Pred. No. 0.58;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 RENLRLTALRY 20
 |||||
 Db 99 RENLRLTALRY 108

RESULT 4
 TEGU_HSV6G STANDARD; PRT; 2077 AA.
 AC P30002;
 DT 01-APR-1993 (Rel. 25, Created)
 DT 01-APR-1993 (Rel. 25, Last sequence update)
 DT 01-OCT-1996 (Rel. 34, Last annotation update)
 DE LARGE TEGUMENT PROTEIN.
 GN U31.
 OS Herpes simplex virus (type 6 / strain GS).
 OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
 OC Betaherpesvirinae; Roseolovirus.
 RN [1]

RP SEQUENCE FROM N.A.
 RX MEDLINE: 91374623.
 RA JOSEPHS S.F., ABLASHI D.V., SALAHUDDIN S.Z., JAGODZINSKI L.L.,
 RA WONG-STAL F., GALLO R.C.;
 RT "Identification of the human herpesvirus 6 glycoprotein H and
 RT putative large tegument protein genes.";
 RL J. Virol. 65:5597-5604(1991).

CC -1- FUNCTION: TEGUMENT PROTEIN.
 CC -1- SIMILARITY: BELONGS TO FAMILY THAT GROUPS TOGETHER HSV-1 UL36,
 CC EHV-1 24, EBV BPLF1, HVS-1 64, VZV 22, AND HCMV UL48.
 CC -----
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CC EMBL: S57540; AAB19786.1; -
 CC PIR: H40511; W2BE24.
 DR SEQUENCE 2077 AA; 239909 MW; 82ACA5DE CRC32;

Query Match 46.5%; Score 46; DB 1; Length 2077;
 Best Local Similarity 38.9%; Pred. No. 19;
 Matches 7; Conservative 8; Mismatches 3; Indels 0; Gaps 0;

QY 1 YRLAIRLNERENLRTAL 18
 |::|: |||: |::|:
 Db 495 YKVAVLLNKKRKEIQEAI 512

RESULT 5
 TEGU_HSV6G STANDARD; PRT; 2077 AA.
 AC P52340;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 01-OCT-1996 (Rel. 34, Last annotation update)
 DE LARGE TEGUMENT PROTEIN.
 GN U31 OR HHRF1.
 OS Herpes simplex virus (type 6 / strain Uganda-1102).
 OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;

OC Betaherpesvirinae; Roseolovirus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 95266321.
 RA GOMPELS U.A., NICHOLAS J., LAWRENCE G., JONES M., THOMSON B.J.,
 RA MARTIN M.E., EFSTATHIOU S., CRAXTON M., MACAULAY H.A.;
 RT "The DNA sequence of human herpesvirus-6: structure, coding content,
 RT and genome evolution.";
 RL Virology 209:29-51(1995).
 CC -1- FUNCTION: TEGUMENT PROTEIN.
 CC -1- SIMILARITY: BELONGS TO FAMILY THAT GROUPS TOGETHER HSV-1 UL36,
 CC EHV-1 24, EBV BPLF1, HVS-1 64, VZV 22, AND HCMV UL48.
 CC -----
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CC EMBL: X83413; CAA58411.1; -
 DR SEQUENCE 2077 AA; 239946 MW; 36FCF7B1 CRC32;

Query Match 46.5%; Score 46; DB 1; Length 2077;
 Best Local Similarity 38.9%; Pred. No. 19;
 Matches 7; Conservative 8; Mismatches 3; Indels 0; Gaps 0;

QY 1 YRLAIRLNERENLRTAL 18
 |::|: |||: |::|:
 Db 495 YKVAVLLNKKRKEIQEAI 512

RESULT 6
 1B40_HUMAN STANDARD; PRT; 359 AA.
 ID 1B40_HUMAN
 AC P10320;
 DT 01-MAR-1989 (Rel. 10, Created)
 DT 01-MAR-1989 (Rel. 10, Last sequence update)
 DT 13-JUL-1999 (Rel. 38, Last annotation update)
 DE HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, BW-44 (B-12) B*4401 ALPHA CHAIN
 DE PRECURSOR (B44.1) (FRAGMENT).
 GN HLA-B OR HLAB.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Eutheria; Primates; Catarrhini; Hominidae; Homo.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 86249389.
 RA KOTTWANN A.H., SEEMANN G.H.A., GUESSEW H.D., ROOS M.H.;
 RT "DNA sequence of the coding region of the HLA-B44 gene.";
 RL Immunogenetics 23:396-400(1986).
 CC -1- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
 CC THE IMMUNE SYSTEM.
 CC -1- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
 CC MICROGLOBULIN).
 CC -----
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CC EMBL: M15470; AAA59619.1; -
 CC PIR: A25295; HLHUB4.
 DR HSP; P30491; IALM.
 DR MIM; 142830; -
 DR PFAM; PF00047; Ig; 1.
 DR PFAM; PF00129; MHC_I; 1.

```

RESULT      8
IDB01_PANTR IDB01_PANTR STANDARD; PRT; 359 AA.
P13750;
01-JAN-1990 (Rel. 13, Created)
01-JAN-1990 (Rel. 13, Last sequence update)
01-APR-1993 (Rel. 25, Last annotation update)
CHLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-1 ALPHA CHAIN PRECURSOR
(FRAGMENT).
Pan troglodytes (Chimpanzee).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Homnidae; Pan.
[1]
SEQUENCE FROM N.A.
MEDLINE; 89030641.
MAYER W.E., JONKER M., KLEIN D., IVANYI P., VAN SEVENTER G.,
KLEIN J.;
"Nucleotide sequences of chimpanzee MHC class I alleles: evidence for
trans-species mode of evolution.";
EMBO J. 7:2765-2774(1988).
[2]
REVISIONS.
MAYER W.;
Submitted (FEB-1989) to the EMBL/GenBank/DBJ databases.
-!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
THE IMMUNE SYSTEM.
-!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
MICROGLOBULIN).
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-----
CC
EMBL; X13115; CAA31507.1; -.
PIR; S03537; S03537.
HSSP; P03989; ILSA.
PROSITE; PS00290; IG_MHC; 1.
PFAM; PF00047; ig; 1.
PFAM; PF00129; MHC-I; 1.
MHC I; Transmembrane; Glycoprotein; Signal.
NON_TER 1
SIGNA <1 20
CHAIN 21 359
CHLA CLASS I HISTOCOMPATIBILITY ANTIGEN,
B-1 ALPHA CHAIN.
EXTRACELLULAR ALPHA-1.
EXTRACELLULAR ALPHA-2.
EXTRACELLULAR ALPHA-3.
CONNECTING PEPTIDE.
CYTOPLASMIC TAIL.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
SEQUENCE 359 AA; 40173 MW; 5395FFC9 CRC32;

Query Match 44.4%; Score 44; DB 1; Length 359;
Best Local Similarity 90.0%; Pred.No. 5.4;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

QY	11	RENRLTALRY	20
Db	95	RENRLTALRY	104
RESULT 9			
		1B01_GORGO	
		ID 1B01_GORGO	STANDARD;
AC	P30379;		
		PRT;	362 AA.

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DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 01-APR-1993 (Rel. 25, Last annotation update)
DE CLASS I HISTOCOMPATIBILITY ANTIGEN, GOGO-B0101 ALPHA CHAIN PRECURSOR.
OS Gorilla gorilla gorilla (Lowland gorilla).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Primates; Catarrhini; Hominidae; Gorilla.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 92078860.
RA LAWLOR D.A., WARREN E., TAYLOR P., PARHAM P.;
RT "Gorilla class I major histocompatibility complex alleles: comparison
RT to human and chimpanzee class I.";
RL J. Exp. Med. 174:1491-1509(1991).
CC -|- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
CC THE IMMUNE SYSTEM.
CC -|- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
CC MICROGLOBULIN).
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CC
CC EMBL; X60255; CAA42807.1; -.
CC PIR; JH0539; JH0539.
CC HSSP; P03989; IHSN.
CC PROSITE; PS00290; IG_MHC; 1.
CC PFAM; PF00047; ig; 1.
CC MHC I; Transmembrane; Glycoprotein; Signal.
CC SIGNAL 1 24
CC CHAIN 25 362
CC CLASS I HISTOCOMPATIBILITY ANTIGEN,
CC GOGO-B0101 ALPHA CHAIN.
CC EXTRACELLULAR ALPHA-1.
CC EXTRACELLULAR ALPHA-2.
CC EXTRACELLULAR ALPHA-3.
CC CONNECTING PEPTIDE.
CC CYTOPLASMIC TAIL.
CC BY SIMILARITY.
CC DISULFID 125 188
CC DISULFID 227 283
CC CARBOHYD 110 110
CC BY SIMILARITY.
CC SEQUENCE 362 AA; 40170 MW; 2E33E2B8 CRC32;

Query Match 44.4%; Score 44; DB 1; Length 362;
Best Local Similarity 90.0%; Pred. No. 5.5;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 11 RENLRLALRY 20
Db [1111111111]
99 RENLRLALRY 108

RESULT 10
1B02_GORGO
ID 1B02_GORGO STANDARD; PRT; 362 AA.
AC P30380;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DE CLASS I HISTOCOMPATIBILITY ANTIGEN, GOGO-B0102 ALPHA CHAIN PRECURSOR.
OS Gorilla gorilla gorilla (Lowland gorilla).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Primates; Catarrhini; Hominidae; Gorilla.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 92078860.
RA LAWLOR D.A., WARREN E., TAYLOR P., PARHAM P.;
RT "Gorilla class I major histocompatibility complex alleles: comparison
RT to human and chimpanzee class I.";
RL J. Exp. Med. 174:1491-1509(1991).
CC -|- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
CC THE IMMUNE SYSTEM.
CC -|- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
CC MICROGLOBULIN).
CC
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RT "Gorilla class I major histocompatibility complex alleles: comparison
RT to human and chimpanzee class I.";
RL J. Exp. Med. 174:1491-1509(1991).
CC -|- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
CC THE IMMUNE SYSTEM.
CC -|- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
CC MICROGLOBULIN).
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CC
CC EMBL; X60593; CAA43101.1; -.
CC PIR; JH0540; JH0540.
CC HSSP; P03989; IHSN.
CC PROSITE; PS00290; IG_MHC; 1.
CC PFAM; PF00047; ig; 1.
CC MHC I; Transmembrane; Glycoprotein; Signal.
CC SIGNAL 1 24
CC CHAIN 25 362
CC CLASS I HISTOCOMPATIBILITY ANTIGEN,
CC GOGO-B0102 ALPHA CHAIN.
CC EXTRACELLULAR ALPHA-1.
CC EXTRACELLULAR ALPHA-2.
CC EXTRACELLULAR ALPHA-3.
CC CONNECTING PEPTIDE.
CC CYTOPLASMIC TAIL.
CC BY SIMILARITY.
CC DISULFID 125 188
CC DISULFID 227 283
CC CARBOHYD 110 110
CC BY SIMILARITY.
CC SEQUENCE 362 AA; 40204 MW; 3CF119AD CRC32;

Query Match 44.4%; Score 44; DB 1; Length 362;
Best Local Similarity 90.0%; Pred. No. 5.5;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 11 RENLRLALRY 20
Db [1111111111]
99 RENLRLALRY 108

RESULT 11
1B03_GORGO
ID 1B03_GORGO STANDARD; PRT; 362 AA.
AC P30381;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DE CLASS I HISTOCOMPATIBILITY ANTIGEN, GOGO-B0103 ALPHA CHAIN PRECURSOR.
OS Gorilla gorilla gorilla (Lowland gorilla).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Primates; Catarrhini; Hominidae; Gorilla.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 92078860.
RA LAWLOR D.A., WARREN E., TAYLOR P., PARHAM P.;
RT "Gorilla class I major histocompatibility complex alleles: comparison
RT to human and chimpanzee class I.";
RL J. Exp. Med. 174:1491-1509(1991).
CC -|- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
CC THE IMMUNE SYSTEM.
CC -|- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
CC MICROGLOBULIN).
CC
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CC -----
 DR EMBL: X60254; CAA42806.1; -
 DR PIR: JH0541; JH0541.
 DR HSP: P03989; ILSA.
 DR PROSITE; PS00290; IG_MHC; 1.
 DR PFAM; PF00047; IG; 1.
 DR PFAM; PF00129; MHC_I; 1.
 KW MHC I; Transmembrane; Glycoprotein; Signal.
 FT SIGNAL 1 24
 FT CHAIN 25 362
 FT DOMAIN 25 114
 FT DOMAIN 115 206
 FT DOMAIN 207 298
 FT DOMAIN 299 308
 FT TRANSMEM 309 332
 FT DOMAIN 333 362
 FT DISULFID 125 188
 FT CARBOHYD 227 283
 FT SEQUENCE 362 AA; 40248 MW; FEAGA941 CRC32;
 SQ

Query Match 44.4%; Score 44; DB 1; Length 362;
 Best Local Similarity 90.0%; Pred. No. 5.5;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 11 RENLRTALRY 20
 Db 99 RENLRTALRY 108

RESULT 12
 1B15_HUMAN
 ID 1B15_HUMAN STANDARD; PRT; 362 AA.
 AC P10317;
 DT 01-MAR-1989 (Rel. 10, Created)
 DT 01-MAR-1989 (Rel. 10, Last sequence update)
 DT 01-APR-1993 (Rel. 25, Last annotation update)
 DE HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-27 B*2702 ALPHA CHAIN
 DE PRECURSOR (B-27K) (B27.2).
 GN HLA-B OR HLAB.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia;
 OC Eutheria; Primates; Catarrhini; Hominidae; Homo.
 [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 86220133.
 RA SEEMANN G.H.A., REIN R.S., BROWN C.S., PLOEGH H.L.;
 RT "Gene conversion-like mechanisms may generate polymorphism in human
 RT class I genes";
 RL EMBO J. 5:547-552(1986).
 [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 86042671.
 RA LOPEZ DE CASTRO J.A.;
 RT "Structural analysis of an HLA-B27 functional variant: identification
 RT of residues that contribute to the specificity of recognition by
 RT cytolytic T lymphocytes";
 RL Proc Natl. Acad. Sci. U.S.A. 82:7394-7398(1985).
 CC -1- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
 CC THE IMMUNE SYSTEM.
 CC -1- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
 CC MICROGLOBULIN).

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CC -----
 DR EMBL: X03664; CAA27301.1; -
 DR EMBL: X03667; CAA27301.1; JOINED.
 DR EMBL: L38504; AAA69724.1; -
 DR PIR: B25092; HLHUBK.
 DR HSP: P03989; ILSA.
 DR MIM: 142830;
 DR PROSITE; PS00290; IG_MHC; 1.
 DR PFAM; PF00047; IG; 1.
 DR PFAM; PF00129; MHC_I; 1.
 KW MHC I; Transmembrane; Glycoprotein; Signal.
 FT SIGNAL 1 24
 FT CHAIN 25 362
 FT DOMAIN 25 114
 FT DOMAIN 115 206
 FT DOMAIN 207 298
 FT DOMAIN 299 308
 FT TRANSMEM 309 332
 FT DOMAIN 333 362
 FT CARBOHYD 110 110
 FT DISULFID 125 188
 FT SEQUENCE 362 AA; 40397 MW; 9798F0BB CRC32;
 SQ

Query Match 44.4%; Score 44; DB 1; Length 362;
 Best Local Similarity 90.0%; Pred. No. 5.5;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 11 RENLRTALRY 20
 Db 99 RENLRTALRY 108

RESULT 13
 1B47_HUMAN
 ID 1B47_HUMAN STANDARD; PRT; 362 AA.
 AC P30487;
 DT 01-APR-1993 (Rel. 25, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 01-FEB-1996 (Rel. 33, Last annotation update)
 DE HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-49(B-21) B*4901 ALPHA CHAIN
 DE PRECURSOR.
 GN HLA-B OR HLAB.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Eutheria; Primates; Catarrhini; Hominidae; Homo.
 [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 89235215.
 RA PARHAM P., LAWLER D.A., LOMEN C.E., ENNIS P.D.;
 RT "Diversity and diversification of HLA-A,B,C alleles";
 RL J. Immunol. 142:3937-3950(1989).
 [2]
 RP REVISION TO 78.
 RX MEDLINE; 93056529.
 RA HILDEBRAND W.H., MADRIGAL J.A., BELICH M.P., ZEMMOUR J., WARD F.E.,
 RA WILLIAMS R.C., PARHAM P.;
 RT "Serologic cross-reactivities poorly reflect allelic relationships in
 RT the HLA-B12 and HLA-B21 groups. Dominant epitopes of the alpha 2
 RT helix";
 RL J. Immunol. 149:3563-3568(1992).
 CC -1- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
 CC THE IMMUNE SYSTEM.


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CC -!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
CC MICROGLOBULIN).
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CC -----
DR EMBL; M24037; AAA02950.1; -.
DR HSSP; P30491; IALM.
DR MIM; 142830; -.
DR PROSITE; PS00290; IG_MHC; 1.
DR PFAM; PF00047; ig; 1.
DR PFAM; PF00129; MHC_I; 1.
DR MHC I; Transmembrane; Glycoprotein; Signal.
KW SIGNAL 1 24
FT CHAIN 25 362
FT DOMAIN 25 114
FT DOMAIN 115 206
FT DOMAIN 207 298
FT DOMAIN 299 309
FT TRANSMEM 310 333
FT DOMAIN 334 362
FT CARBOHYD 110 110
FT DISULFID 125 188
FT DISULFID 227 283
SQ SEQUENCE 362 AA; 40581 MW; E996F82F CRC32;

Query Match 44.4%; Score 44; DB 1; Length 362;
Best Local Similarity 90.0%; Pred. No. 5.5;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 11 RENLRTALRY 20
DB 99 RENLRLALRY 108

RESULT 14
ID 1B49_HUMAN STANDARD; PRT; 362 AA.
AC P18464.
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 01-FEB-1996 (Rel. 33, Last annotation update)
DE HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-51(B-5) B*5101 ALPHA CHAIN
DE PRECURSOR.
CN HLA-B OR HLAB.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Primates; Catarrhini; Hominidae; Homo.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 90207291.
RA ENNIS P.D., ZEMMOUR J., SALTER R.D., PARHAM P.;
RT "Rapid cloning of HLA-A,B cDNA by using the polymerase chain
RT reaction: frequency and nature of errors produced in amplification.";
RL proc. Natl. Acad. Sci. U.S.A. 87:2833-2837(1990).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE; 89080265.
RA HAYASHI H., ENNIS P.D., ARIGA H., SALTER R.D., PARHAM P., KANO K.,
RA TAKIGUCHI M.;
RT "HLA-B*51 and HLA-B*52 differ by only two amino acids which are in the
RT helical region of the alpha 1 domain.";
RL J. Immunol. 142:306-311(1989).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE; 89233295.

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RA POHLA H., KUON W., TABACZEWSKI P., DOERNER C., WEISS E.H.;
RT "Allelic variation in HLA-B and HLA-C sequences and the evolution of
RT the HLA-B alleles.";
RL Immunogenetics 29:297-307(1989).
CC -!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
CC THE IMMUNE SYSTEM.
CC -!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
CC MICROGLOBULIN).
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CC -----
DR EMBL; M32319; AAA36232.1; -.
DR EMBL; M22792; AAA59620.1; ALT_SEQ.
DR EMBL; M22786; AAA59620.1; JOINED.
DR EMBL; M22787; AAA59620.1; JOINED.
DR EMBL; M22788; AAA59620.1; JOINED.
DR EMBL; M22789; AAA59620.1; JOINED.
DR EMBL; M22790; AAA59620.1; JOINED.
DR EMBL; M22791; AAA59620.1; JOINED.
DR EMBL; M41087; AAA64513.1; -.
DR EMBL; M41086; AAA64513.1; JOINED.
DR PIR; A30345; A30345.
DR PIR; A30548; A30548.
DR HSSP; P30491; IALM.
DR MIM; 142830; -.
DR PROSITE; PS00290; IG_MHC; 1.
DR PFAM; PF00047; ig; 1.
DR PFAM; PF00129; MHC_I; 1.
KW MHC I; Transmembrane; Glycoprotein; Signal.
FT SIGNAL 1 24
FT CHAIN 25 362
FT DOMAIN 25 114
FT DOMAIN 115 206
FT DOMAIN 207 298
FT DOMAIN 299 308
FT TRANSMEM 309 332
FT DOMAIN 333 362
FT CARBOHYD 110 110
FT DISULFID 125 188
FT DISULFID 227 283
SQ SEQUENCE 362 AA; 40566 MW; 4D846F30 CRC32;

Query Match 44.4%; Score 44; DB 1; Length 362;
Best Local Similarity 90.0%; Pred. No. 5.5;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 11 RENLRTALRY 20
DB 99 RENLRLALRY 108

RESULT 15
ID 1B52_HUMAN STANDARD; PRT; 362 AA.
AC P30489.
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 01-APR-1993 (Rel. 25, Last annotation update)
DE HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-51(B-5) B*5104 ALPHA CHAIN
DE PRECURSOR.
CN HLA-B OR HLAB.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Primates; Catarrhini; Hominidae; Homo.
RN [1]

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RP SEQUENCE FROM N.A.
RX MEDLINE; 92269955.
RA BELICH M.P., MADRICAL J.A., HILDEBRAND W.H., ZEMMOUR J.,
RA WILLIAMS R.C., LUZ R., PETZL-ERLER M.L., FARHAM P.;
RT "Unusual HLA-B alleles in two tribes of Brazilian Indians.";
RL Nature 357:326-329(1992).
CC -1- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
CC THE IMMUNE SYSTEM.
CC -1- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
CC MICROGLOBULIN).
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CC -----
CC EMBL; Z15143; CAA78849.1; -
CC HSP; P30491; IALM.
CC MM; 142830; -
CC PROSITE; PS00290; IG_MHC; 1.
CC PFAM; PF00047; Ig; 1.
CC PFAM; PF00129; MHC_I; 1.
CC MHC I; Transmembrane; Glycoprotein; Signal.
CC SIGNAL 1 24
CC CHAIN 25 362 HLA CLASS I HISTOCOMPATIBILITY ANTIGEN,
CC B-51(B-5) B*5104 ALPHA CHAIN.
CC DOMAIN 25 114 EXTRACELLULAR ALPHA-1.
CC DOMAIN 115 206 EXTRACELLULAR ALPHA-2.
CC DOMAIN 207 298 EXTRACELLULAR ALPHA-3.
CC DOMAIN 299 308 CONNECTING PEPTIDE.
CC TRANSMEM 309 332 CYTOPLASMIC TAIL.
CC DOMAIN 333 362 BY SIMILARITY.
CC CARBOHYD 110 110 BY SIMILARITY.
CC DISULFID 125 188 BY SIMILARITY.
CC DISULFID 227 283 BY SIMILARITY.
CC SEQUENCE 362 AA; 40560 MW; F22F08AB CRC32;
SQ

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Query Match 44.4%; Score 44; DB 1; Length 362;
Best Local Similarity 90.0%; Pred. No. 5.5;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 11 RNLRTALRY 20
Db 99 RNLRTALRY 108

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Search completed: February 8, 2000, 01:26:00
Job time: 1560 sec

Result No.	Score	Query			DB	ID	Description
		Match	Length				
1	50	50.5	89	7	O19674	O19674 homo sapien	
2	50	50.5	89	7	O19565	O19565 homo sapien	
3	50	50.5	131	7	O97998	O97998 homo sapien	
4	50	50.5	131	7	O97999	O97999 homo sapien	
5	50	50.5	181	7	O19779	O19779 homo sapien	
6	50	50.5	181	7	O30197	O30197 homo sapien	
7	50	50.5	181	7	O19669	O19669 homo sapien	
8	50	50.5	181	7	O78028	O78028 homo sapien	
9	50	50.5	355	7	O29853	O29853 homo sapien	
10	50	50.5	361	7	O9XR50	O9XR50 pongo pygma	
11	50	50.5	362	7	O29637	O29637 homo sapien	
12	50	50.5	362	7	O29935	O29935 homo sapien	
13	50	50.5	362	7	P79524	P79524 homo sapien	
14	50	50.5	362	7	O29850	O29850 homo sapien	
15	50	50.5	362	7	O29661	O29661 homo sapien	
16	50	50.5	362	7	O78180	O78180 homo sapien	
17	50	50.5	362	7	O29933	O29933 homo sapien	
18	46	46.5	302	5	O25608	O25608 onchocerca	
19	46	46.5	346	7	O95459	O95459 rattus norv	
20	46	46.5	346	7	O78088	O78088 rattus norv	

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RESULT 1
O19674
IID O19674 PRELIMINARY; PRT; 89 AA.
AC O19674;
DT 01-JAN-1998 (TReMBLrel. 05, Created)
DDT 01-JAN-1998 (TReMBLrel. 05, Last sequence update)
DDT 01-NOV-1998 (TReMBLrel. 08, Last annotation update)
DE HLA-B*13 (FRAGMENT).
HLA-B*13.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Primates; Catarrhini; Hominidae; Homo.
RN [1]
RP SEQUENCE FROM N.A.
RR MAERTENS R., DE CANCK I.;
RS Submitted (APR-1997) to the EMBL/GenBank/DBJ databases.
RD EMBL; Y12378; CAA73021.1; -.
DR PFAM; PF00129; MHC_I; 1.
KW MHC.
FT NON_TER 1
FT NON_TER 89
SQ SEQUENCE 89 AA; 10581 MW; 9AC7631C CRC32;

Query Match 50.5%; Score 50; DB 7; Length 89;
Best Local Similarity 100.0%; Pred. No. 0.8;
Matches 10; Conservative 0; Mismatches 0; Indels 0

QY 11 RNLRTALRY 20
Ddb 74 RNLRTALRY 83
|||||||

RESULT 2
O19565
IID O19565 PRELIMINARY; PRT; 89 AA.
AC O19565;
DT 01-JAN-1998 (TReMBLrel. 05, Created)
DDT 01-MAY-1999 (TReMBLrel. 10, Last sequence update)
DDT 01-MAY-1999 (TReMBLrel. 10, Last annotation update)
DE MHC CLASS I ANTIGEN (FRAGMENT).
HLA-B.
OS Homo sapiens (Human).

```

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Eutheria; Primates; Catarrhini; Hominidae; Homo.
 RN [1]
 RP SEQUENCE FROM N.A.
 RA CAO K., BURDETT L., ZHANG G., FERNANDEZ-VINA M.;
 RL Submitted (AUG-1997) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF017316; AAB70282.2; -.
 KW MHC.
 FT NON_TER 1 1
 FT NON_TER 89 89
 SQ SEQUENCE 89 AA; 10581 MW; 9AC7631C CRC32;

Query Match 50.5%; Score 50; DB 7; Length 89;
 Best Local Similarity 100.0%; Pred. No. 0.8; Indels 0; Gaps 0;
 Matches 10; Conservative 0; Mismatches 0;

QY 11 RENLRTALRY 20
 Db 74 RENLRTALRY 83

RESULT 3
 O97998
 ID O97998 PRELIMINARY; PRT; 131 AA.
 AC O97998;
 DT 01-MAY-1999 (TREMBLrel. 10, Created)
 DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
 DT 01-MAY-1999 (TREMBLrel. 10, Last annotation update)
 DE MHC CLASS I ANTIGEN (FRAGMENT).
 GN HLA-B.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Eutheria; Primates; Catarrhini; Hominidae; Homo.
 RN [1]
 RP SEQUENCE FROM N.A.
 RA HOLDSWORTH R.;
 RL Submitted (NOV-1997) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF035648; AAD02035.1; -.
 KW MHC.
 FT NON_TER 1 1
 FT NON_TER 131 131
 SQ SEQUENCE 131 AA; 15134 MW; 931C8D27 CRC32;

Query Match 50.5%; Score 50; DB 7; Length 131;
 Best Local Similarity 100.0%; Pred. No. 1.2; Indels 0; Gaps 0;
 Matches 10; Conservative 0; Mismatches 0;

QY 11 RENLRTALRY 20
 Db 40 RENLRTALRY 49

RESULT 4
 O97999
 ID O97999 PRELIMINARY; PRT; 131 AA.
 AC O97999;
 DT 01-MAY-1999 (TREMBLrel. 10, Created)
 DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
 DT 01-MAY-1999 (TREMBLrel. 10, Last annotation update)
 DE MHC CLASS I ANTIGEN (FRAGMENT).
 GN HLA-B.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Eutheria; Primates; Catarrhini; Hominidae; Homo.
 RN [1]
 RP SEQUENCE FROM N.A.
 RA HOLDSWORTH R.;
 RL Submitted (NOV-1997) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF035649; AAD02036.1; -.
 KW MHC.
 FT NON_TER 1 1

FT NON_TER 131 131
 SQ SEQUENCE 131 AA; 15057 MW; 32C865A3 CRC32;
 Query Match 50.5%; Score 50; DB 7; Length 131;
 Best Local Similarity 100.0%; Pred. No. 1.2;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 11 RENLRTALRY 20
 Db 40 RENLRTALRY 49

RESULT 5
 O19779
 ID O19779 PRELIMINARY; PRT; 181 AA.
 AC O19779;
 DT 01-JAN-1998 (TREMBLrel. 05, Created)
 DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
 DT 01-NOV-1999 (TREMBLrel. 12, Last annotation update)
 DE MHC CLASS I ANTIGEN (FRAGMENT).
 GN HLA-B.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Eutheria; Primates; Catarrhini; Hominidae; Homo.
 RN [1]
 RP SEQUENCE FROM N.A.
 RA STEINER N.K., NG J., BUSH J., HARTZMAN R.J., JOHNSON-DOW L.,
 RA HURLEY C.K.;
 RL Hum. Immunol. 56:0-0(1997).
 DR EMBL; U90241; AAB82305.1; -.
 DR EMBL; U90240; AAB82305.1; JOINED.
 DR HSSP; P10318; IROG.
 DR PFAM; PF00129; MHC_I; 1.
 KW MHC.
 FT NON_TER 1 1
 FT NON_TER 181 181
 SQ SEQUENCE 181 AA; 21095 MW; 97EC2597 CRC32;

Query Match 50.5%; Score 50; DB 7; Length 181;
 Best Local Similarity 100.0%; Pred. No. 1.7;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 RENLRTALRY 20
 Db 74 RENLRTALRY 83

RESULT 6
 O30197
 ID O30197 PRELIMINARY; PRT; 181 AA.
 AC O30197;
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
 DT 01-NOV-1999 (TREMBLrel. 12, Last annotation update)
 DE MHC CLASS I ANTIGEN (FRAGMENT).
 GN HLA-B.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Eutheria; Primates; Catarrhini; Hominidae; Homo.
 RN [1]
 RP SEQUENCE FROM N.A.
 RA HURLEY C.K., HOYER R.J.;
 RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
 DR EMBL; U63560; AAB05925.1; -.
 DR EMBL; U63559; AAB05925.1; JOINED.
 DR HSSP; P10318; IROG.
 DR PFAM; PF00129; MHC_I; 1.
 KW MHC.
 FT NON_TER 1 1
 FT NON_TER 181 181
 SQ SEQUENCE 181 AA; 20997 MW; 7DFABE37 CRC32;

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Query Match      50.5%; Score 50; DB 7; Length 181;
Best Local Similarity 100.0%; Pred. No. 1.7;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 RENLRTALRY 20
DB 74 RENLRTALRY 83
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RESULT 7
ID O19669 PRELIMINARY; PRT; 181 AA.
AC O19669;
DT 01-JAN-1998 (TREMELREL. 05, Created)
DT 01-JAN-1998 (TREMELREL. 05, Last sequence update)
DT 01-NOV-1999 (TREMELREL. 12, Last annotation update)
DE MHC CLASS I ANTIGEN SHCHA (FRAGMENT).
GN HLA-B.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Primates; Catarrhini; Hominidae; Homo.
RN [1]
RP SEQUENCE FROM N.A.
RA HURLEY C.K., STEINER N.K.;
RL Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; U58470; AAB02607.1; -.
DR EMBL; U58469; AAB02607.1; JOINED.
DR HSSP; P10318; 1ROG.
DR PFAM; PF00129; MHC_I; 1.
KW MHC.
FT NON_TER 1
NON_TER 181
SEQUENCE 181 AA; 21028 MW; EC872642 CRC32;

Query Match      50.5%; Score 50; DB 7; Length 181;
Best Local Similarity 100.0%; Pred. No. 1.7;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 RENLRTALRY 20
DB 74 RENLRTALRY 83
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RESULT 8
ID O78028 PRELIMINARY; PRT; 181 AA.
AC O78028;
DT 01-NOV-1998 (TREMELREL. 08, Created)
DT 01-NOV-1998 (TREMELREL. 08, Last sequence update)
DT 01-NOV-1999 (TREMELREL. 12, Last annotation update)
DE HLA-B*15MD.
GN HLA-B*15MD.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Primates; Catarrhini; Hominidae; Homo.
RN [1]
RP SEQUENCE FROM N.A.
RA GAO X., MATHESON B.;
RL Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; U58316; AAB87723.1; -.
DR EMBL; U58315; AAB87723.1; JOINED.
DR HSSP; P10318; 1ROG.
DR PFAM; PF00129; MHC_I; 1.
KW MHC.
FT NON_TER 1
NON_TER 181
SEQUENCE 181 AA; 21029 MW; C35A18BE CRC32;

Query Match      50.5%; Score 50; DB 7; Length 181;
Best Local Similarity 100.0%; Pred. No. 1.7;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 RENLRTALRY 20
DB 74 RENLRTALRY 83
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RESULT 9
ID Q29853 PRELIMINARY; PRT; 355 AA.
AC Q29853;
DT 01-NOV-1996 (TREMELREL. 01, Created)
DT 01-NOV-1996 (TREMELREL. 01, Last sequence update)
DT 01-NOV-1999 (TREMELREL. 12, Last annotation update)
DE HLA-B ALPHA-CHAIN (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Primates; Catarrhini; Hominidae; Homo.
RN [1]
RP SEQUENCE FROM N.A.
RA GAUCHAT-FEISS D., BREUR-VRISENDORP B.S., RUFER N., JEANNET M.,
RT "Sequencing of a novel functional HLA-B*44 subtype differing in two
RT residues in the alpha 2 domain.";
RL Tissue Antigens 44:261-264(1994).
DR EMBL; X75953; CAA53566.1; -.
DR HSSP; P30491; 1A1M.
DR PROSITE; PS00290; IG_MHC; 1.
DR PFAM; PF00047; Ig; 1.
DR PFAM; PF00129; MHC_I; 1.
KW MHC.
FT NON_TER 355
NON_TER 355 AA; 39845 MW; EF81934E CRC32;

Query Match      50.5%; Score 50; DB 7; Length 355;
Best Local Similarity 100.0%; Pred. No. 3.3;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 RENLRTALRY 20
DB 99 RENLRTALRY 108
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ID Q9XRY0 PRELIMINARY; PRT; 361 AA.
AC Q9XRY0;
DT 01-NOV-1999 (TREMELREL. 12, Created)
DT 01-NOV-1999 (TREMELREL. 12, Last sequence update)
DT 01-NOV-1999 (TREMELREL. 12, Last annotation update)
DE MHC CLASS I ANTIGEN (FRAGMENT).
GN POPY B.
OS Pongo pygmaeus (Orangutan).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Primates; Catarrhini; Hominidae; Pongo.
RN [1]
RP SEQUENCE FROM N.A.
RA ADAMS E.J., THOMSON G., PARHAM P.;
RT "Evidence for an HLA-C-like locus in the orangutan Pongo pygmaeus.";
RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF118895; AAD28435.1; -.
DR PROSITE; PS00290; IG_MHC; 1.
DR NON_TER 1
NON_TER 361 AA; 40466 MW; CB177B4F CRC32;

Query Match      50.5%; Score 50; DB 7; Length 361;
Best Local Similarity 100.0%; Pred. No. 3.4;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 11 RENLRTALRY 20
Db 98 RENLRTALRY 107
RESULT 11
Q29637 PRELIMINARY; PRT; 362 AA.
AC Q29637;
DT 01-NOV-1996 (TRENBLrel. 01, Created)
DT 01-NOV-1996 (TRENBLrel. 01, Last sequence update)
DT 01-NOV-1999 (TRENBLrel. 12, Last annotation update)
DE MHC CLASS I ANTIGEN.
GN HLA-B.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Primates; Catarrhini; Hominidae; Homo.
RN [1]
RP SEQUENCE FROM N.A.
RA DOMENA J.D., PARHAM P.;
RL Submitted (DEC-1993) to the EMBL/GenBank/DBJ databases.
DR EMBL; U04244; AA87397.1; -.
DR HSSP; P30460; IALM.
DR PROSITE; PS00290; IG_MHC; 1.
DR PFAM; PF00047; Ig; 1.
DR PFAM; PF00129; MHC_I; 1.
KW MHC.
SQ SEQUENCE 362 AA; 40359 MW; E8A895D7 CRC32;

Query Match 50.5%; Score 50; DB 7; Length 362;
Best Local Similarity 100.0%; Pred. No. 3.4;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 RENLRTALRY 20
Db 99 RENLRTALRY 108
RESULT 12
Q29935 PRELIMINARY; PRT; 362 AA.
AC Q29935;
DT 01-NOV-1996 (TRENBLrel. 01, Created)
DT 01-NOV-1996 (TRENBLrel. 01, Last sequence update)
DT 01-NOV-1999 (TRENBLrel. 12, Last annotation update)
DE MHC CLASS I HLA-B*3802.
GN HLA-B.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Primates; Catarrhini; Hominidae; Homo.
RN [1]
RP SEQUENCE FROM N.A.
RA LITTLE A.M.M., DOMENA J.D., HILDEBRAND W.H., PARHAM P.;
RL Submitted (FEB-1994) to the EMBL/GenBank/DBJ databases.
DR EMBL; L22028; AAA59618.1; -.
DR HSSP; P30491; IALM.
DR PROSITE; PS00290; IG_MHC; 1.
DR PFAM; PF00047; Ig; 1.
DR PFAM; PF00129; MHC_I; 1.
KW MHC.
SQ SEQUENCE 362 AA; 40404 MW; 83A8399C CRC32;

Query Match 50.5%; Score 50; DB 7; Length 362;
Best Local Similarity 100.0%; Pred. No. 3.4;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 RENLRTALRY 20
Db 99 RENLRTALRY 108

RESULT 13
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ID P79524 PRELIMINARY; PRT; 362 AA.
AC P79524;
DT 01-MAY-1997 (TRENBLrel. 03, Created)
DT 01-MAY-1997 (TRENBLrel. 03, Last sequence update)
DT 01-NOV-1999 (TRENBLrel. 12, Last annotation update)
DE MHC CLASS I HLA-B*440.
GN HLA-B.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Primates; Catarrhini; Hominidae; Homo.
RN [1]
RP SEQUENCE FROM N.A.
RA ARNETT K.L., DARKE C., PARHAM P.;
RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; U64801; AAB40632.1; -.
DR HSSP; P30491; IALM.
DR PROSITE; PS00290; IG_MHC; 1.
DR PFAM; PF00047; Ig; 1.
DR PFAM; PF00129; MHC_I; 1.
KW MHC.
SQ SEQUENCE 362 AA; 40396 MW; AC0FAF3C CRC32;

* Query Match 50.5%; Score 50; DB 7; Length 362;
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Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 RENLRTALRY 20
Db 99 RENLRTALRY 108

RESULT 14
Q29850 PRELIMINARY; PRT; 362 AA.
ID Q29850;
AC Q29850;
DT 01-NOV-1996 (TRENBLrel. 01, Created)
DT 01-NOV-1996 (TRENBLrel. 01, Last sequence update)
DT 01-NOV-1999 (TRENBLrel. 12, Last annotation update)
DE HLA-B ALPHA CHAIN B*4407 PRECURSOR.
GN HLA-B*4407.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Primates; Catarrhini; Hominidae; Homo.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 97004417.
RA VILCHES C., SANZ L., DE PABLO R., MORENO M.E., PUENTE S., KREISLER M.;
RT "Molecular characterization of the new alleles HLA-B*8101 and B*4407.";
RL Tissue Antigens 47:139-142(1996).
DR EMBL; X90391; CAA62036.1; -.
DR HSSP; P30491; IALM.
DR PROSITE; PS00290; IG_MHC; 1.
DR PFAM; PF00047; Ig; 1.
DR PFAM; PF00129; MHC_I; 1.
KW Signal; MHC.
FT SIGNAL 1 24 POTENTIAL.
FT CHAIN 25 362 HLA-B ALPHA CHAIN B*4407.
SQ SEQUENCE 362 AA; 40449 MW; 07B5245D CRC32;

Query Match 50.5%; Score 50; DB 7; Length 362;
Best Local Similarity 100.0%; Pred. No. 3.4;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 RENLRTALRY 20
Db 99 RENLRTALRY 108

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RESULT 15
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AC Q29661;
DT 01-NOV-1996 (TREMELREL. 01, Created)
DT 01-NOV-1996 (TREMELREL. 01, Last sequence update)
DT 01-NOV-1999 (TREMELREL. 12, Last annotation update)
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DE HLA-B*1303.
GN Homo sapiens (Human).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Primates; Catarrhini; Hominidae; Homo.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-BLOOD;
RX MEDLINE: 96232969.
RA BALAS A., GARCIA-SANCHEZ F., VICARIO J.L.;
RT "HLA-B*1303: a new example of poor correlation between serology and
RT structure.";
RL Hum. Immunol. 45:32-36(1996).
DR EMBL: U14943; AAB06829.1; -.
DR HSP: P30491; IAIW.
DR PROSITE: PS00290; IG_MHC; 1.
DR PFAM: PF00047; Ig; 1.
DR PFAM: PF00129; MHC_I; 1.
KW Signal; MHC.
FT SIGNAL 1 24 POTENTIAL.
FT CHAIN 25 362 MHC ANTIGEN HLA-B*1303.
SQ SEQUENCE 362 AA; 40501 MW; 9277DEFB CRC32;

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Query Match 50.5%; Score 50; DB 7; Length 362;
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QY 11 RENLRTALRY 20
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  LOCUS HSB44HLA2 187 bp DNA PRI 15-APR-1994
  DEFINITION H.sapiens HLA-B gene, exon 2.
  ACCESSION X78426
  VERSION X78426.1 GI:473237
  KEYWORDS heavy chain; HLA-B*4404 gene; MHC class I associated.
  SOURCE human.
  ORGANISM Homo sapiens
    Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
    Primates; Catarrhini; Hominidae; Homo.
  REFERENCE
    1 (bases 1 to 187)
  AUTHORS Yao.Z. and Albert.E.
  TITLE Identification of two major HLA-B44 subtypes an a novel B44
    sequence: oligotyping
  JOURNAL Unpublished
  AUTHORS Yao.Z.
  TITLE Direct Submission
  JOURNAL Submitted (18-MAR-1994) Z. Yao, Immunogenetics Laboratory,
    Kinderpoliklinik University of Munich, Pettenkaferstr 8a, 80336
    Munich, FRG
  REMARK revised by [3] MAT
  REFERENCE 3 (bases 1 to 187)
  AUTHORS Yao.Z.
  TITLE Direct Submission
  JOURNAL Submitted (15-APR-1994) Z. Yao, Immunogenetics Laboratory,
    Kinderpoliklinik University of Munich, Pettenkaferstr 8a, 80336
    Munich, FRG
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DEFINITION Homo sapiens HLA-B gene, allele HLA-B*0802, exon 2.

ACCESSION Y18648

VERSION Y18648.1 GI:4160522

KEYWORDS HLA-B gene; HLA-B*0802 allele; human leucocyte antigen B; major histocompatibility complex; MHC class I antigen.

SOURCE human.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
Primates; Catarrhini; Hominidae; Homo.

REFERENCE

1 (bases 1 to 270)

AUTHORS

Guttridge,M.G

TITLE

Direct Submission

JOURNAL

Submitted (12-JAN-1999) M.G. Guttridge, Welsh Blood Service, Ely Valley Road, Talbot Green, Pontyclun, CF72 9WB, UK

FEATURES

Location/Qualifiers

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/note="B*0802 allele"

/number=2

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/gene="HLA-B"

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ORIGIN

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US-08-653-294-29 x HOSA18648 ..

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 DEFINITION AJ132659
 ACCESSION
 VERSION AJ132659.1 GI:4218239
 KEYWORDS HLA-B gene; HLA-B*4408 allele; human leucocyte antigen B; major histocompatibility complex; MHC class I antigen.

SOURCE human.
 ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 270)
 AUTHORS Guttridge M.G.
 TITLE Direct Submission
 JOURNAL Submitted (01-FEB-1999) Guttridge M.G., Tissue Typing, Welsh Blood Service, Ely Valley Road, Talbot Green, Pontyclun, Cardiff, CF72

REFERENCE 2 (bases 1 to 270)
 AUTHORS Guttridge M.G.
 TITLE Serology and confirmatory sequence of HLA-B*4408
 JOURNAL Unpublished
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BASE COUNT 57 a 91 c 85 g 37 t
 ORIGIN

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 Percent Similarity: 100.000 Percent Identity: 100.000

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seq_name: gb_pri: HSHLAB132

seq_documentation_block: 270 bp DNA PRI 06-OCT-1999
 LOCUS HSA249724 Homo sapiens partial HLA-B gene for MHC class I antigen, HLA-B*44
 DEFINITION variant, exon 2.
 ACCESSION AJ249724
 VERSION AJ249724.1 GI:5919229
 KEYWORDS HLA-B gene; HLA-B*44 variant; human leucocyte antigen B; major histocompatibility complex; MHC class I antigen.

SOURCE human.
 ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 270)
 AUTHORS Elsner, H.A., Schmitz, G. and Blasczyk, R.

seq_documentation_block: 270 bp DNA PRI 28-APR-1997
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 DEFINITION Y12378
 ACCESSION Y12378.1 GI:1934896
 VERSION Y12378.1
 KEYWORDS exon 2; HLA-B*13.
 SOURCE human.
 ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 270)
 AUTHORS Maertens, R. and De Canck, I.
 JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 270)
 AUTHORS De Canck, I.
 TITLE Direct Submission
 JOURNAL Submitted (07-APR-1997) I. De Canck, INNOGENETICS N.V., Industriepark Zwijnaarde 7 box 4, B-9052 Gent, BELGIUM

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 /gene="HLA-B*13"
 <1..>270
 /gene="HLA-B*13"
 /codon_start=3
 /protein_id="CAA73021.1"
 /db_xref="GI:1934897"
 /db_xref="SPTREMBL:O19674"
 /translation="SHSMRYFYTAMSRPGRGEPRFITVGVYDDTFVRFSDAASPRM
 APRAPWIEQSGPEYWDRETQISKNTQYRENLTALRYNQSEA"

BASE COUNT 59 a 92 c 83 g 36 t
 ORIGIN

alignment_scores:
 Quality: 50.00 Length: 10
 Ratio: 5.000 Gaps: 0
 Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
 US-08-653-294-29 x HSHLAB132
 Align seg 1/1 to: HSHLAB132 from: 1 to: 270
 11 ArgGluAsnLeuArgThrAlaLeuArgTyr 20
 |||
 222 CGAGAGAACCTGGCCACCGCTCCGCTAC 251

seq_name: gb_pr2: HSA249724

seq_documentation_block: 270 bp DNA PRI 06-OCT-1999
 LOCUS HSA249724 Homo sapiens partial HLA-B gene for MHC class I antigen, HLA-B*44
 DEFINITION variant, exon 2.
 ACCESSION AJ249724
 VERSION AJ249724.1 GI:5919229
 KEYWORDS HLA-B gene; HLA-B*44 variant; human leucocyte antigen B; major histocompatibility complex; MHC class I antigen.

SOURCE human.
 ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 270)
 AUTHORS Elsner, H.A., Schmitz, G. and Blasczyk, R.

```

TITLE      A new HLA-B*44 variant
JOURNAL    Unpublished
REFERENCE  2 (bases 1 to 270)
AUTHORS    Blasczyk, R.
TITLE      Direct Submission
JOURNAL    Medicine, Hannover Medical School, Carl-Neuberg-Str. 1, Hannover,
           30625, GERMANY

FEATURES   Location/Qualifiers
            source
            1..270
            /organism="Homo sapiens"
            /isolate="MH997336/B*1268"
            /db_xref="taxon:9606"
            /chromosome="6"
            /map="6p21"
            1..270
            /gene="HLA-B"
            /note="HLA-B*44 variant"
            /number=2
            1..270
            /gene="HLA-B"
            /gene="HLA-B"
            /standard_name="MHC class I antigen"
            /note="HLA-B*44 variant"
            /codon_start=3
            /label="HLA-B*44_CDS"
            /product="human leucocyte antigen B"
            /protein_id="CAB56342.2"
            /db_xref="GI:6015538"
            /translation="SHSMRYFYTAMSRGGRGEPRITVGYDDTLFVRFDSATSPRK
            EPRAPWIEGEGPEYDRETIQISKNTQTYRENLRALRYNOSEA"

BASE COUNT 60 a 89 c 85 g 36 t
ORIGIN

alignment_scores:
  Quality: 50.00 Length: 10
  Ratio: 5.000 Gaps: 0
  Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
  US-08-653-294-29 x HSA249724 ..
  Align seg 1/1 to: HSA249724 from: 1 to: 270
  11 ArgGluAsnLeuArgThrAlaLeuArgTyr 20
  |||||
  222 CGAGAGAACCTGCGACCGCGCTCCGCTAC 251
  seq_name: gb_pr2:HSSHCHA01

seq_documentation_block:
  LOCUS HSSHCHA01 270 bp DNA PRI 18-JUN-1996
  DEFINITION Human MHC class I antigen SHCHA (HLA-B*4403 variant) gene, exon 2.
  ACCESSION U58469
  VERSION U58469.1 GI:1378136
  KEYWORDS
  SEGMENT 1 of 2
  SOURCE human.
  ORGANISM Homo sapiens
  Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia;
  Eutheria; Primates; Catarrhini; Hominidae; Homo.
  REFERENCE 1 (sites)
  AUTHORS Hurley, C.K. and Steiner, N.K.
  TITLE Novel HLA-B alleles
  JOURNAL Unpublished
  REFERENCE 2 (bases 1 to 270)
  AUTHORS Hurley, C.K. and Steiner, N.K.
  TITLE Direct Submission
  JOURNAL Submitted (16-MAY-1996) C.K. Hurley, Microbiology & Immunology,
  Georgetown University, 3970 Reservoir Rd.NW, Washington, DC 20007,
  USA

FEATURES   Location/Qualifiers
            source
            1..270
            /organism="Homo sapiens"
            /db_xref="taxon:9606"
            /chromosome="6"
            /map="6p21"
            /cell_line="MD674"
            /cell_type="lymphocyte"
            /tissue_type="blood"
            1..270
            /gene="HLA-B*15MD"
            /number=2
            58 a 91 c 85 g 36 t
            BASE COUNT
            ORIGIN

alignment_scores:
  Quality: 50.00 Length: 10
  Ratio: 5.000 Gaps: 0
  Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
  US-08-653-294-29 x HSSHCHA01 ..
  Align seg 1/1 to: HSSHCHA01 from: 1 to: 270
  11 ArgGluAsnLeuArgThrAlaLeuArgTyr 20
  |||||
  222 CGAGAGAACCTGCGACCGCGCTCCGCTAC 251
  seq_name: gb_pr3:HSHLAB15M1

seq_documentation_block:
  LOCUS HSHLAB15M1 270 bp DNA PRI 01-DEC-1997
  DEFINITION Human HLA-B*15MD gene, exon 2.
  ACCESSION U58315
  VERSION U58315.1 GI:2654406
  KEYWORDS
  SEGMENT 1 of 2
  SOURCE human.
  ORGANISM Homo sapiens
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
  Eutheria; Primates; Catarrhini; Hominidae; Homo.
  REFERENCE 1 (sites)
  AUTHORS Gao, X. and Matheson, B.
  TITLE A novel B*15 variant found in oceanic populations
  JOURNAL Unpublished
  REFERENCE 2 (bases 1 to 270)
  AUTHORS Gao, X.
  TITLE Direct Submission
  JOURNAL Submitted (15-MAY-1996) Xiaojiang Gao, The Australian National
  University, Human Genetics Group, Acton, Canberra, Act, Australia,
  2601

FEATURES   Location/Qualifiers
            source
            1..270
            /organism="Homo sapiens"
            /db_xref="taxon:9606"
            /chromosome="6"
            /map="6p21"
            /cell_line="MD674"
            /cell_type="lymphocyte"
            /tissue_type="blood"
            1..270
            /gene="HLA-B*15MD"
            /number=2
            58 a 91 c 85 g 36 t
            BASE COUNT
            ORIGIN

alignment_scores:
  Quality: 50.00 Length: 10
  Ratio: 5.000 Gaps: 0
  Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
  US-08-653-294-29 x HSSHCHA01 ..
  Align seg 1/1 to: HSSHCHA01 from: 1 to: 270
  11 ArgGluAsnLeuArgThrAlaLeuArgTyr 20
  |||||
  222 CGAGAGAACCTGCGACCGCGCTCCGCTAC 251
  seq_name: gb_pr3:HSHLAB15M1

```

1

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alignment_scores:
  Quality: 50.00      Length: 10
  Ratio: 5.000       Gaps: 0
  Percent Similarity: 100.000  Percent Identity: 100.000

alignment_block:
US-08-653-294-29 x HB38021G1 ..
Align seg 1/1 to: HB38021G1 from: 1 to: 270

11 ArgGluAsnLeuArgThrAlaLeuArgTyr 20
|||||
222 CGAGAGAACCTGCGCACCAGCGCTCGCTAC 251

seq_name: gb_pr4:HS44032S1

seq_documentation_block:
LOCUS HS44032S1 270 bp DNA PRI 21-JUN-1999
DEFINITION Human MHC class I antigen HLA-B (HLA-B*4410 allele) gene, exon 2.
ACCESSION U63559
VERSION U63559.1 GI:1488303
KEYWORDS
SEGMENT 1 of 2
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Hurley,C.K. and Hoyer,R.J.
TITLE Human MHC Class I Antigen HLA-B*4410
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 270)
AUTHORS Hurley,C.K. and Hoyer,R.J.
TITLE Direct Submission
JOURNAL Submitted (11-JUL-1996) Dept. of Microbiology and Immunology,
Georgetown University, 3970 Reservoir Rd., NW, Washington, DC
20007, USA
FEATURES
source
1..270
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="6"
/cell_type="white blood cells from whole blood"
1..270
/gene="HLA-B"
/number=2
BASE COUNT 60 a 89 c 85 g 36 t
ORIGIN

alignment_scores:
  Quality: 50.00      Length: 10
  Ratio: 5.000       Gaps: 0
  Percent Similarity: 100.000  Percent Identity: 100.000

alignment_block:
US-08-653-294-29 x HS44032S1 ..
Align seg 1/1 to: HS44032S1 from: 1 to: 270

11 ArgGluAsnLeuArgThrAlaLeuArgTyr 20
|||||
222 CGAGAGAACCTGCGCACCAGCGCTCGCTAC 251

seq_name: gb_pr4:AF035648

seq_documentation_block:
LOCUS AF035648 395 bp DNA PRI 05-JAN-1999
DEFINITION Homo sapiens MHC class I antigen HLA-B gene (HLA-B*4402 variant allele), partial cds.
ACCESSION AF035648
VERSION AF035648.1 GI:4104422

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KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 395)
AUTHORS Holdsworth,R.
TITLE Direct Submission
JOURNAL Submitted (24-NOV-1997) Tissue Typing, Red Cross Blood Service,
South Melbourne, Melbourne, Victoria 3205, Australia
FEATURES
source
1..395
Location/Qualifiers
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="6"
<1..>395
/gene="HLA-B"
/product="MHC class I antigen"
<1..>395
/gene="HLA-B"
/allele="HLA-B*4402 variant"
<1..>395
/gene="HLA-B"
/codon_start=3
/product="MHC class I antigen"
/protein_id="AAD02035.1"
/db_xref="GI:4104423"
/translation="FSDATSPKPEPRAPWISQEGPEYWDRETOISKNTQTYRENLR
TALRYNQSEAGSHIIQRMYGDPDGRLLRGYDQDAYDGDYIALNEDLSSWTAAD
TAAQITQRKEAARVAEODRAYLEGECVE"
BASE COUNT 89 a 120 c 141 g 45 t
ORIGIN

alignment_scores:
  Quality: 50.00      Length: 10
  Ratio: 5.000       Gaps: 0
  Percent Similarity: 100.000  Percent Identity: 100.000

alignment_block:
US-08-653-294-29 x AF035648 ..
Align seg 1/1 to: AF035648 from: 1 to: 395

11 ArgGluAsnLeuArgThrAlaLeuArgTyr 20
|||||
120 CGAGAGAACCTGCGCACCAGCGCTCGCTAC 149

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seq name:	N	Geneseq	36:T07447
N_Geneseq_36:V75169	+	40.00	108.05
N_Geneseq_36:T84985	+	40.00	106.72
N_Geneseq_36:T84986	+	40.00	101.42
N_Geneseq_36:V35645	+	40.00	101.32
N_Geneseq_36:V75169	+	40.00	203.47
N_Geneseq_36:T84985	+	40.00	241.43
N_Geneseq_36:T84986	+	40.00	476.19
N_Geneseq_36:V35645	+	40.00	482.35

seq_documentation_block:
ID T07447 standard; DNA; 362 BP.
AC T07447;
DE 27-APR-1996 (first entry)
DT B. subtilis aprE target DNA.
KW DNA; nucleic acid; analyte; lateral flow detection; PCR;
KW polymerase chain reaction; capture probe; hybridisation; aprE gene;
KW ss.
OS Bacillus subtilis.
PN W09527081-A1.
PD 12-OCT-1995.
PE 30-MAR-1995: 703773

PR 31-MAR-1994; US-221769.
PA (DIPO) DU PONT DE NEMOURS & CO ET

PI Ebersole RC, Fitzpatrick-McElligott S, Hendrickson ER:
(DORC) LE FONT DE NETWORKS & CO E I.

PI Majarian WR, Payne MS, Rafalski JA;

DR WPI; 95-358650/46.

PT Detecting the presence of a nucleic acid analyte - by contact with a

test strip having immobilised capture moieties.

PS Example 1; Page 43; 82pp; English.

CC A specific segment (T07447) of the B. subtilis aprE gene was amplified
CC by PCR using primers 3 (T07448) and 4 (T07449) in the presence of

CC DIOCTYL-14-GALF and arizoximin-11-GALF. Detection of the PCR product
CC was performed using a lateral flow nucleic acid detection system in

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CC which anti-dioxigenin coupled to alkaline phosphatase was
CC deposited on the 'application zone' of a nitrocellulose membrane,
CC and avidin on the 'capture zone'. Amplified aprE target DNA was
CC applied to the application zone and allowed to wick to the capture
CC zone, where it was detected by colorimetry. In another method,
CC target aprE DNA amplified in the presence of biotin-labeled dNTP
CC was hybridized in solution with aprE DNA amplified in the presence
CC of dioxigenin-labeled dNTP to demonstrate lateral flow detection of a
CC bifunctional nucleic acid hybrid.
SQ Sequence 362 BP; 99 A; 89 C; 82 G; 92 T;

alignment_scores:
    Quality: 46.00
    Ratio: 2.875
    Percent Similarity: 94.118    Percent Identity: 52.941

alignment_block:
US-08-653-294-29 x T07447/rev ..

Align seg 1/1 to reverse of: T07447 from: 1 to: 362

      3  LeuAlaIleArgLeuAsnGluArGArGGLuAsnLeuArgThrAlaLeuAr 19
      ::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
    111 GTAGCCCTTGAGAGTGAGAGCCGCGCTTTAAATTGGAGAAATGCCATPAG 62

      19 g 19
      |
      61 G 61

seq_name: N_Geneseq_36:N80745

seq_documentation_block:
ID ID N80745 standard; DNA; 1220 BP.
AC N80745;
DT 14-SEP-1990 (first entry)
DE Coding region of the aprA gene encoding subtilisin in Bacillus subtilis
KW Bacillus subtilis strain Q8127 (trpC2 leuA8 sacUdh200); subtilisin;
KW thermal stability; pH stability; specific activity;
KW substrate specificity; detergency; ss.
OS Bacillus subtilis strain Q8127 (trpC2 leuA8 sacUdh200).
Key Location/Qualifiers

```

seq name: N Geneseq 36:N80745

seq_documentation_block:

ID N80745 standard; DNA; 1220 BP.

AC N80745;

DT 14-SEP-1990 (first entry)

DE Coding region of the aprA gene encoding subtilisin in *Bacillus subtilis*

KW *Bacillus subtilis* strain QBI27 (trpC2 leuA8 sacU_H200); subtilisin; thermal stability; pH stability; specific activity.

KW thermal stability; pH stability; specific activity;
 KW substrate specificity; detergency; ss

OS *Bacillus subtilis* strain OB127 (trpC2 leuA8 sacU^h200).

EH	Key	Location/Qualifiers
00		

```

FT mat_peptide 1..1143
FT /*tag= a
PN WO808033-A.
PD 20-OCT-1988.
PF 28-MAR-1988; U01038.
PR 10-APR-1988; US-036872.
PA (AMGE-) Amgen Inc.
PI Zurovski MM, Stabinsky Y, Levitt M;
DR WPI: 88-307568/43.
DR P-PSDB; P80744.
PT New subtilisin analogues -
PT have aminoacid(s) present in calcium binding site replaced by
PT negatively charged aminoacid(s)
PS Example 2: Table 1, pages 22-24; 60pp; English.
CC Genomic DNA was isolated from cells of B. subtilis strain QBI27 (trpC2
CC 'leuA8 sacuH200'). The coding region of the aprA gene was sequenced and
CC the results of the sequence are given in n80745. The specific identity
CC of the initial 5 codons of the leader region is attributable to the
CC report of Stahl, et al., J. Bacteriol., 158, 411-418, (1984) and Wong,
CC et al P.N.A.S., 81, 1184-1188 (1984). There exist codon sequence
CC differences from Stahl, et al., at amino acid positions 84 and 85.
CC Specifically, Stahl, et al., reports a codon GTT (coding for valine) at
CC amino acid position 84 while the codon GTA (also coding for valine)
CC appears in n80745. Stahl, et al., also reports a codon AGC (coding for
CC serine) at amino acid position 85 as opposed to the codon GCG (coding for
CC alanine) in n80745. The patent concerns a novel subtilisin analogue
CC which has an amino acid sequence of a naturally occurring Bacillus
CC subtilisin which has been modified by having: one or more of the amino
CC acids present in a calcium binding site of the naturally occurring
CC Bacillus subtilisin replaced by a negatively charged amino acid, and
CC one or more of any Asn-Gly sequence of the naturally occurring Bacillus
CC subtilisin deleted or replaced by a different amino acid. Pref. it is
CC an analogue of subtilisin Carlsberg, subtilisin DY, subtilisin BPN', an
CC aprA subtilisin of B. subtilis or subtilisin from B. mesentericus. The
CC subtilisin analogues exhibit improved thermal and pH stability,
CC increased specific activity and broad substrate specificity thereby
CC increasing the detergency of detergent formulations contg. such
CC analogues.
SQ Sequence 1220 BP; 355 A; 281 C; 283 G; 301 T;

alignment_scores:
Quality: 46.00 Length: 17
Ratio: 2.875 Gaps: 0
Percent Similarity: 94.118 Percent Identity: 52.941

alignment_block:
US-08-653-294-29 x N80745/rev ..
Align seg 1/1 to reverse of: N80745 from: 1 to: 1220

3 LeuAlaIleArgLeuAsnGluArgGluAsnLeuArgThrAlaLeuAr 19
:::|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
381 GTAGCCTTGAGTGAAGAGCGCGCTTTAATTGAGAAATGCCATAAG 332
19 g 19
331 G 331

seq_name: N_Geneseq_36:006587
seq_documentation_block:
ID Q06587 standard; DNA; 1220 BP.
AC N80745;
DT 26-FEB-1991 (first entry)
DE Thermostable Bacillus subtilisin encoded by aprA gene.
KW aprA gene; subtilisin; thermostable enzyme; protease; surfactant; ds.
OS Bacillus subtilis.
FH Key Location/Qualifiers
FT cds 1..1143
FT /*tag= a
FT mat_peptide 316..1143
FT /*tag= b
FT /label= aprA gene
PN WO8704461-A.
PD 30-JUL-1987.
PF 07-JAN-1987; U00027.
PR 15-JAN-1986; US-819241.
PA (AMGE-) AMGEN.
PI Stabinsky Y, Zukowski M;
DR WPI: 87-221262/31.
DR P-PSDB; P70555.
PT Thermally stable and pH stable subtilisin analogues - produced by
PT deleting or replacing at least one of the asparagine-glycine
PT sequences.
PS Disclosure; Table 1; 56pp; English.
CC Modified subtilisin may be used in detergent compositions, it has
CC an improved pH and heat stability. See also P70556.
CC Sequence 1220 BP; 355 A; 283 C; 281 G; 301 T;

```

```

FT cds 1..1143
FT /*tag= b
FT mat_peptide 319..1143
FT /*tag= c
PN EP-398539-A.
PD 22-NOV-1990.
PF 01-MAY-1990; 304715.
PR 17-MAY-1989; US-353124.
PA (AMGE-) AMGEN INC.
PI Zukowski MM, Narhi LO, Levitt M;
DR WPI: 90-350298/47.
DR P-PSDB; R07970.
PT Bacillus subtilin analogues - with improved pH thermal and oxidn.
PT stability useful in cleaning compans.
PS Claim 20: Table 1; 39pp; English.
CC Modified analogues of subtilisin are useful in cleaning fabrics, and
CC have an improved resistance to oxidation, heat and pH extremes.
CC Analogues have one or more negative AAs present in the calcium
CC binding site (CBS) and may also be used in manufacture of protein
CC hydrolysates, and detection of incomplete Abs in serology.
CC Sequence 1220 BP; 355 A; 281 C; 283 G; 301 T;
SQ

alignment_scores:
Quality: 46.00 Length: 17
Ratio: 2.875 Gaps: 0
Percent Similarity: 94.118 Percent Identity: 52.941

alignment_block:
US-08-653-294-29 x Q06587/rev ..
Align seg 1/1 to reverse of: Q06587 from: 1 to: 1220

3 LeuAlaIleArgLeuAsnGluArgGluAsnLeuArgThrAlaLeuAr 19
:::|||||:|||||:|||||:|||||:|||||:|||||:|||||:
381 GTAGCCTTGAGTGAAGAGCGCGCTTTAATTGAGAAATGCCATAAG 332
19 g 19
331 G 331

seq_name: N_Geneseq_36:N70890
seq_documentation_block:
ID N70890 standard; DNA; 1220 BP.
AC N70890;
DT 26-FEB-1991 (first entry)
DE Thermostable Bacillus subtilisin encoded by aprA gene.
KW aprA gene; subtilisin; thermostable enzyme; protease; surfactant; ds.
OS Bacillus subtilis.
FH Key Location/Qualifiers
FT cds 1..1143
FT /*tag= a
FT mat_peptide 316..1143
FT /*tag= b
FT /label= aprA gene
PN WO8704461-A.
PD 30-JUL-1987.
PF 07-JAN-1987; U00027.
PR 15-JAN-1986; US-819241.
PA (AMGE-) AMGEN.
PI Stabinsky Y, Zukowski M;
DR WPI: 87-221262/31.
DR P-PSDB; P70555.
PT Thermally stable and pH stable subtilisin analogues - produced by
PT deleting or replacing at least one of the asparagine-glycine
PT sequences.
PS Disclosure; Table 1; 56pp; English.
CC Modified subtilisin may be used in detergent compositions, it has
CC an improved pH and heat stability. See also P70556.
CC Sequence 1220 BP; 355 A; 283 C; 281 G; 301 T;

```

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seq_documentation_block:
ID   N71241 standard; DNA; 1500 BP.
AC   N71241;
DT   02-MAY-1991 (first entry)
DE   Subtilisin gene from Bacillus subtilis.
KW   subtilisin; extracellular protease; amylase production; ss.
OS   Bacillus subtilis.
FH   Key
FT   signal_peptide 137..205
FT   mat_peptide 455..1279
FT   misc_rna 206..454
FT   tag= b
FT   tag= c
FT   label= pro sequence
PN
PD   EP-246678-A.
PD   25-NOV-1987.
PF   01-JAN-1987; 200690.
PR   24-JUN-1983; US-507419.
PR   29-MAY-1984; US-614491.
PR   29-MAY-1984; US-614616.
PR   29-MAY-1984; US-614612.
PR   29-MAY-1984; US-614617.
PR   29-MAY-1984; US-614615.
PR   01-JAN-1987; EP-200690.
PA   (GETH ) GENENTECH INC.
PI   Bott RR, Ferrari E, Wells JA, Estell DA, Henner DJ;
DR   WI: 87-328920/47.
DR   P-PSDB; P71060.
PT   Bacillus strains not excreting subtilisin or neutral protease -
PT   obt'd. by recombinant DNA procedures, useful for enzyme prodn.
PT   esp. of hydrolase(s) such as amylase
PS   Example; Fig 7: 71pp; English.
CC   B.subtilis i168 chromosomal DNA was digested with EcoRI. A single
CC   6kb fragment hybridised to a fragment from the C-terminus of the
CC   subtilisin structural gene in pS4 (see N71240). It was ligated to
CC   EcoRI-cut pBS42 and the ligation mixture used to transform E.coli
CC   ATCC 31446. Plasmid DNA was prepared from a pooled suspension of
CC   transformant colonies and used to transform a protease deficient
CC   strain of B.subtilis (BG84). Plasmid DNA from protease producing
CC   colonies was digested with EcoRI and examined by Southern blot
CC   analysis to isolate the 6kb fragment. A positive clone was identified
CC   containing a plasmid designated psi68.1. Three HincII fragments
CC   and a HincIII-EcoRI fragment were ligated into M13 vectors and
CC   sequenced to obtain the entire subtilisin sequence.
SQ   Sequence 1500 BP; 443 A; 343 C; 328 G; 386 T;

alignment_scores:
Quality: 46.00 Length: 17
Ratio: 2.875 Gaps: 0
Percent Similarity: 94.118 Percent Identity: 52.941

alignment_block:
US-08-653-294-29 x N71241/rev ..
Align seg 1/1 to reverse of: N71241 from: 1 to: 1500

3 LeuAlaIleArgLeuAsnGluArgArgGluAsnLeuArgThrAlaLeuAr 19
:::|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
517 GTAGCCTTGAGAGTGAAGAGCGCGCGCTTAAATTGAGAAATGCCATAAG 468

19 g 19
457 G 457

seq_name: N_Geneseq_36:N70058

seq_documentation_block:
ID   N70058 standard; DNA; 1500 BP.
AC   N70058;
DT   20-JAN-1991 (first entry)
DE   Bacillus subtilis subtilisin gene.

```

```

KW Bacillus subtilis; subtilisin; enzyme; ss.
FH Key Location/Qualifiers
FT cds 137..1280
FT /*tag= a
FT /product=subtilisin
PN EP-247647-A.
PD 02-DEC-1987.
PF 22-JUN-1984; 200689.
PR 24-JUN-1983; US-507419.
PR 29-MAY-1984; US-614491.
PA (GETH) Genentech Inc.
PI Bott RR,
PI Ferrari E,
PI Wells JA,
PI Estell DA,
PI Henner DJ,
DR WPI; 87-336315/48.
DR P-PSDB; P70053.
DR DNA mutagenesis proces - by introducing restriction enzyme sites,
PT digesting and introducing oligonucleotides capable of annealing at
PT the restriction enzyme sites.
PS Disclosure; Fig 7; 61pp; English.
CC This recombinant sequence may be used for the industrial production
CC of subtilisin. See also N70057, N70059 and P70054.
SQ Sequence 1500 BP; 443 A; 342 C; 330 G; 385 T;

alignment_scores:
    Quality: 46.00 Length: 17
    Ratio: 2.875 Gaps: 0
Percent Similarity: 94.118 Percent Identity: 52.941

alignment_block:
US-08-653-294-29 x N70058/rev ..
Align seg 1/1 to reverse of: N70058 from: 1 to: 1500

3 LeuAlaIleArgLeuAsnGluArgGluAsnLeuArgThrAlaLeuAr 19
:::|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
517 GTAGCCTTGAGAGTGAGAGCGCGCTTTAATTGCGAATGCCATAG 468

19 g 19
467 G 467

seq_name: N_Geneseq_36:Q90042
seq_documentation_block:
ID Q90042 standard; DNA; 1500 BP.
AC Q90042;
DT 10-JAN-1996 (first entry)
DE B.subtilis subtilisin gene.
KW Bacillus amyloliquefaciens subtilisin; carbonyl hydrolase; protease;
KW fusion protein; preproprotein; transport; cell membrane; B.subtilis;
KW autoproteolysis; maturation; ss.
OS Bacillus subtilis.
FH Key Location/Qualifiers
FT cds 137..1282
FT /*tag= a
FT /product= subtilisin
FT /transl_except= 137..139 a.a.: fMet
FT signal_peptide 137..454
FT /*tag= b
FT mat_peptide 455..1279
FT /*tag= c
FT US5411873-A.
PN PD 02-MAY-1995.
PF 29-MAY-1984; 614612.
PR 29-MAY-1984; US-614612.
PR 01-APR-1986; US-846627.
PR 27-FEB-1990; US-488433.
PR 11-AUG-1992; US-928697.
PA (GENV) GENENCOR INC.

```

```

PI Adams RM, Power SD, Powers DB, Wells JA, Yansura DG;
DR WPI: 95-178127/23.
DR P-PSDB; R74224.
PT Recovery of recombinant subtilisin mutants from host cells - by
PT treatment with active subtilisin to cleave mutant from its
PT pro-sequence.
PS Disclosure; Fig 2; 32pp; English.
CC The nucleotide sequence of the Bacillus subtilis subtilisin gene. The
CC gene is used in a method to produce a carbonyl hydrolase (subtilisin)
CC e.g. the B.amyloliquefaciens subtilisin (Q90041) or other heterologous
CC protein (produced as a fusion protein) e.g. human growth hormone, such
CC that the desired protein is translated as a preproprotein which can be
CC transported across the cell membrane but is not released as an
CC enzymatically functional protein until the application of an external
CC protease or a protease encoded by the host cell e.g. B.subtilis
CC subtilisin or neutral protease (Q90043). The preproprotein sequence is
CC mutated so that it is incapable of autoproteolytic maturation. The
CC B.amyloliquefaciens sequence was mutated using the primers Q90044-5 and
CC Q****-*, specifically at S221N, D32N, A48R or contained a deletion of
CC 166 amino acids from the C-terminus of the protein. 386 T;
SQ Sequence 1500 BP; 443 A; 343 C; 328 G; 386 T;

alignment_scores:
    Quality: 46.00 Length: 17
    Ratio: 2.875 Gaps: 0
Percent Similarity: 94.118 Percent Identity: 52.941

alignment_block:
US-08-653-294-29 x Q90042/rev ..
Align seg 1/1 to reverse of: Q90042 from: 1 to: 1500

3 LeuAlaIleArgLeuAsnGluArgGluAsnLeuArgThrAlaLeuAr 19
:::|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
517 GTAGCCTTGAGAGTGAGAGCGCGCTTTAATTGAGAAATGCCATAG 468

19 g 19
467 G 467

seq_name: N_Geneseq_36:N60475
seq_documentation_block:
ID N60475 standard; DNA; 1524 BP.
AC N60475;
DT 24-AUG-1991 (first entry)
DE Sequence of the apr [Bsu] gene encoding subtilisin.
KW Alkaline serine protease; exoprotease; enzyme; proteolytic;
KW degradation; Bacillus host strains; ss.
OS Bacillus subtilisin.
FH Key Location/Qualifiers
FT signal_peptide 283..369
FT /*tag= a
FT /transl_except= (pos:283..285,aa:Met)
FT cds 370..600
FT /*tag= b
FT /label= pro sequence
FT mat_peptide 601..1428
FT /*tag= c
FT WO8601825-A.
PN PD 27-MAR-1986.
PF 20-SEP-1985; 905017.
PR 21-SEP-1984; US-652968.
PR 13-MAY-1985; US-733379.
PR (GENE-) GENEX CORP.
PA Farnestock SR, Fisher KE;
DR WPI; 86-094078/14.
DR P-PSDB; P60571.
PT Bacillus strains with reduced extra-cellular protease levels -
PT useful as hosts for secretion of heterologous polypeptide(s) and
PT proteins.
PS Example; Fig 2; 30pp; English.

```



```
FT      EP-354580-A.
PN      14-FEB-1990.
PD      10-AUG-1989.
PR      11-AUG-1988; JP-200758.
PA      (OLYU) Olympus Optical Co., Ltd.
PI      Kano K, Takiguchi;
DR      WPI; 90-046289/07.
DR      P-PSDB; R03142.
PT      New DNA for class 1 human leucocyte antigens and derived probes and
PT      transformed cells, useful for DNA typing, as immunogens etc.
PS      Claim 2; pp11-12; 23pp; English.
CC      The HLA class I DNA can be used as a source of probes for use in DNA
CC      typing. Transformed cells, which are useful as immunogens, can be
CC      obtained by introducing these DNAs into eucaryotic cells.
SQ      Sequence 1086 BP; 223 A; 335 C; 358 G; 170 T;

alignment_scores:
  Quality: 44.00      Length: 10
  Ratio: 4.889      Gaps: 0
  Percent Similarity: 90.000      Percent Identity: 90.000

alignment_block:
US-08-653-294-29 x Q01822  ..

Align seg 1/1 to: Q01822 from: 1 to: 1086

11  ArgGluAsnLeuArgThrAlaLeuArgTyr 20
|||||
294 CGAGAGAACCTCGGATCGGCTCGCTAC 323
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OM of: US-08-653-294-29 to: EST:* out_format : pfs

Date: Feb 8, 2000 6:23 AM

About: Results were produced by the GenCore software, version 4.5,
Copyright (c) 1993-2000 Compugen Ltd.

Command line parameters:

-MODEL=framet.p2n.model -DEV=xlp
-Q=/cgnl_1/USPTO.spool/US08653294/runat_04022000_160700_15770/app_query.fasta.2
-DB=EST -QFMT=fastap -SUFFIX=est -GAPOP=12.000 -GAPEXT=4.000
-MINMATCH=0.100 -LOOPCL=0.000 -LOOPEXT=0.000 -GAPOP=4.500
-GAPEXT=0.050 -XGAPOP=10.000 -XGAPEXT=0.500 -FGAPOP=6.000
-FGAPEXT=7.000 -YGAPOP=10.000 -YGAPEXT=0.500 -DELOP=6.000
-DELXT=7.000 -START=1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOALIGN=200 -THR_SCORE=pct -ALIGN=15 -MODE=LOCAL
-OUTFMT=pfs -NORM=ext -MINLEN=0 -MAXLEN=1000000 -USER=US08653294
-NCPU=6 -ICPU=3 -NO_XLPXY -WAIT -THREADS=1

Search information block:

Query: US-08-653-294-29

Query length: 20

Database: EST:

Database sequences: 4538634

Database length: 1887831982

Search time (sec): 7600.090000

score_list:

Sequence	Strd	Orig	ZScore	Escore	Len	Documentation
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gb_est28:AI488819	-	52.00	147.60	18.66	647	! AI488819 EST247158 tomato ovary
gb_est11:D33316	+	50.00	146.82	20.62	360	! D33316 CELK0196ZF yuji Kohara u
gb_est11:D33321	+	50.00	146.82	20.62	360	! D33321 CELK0196GF yuji Kohara u
gb_est11:D33579	+	50.00	146.82	20.62	360	! D33579 CELK0226GF yuji Kohara u
gb_est17:C69731	+	50.00	146.82	20.62	360	! C69731 C69731 yuji Kohara unpub
gb_est17:C69775	+	50.00	146.82	20.62	360	! C69775 C69775 yuji Kohara unpub
gb_est17:C69958	+	50.00	146.82	20.62	360	! C69958 C69958 yuji Kohara unpub
gb_est17:D37592	+	50.00	145.88	23.28	399	! D37592 CELK004C4F yuji Kohara u
gb_est23:AI124815	+	50.00	145.54	24.31	414	! AI124815 am5606.xl Johnston f
gb_gss15:A0640208	+	48.00	138.17	62.56	472	! A0640208 927P1-2F1.TP 927P1 Try
gb_gss15:A0655562	+	48.00	135.56	87.43	627	! A0655562 Sheared DNA-9C11.TF SH
gb_gss14:A0576359	+	48.00	134.64	98.37	693	! A0576359 nbx00808E07f CUGI Rice
gb_gss6:A0861681	+	48.00	133.35	115.99	797	! A0861681 nbx0017E18f CUGI Rice
gb_gss1:CNS0078F	+	47.00	135.94	83.23	430	! AL089373 Arabidopsis thaliana g
gb_gss1:CNS000WJ5	-	47.00	134.72	97.31	491	! AL093647 Arabidopsis thaliana g
gb_gss3:B28953	-	47.00	131.41	148.80	704	! B28953 T22N177R TAMU Arabidopsi
gb_gss1:CNS000WLA	+	47.00	129.79	183.24	840	! AL093724 Arabidopsis thaliana g
gb_est25:A1248474	+	46.50	135.56	87.40	379	! AI248474 gb71d01.xl Soares.feta
gb_gss10:A0201243	-	46.50	131.13	154.33	614	! A0201243 RPI111-4512A.TJ RPI1-1
gb_est37:AI938226	-	46.00	135.07	93.05	338	! A938226 sc41802.y1 Gm-cl014 GI
gb_gss4:AO721357	+	46.00	131.18	153.21	516	! AO721357 HS_5559_A2_A12-T7A RPI
gb_est19:AA782242	-	46.00	130.30	171.56	568	! AA782242 ai31d04.s1 Soares.para
gb_gss15:A0649574	+	46.00	128.41	218.73	698	! A0649574 Sheared DNA-28D9.TF SH
gb_gss6:A0855602	+	45.50	127.26	253.48	791	! A0855602 Cpg1696A CpiOWagDNAL C
gb_est39:AW108889	+	45.50	127.78	237.09	632	! AW108889 gate0002G03f Gossypium
gb_est40:AW143668	+	45.00	131.75	142.52	347	! AW143668 EST293964 Normalized r
gb_est22:AA008269	+	45.00	128.86	206.34	475	! AA008269 AU008269 Schizosacchar
gb_est20:AA881004	+	45.00	127.12	257.92	574	! AA881004 vx35b04.r1 Stratagene
gb_est9:AA106132	+	45.00	126.22	289.44	633	! AA106132 mm20f05.r1 Stratagene
gb_gss1:CTBE12	+	45.00	125.82	304.59	661	! AJ227511 Clona intestinalis ger
gb_gss3:BI2131	-	45.00	121.26	546.84	1086	! BI2131 F13C15-T7 IGF Arabidops
gb_est8:CO3945	-	44.00	132.36	131.67	232	! C03945 C03945 Human heart cDNA
gb_gss3:B22867	-	44.00	131.57	145.83	253	! B22867 F22K6TR IGF Arabidopsi
gb_est10:AA151891	+	44.00	131.50	147.19	255	! AA151891 zool1f06.r1 Stratagene
gb_gss1:AA500004	-	44.00	131.00	156.76	269	! AL085978 Arabidopsis thaliana g
gb_est11:AA263158	+	44.00	130.54	166.41	283	! AA263158 PMY0534 KGI-a Lambda Z
gb_est11:D35886	+	44.00	128.33	220.99	360	! D35886 CELK028E7F yuji Kohara u
gb_est27:AI466429	+	44.00	128.17	225.34	366	! AI466429 vx35b04.y1 Stratagene
gb_est6:D82221	+	44.00	127.95	231.88	375	! D82221 HUMHBC4626 Human pancrea
gb_est37:AI944684	+	44.00	127.36	250.21	400	! AI944684 bs04b11.y1 Drosophila
gb_gss9:AO148510	-	44.00	126.95	263.53	418	! AO148510 HS_2243_B2_D01_MR CIT

gb_gss15:A0638856 - 44.00 126.32 285.96 448 ! A0638856 927P1-6F7.TV 927P1
gb_gss4:AO676371 - 44.00 126.26 288.22 451 ! A0676371 HS_2145_B2_B03.T7C
gb_gss1:CNS000B4 - 44.00 126.13 292.75 457 ! AL082990 Arabidopsis thalian

seq_name: gb_gss4:AO720034

seq_documentation_block:

LOCUS AO720034 532 bp DNA GSS 14-JUL-1999
DEFINITION HS_5541_A2_G07_SP6E RPI1-11 Human Male BAC Library Homo sapiens
genomic clone Plate-1117 Col-14 Row-M, genomic survey sequence.
ACCESSION AO720034
VERSION AO720034.1 GI:5479703
KEYWORDS GSS.
SOURCE human.

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;

Eutheria; Primates; Catarrhini; Hominoidea; Homo.

1 (bases 1 to 532)

MAHAIAS.G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,
Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and
Hood,L.

Sequence-tagged connectors: A sequence approach to mapping and

scanning the human genome

Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999)

99380589

Contact: Mahairas GG, Wallace JC, Hood L

High Throughput Sequencing Center

University of Washington

401 Queen Anne Avenue North, Seattle, WA 98109, USA

Tel: (206) 616-3618

Fax: (206) 616-3887

Email: jwallace@u.washington.edu

Clones are derived from the human BAC library RPI1-11. For BAC

library availability, please contact Pieter de Jong

(pieterdejong.med.buffalo.edu). Clones may be purchased from

BACPAC Resources (http://bacpac.med.buffalo.edu/ordering_bac.htm)

or from Resear h Genetics (info@resgen.com). BAC end Web Server:

http://www.htsc.washington.edu

Plate: 1117 row: M column: 14

Seq primer: SP6

Class: BAC ends

High quality sequence stop: 532.

Location/Qualifiers

source

1. 532

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone_lib="RPI1-11 Human Male BAC Library"

/sex="male"

/notes="Vector: pBACE3.6; Genomic sequence of BAC ends"

BASE COUNT 145 a 119 c 104 g 158 t 6 others

ORIGIN

alignment_scores:

Quality: 52.00 Length: 16

Ratio: 3.467 Gaps: 0

Percent Similarity: 93.750 Percent Identity: 62.500

alignment_block:

US-08-653-294-29 x AO720034

Align seg 1/1 to: AO720034 from: 1 to: 532

1 TyrArgLeuAlaIleArgLeuAsnGluArgGluAsnLeuArgThr 16

|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

433 TATAAAGTGGCTTTAGACTCACTCACTAGGCGAGAGAGTTGCATACA 480

seq_name: gb_est28:AI488819

seq_documentation_block:

LOCUS AI488819 647 bp mRNA EST 29-JUN-1999

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DEFINITION EST247158 tomato ovary, TAMU Lycopersicon esculentum cDNA clone
ACCESSION CLE018L8, mRNA sequence.
VERSION AI488819.1 GI:4394190
KEYWORDS EST.
SOURCE tomato.
ORGANISM Lycopersicon esculentum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons; core
eudicots; Asteridae; euasterids I; Solanales; Solanaceae; Solanum;
Potatoe; Lycopersicon.
REFERENCE 1 (bases 1 to 647)
AUTHORS Alcala,J., Vrebalov,J., White,R., Matern,A.L., Vision,T.,
Holt,I.E., Liang,F., Upton,J., Ronning,C.M., Craven,M.B.,
Fujii,C.Y., Bowman,C.L., Nierman,W., Fraser,C.M., Venter,J.C.,
Martin,G.B., Tanksley,S.D. and Giovannoni,J.
Generation of ESTs from tomato carpel tissue
Unpublished (1999)
On May 18, 1998 this sequence version replaced gi:3138293.
COMMENT Contact: David Frisch
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 4366
Fax: 864 656 4293
Email: dfrisch@CLEMSON.EDU.
FEATURES
Source
1..647
/organism="Lycopersicon esculentum"
/cultivar="TA496"
/db_xref="taxon:4081"
/clone="CLE018L8"
/clone_lib="tomato ovary, TAMU"
/tissue_type="carpel"
/dev_stage="5 days pre-anthesis to 5 days post-anthesis"
/lab_host="XL1-Blue MRF"
/notes="Vector: pBlueScript SK(-); Site_1: EcoRI; Site_2:
XhoI; cLED - Tomato Carpel EST Library. OligodT-primed and
directionally cloned cDNA in vector Lambda ZAP II with 5'
and 3' ends located at the EcoRI and XhoI sites,
respectively."
BASE COUNT 198 a 116 c 148 g 185 t
ORIGIN
111 G 111
alignment_scores:
Quality: 52.00 Length: 20
Ratio: 3.714 Gaps: 0
Percent Similarity: 70.000 Percent Identity: 60.000
seq_documentation_block:
US-08-653-294-29 x AI488819/rev ..
Align seg 1/1 to reverse of: AI488819 from: 1 to: 647
1 TTTArgLeuAlaIleArgLeuAsnGluArgGluAsnLeuArgThrAl 17
|||||
384 TATGTCTCCATACCATGATGACAGATCTGGACACATTCAGGACAG 335
17 aLeuArgTyr 20
|||||
334 GTTGAGGTAT 325
seq_name: gb_est1:D35316
seq_documentation_block:
LOCUS D35316 360 bp. mRNA EST 08-AUG-1994
DEFINITION CELK019CZF Yuji Kohara unpublished cDNA Caenorhabditis elegans CDNA
clone yk19g12 5', mRNA sequence.
ACCESSION D35316
VERSION D35316.1 GI:526832
KEYWORDS EST.
SOURCE Caenorhabditis elegans.
ORGANISM Caenorhabditis elegans
Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida;
Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
REFERENCE 1 (bases 1 to 360)
AUTHORS Kohara,Y., Mitsuki,H., Nishigaki,A., Motohashi,T., Sugimoto,A. and
Tabara,H.
Toward an expression map of the C.elegans genome
Unpublished (1994)
COMMENT Contact: Yuji Kohara
Gene Library Lab
National Institute of Genetics
Yata 1111, Mishima, Shizuoka 411, Japan
Tel: 81-559-81-6854
Fax: 81-559-81-6855
Email: ykohara@lab.nig.ac.jp.
LOCATION/Qualifiers
1..360
/organism="caenorhabditis elegans"
/strain="CB1489 him-8(e1489)"
/db_xref="taxon:6239"
/clone="yk19g12"
/clone_lib="yuji kohara unpublished cDNA"
/sex="hermaphrodite, male"
/tissue_type="whole animal"
/dev_stage="varied"
BASE COUNT 111 a 87 c 82 g 77 t 3 others
ORIGIN
111 G 111
seq_name: gb_est1:D35321
seq_documentation_block:
LOCUS D35321 360 bp. mRNA EST 08-AUG-1994
DEFINITION CELK019G6F Yuji Kohara unpublished cDNA Caenorhabditis elegans CDNA
clone yk19g6 5', mRNA sequence.
ACCESSION D35321
VERSION D35321.1 GI:526826
KEYWORDS EST.
SOURCE Caenorhabditis elegans.
ORGANISM Caenorhabditis elegans
Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida;
Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
REFERENCE 1 (bases 1 to 360)
AUTHORS Kohara,Y., Mitsuki,H., Nishigaki,A., Motohashi,T., Sugimoto,A. and
Tabara,H.
Toward an expression map of the C.elegans genome
Unpublished (1994)
COMMENT Contact: Yuji Kohara
Gene Library Lab
National Institute of Genetics
Yata 1111, Mishima, Shizuoka 411, Japan
Tel: 81-559-81-6854
Fax: 81-559-81-6855
Email: ykohara@lab.nig.ac.jp.
LOCATION/Qualifiers
111 G 111

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source
1..360
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/strain="CB1489 him-8(e1489)"
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/clone="yk1996"
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/sex="hermaphrodite, male"
/tissue_type="whole animal"
/dev_stage="varied"
116 a 85 c 79 g 80 t
BASE COUNT
ORIGIN

alignment_scores
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Ratio: 3.571 Gaps: 0
Percent Similarity: 82.353 Percent Identity: 64.706

alignment_block:
US-08-653-294-29 x D35321 ..
Align seg 1/1 to: D35321 from: 1 to: 360
2 ArgLeuAlaileArgLeuAsnGluArgGluAsnLeuArgThrAlaLe 18
||| |||:|||||:|||||:|||||:|||||:|||||:|||||:
79 AGATCCGCGTTAAGGTTGACGGAAGAAGATCCAATCTGAGGATTATTCT 128
18 u 18
129 G 129

seq_name: gb_est1:D35579

seq_documentation_block:
LOCUS D35579 360 bp mRNA EST 08-AUG-1994
DEFINITION CELK02269F Yuji Kohara unpublished cDNA Caenorhabditis elegans cDNA
clone yk2269 5', mRNA sequence.
ACCESSION D35579
VERSION D35579.1 GI:527030
KEYWORDS EST.
SOURCE Caenorhabditis elegans.
ORGANISM Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditidae;
Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
Kohara, Y., Mitsuki, H., Nishigaki, A., Mochashi, T., Sugimoto, A. and
Tabara, H.
Toward an expression map of the C.elegans genome
Unpublished (1994)
Contact: Yuji Kohara
Gene Library Lab
National Institute of Genetics
Yata 1111, Mishima, Shizuoka 411, Japan
Tel: 81-559-81-6854
Fax: 81-559-81-6855
Email: ykohara@lab.nig.ac.jp.
FEATURES
Source
1..360
/organism="Caenorhabditis elegans"
/strain="CB1489 him-8(e1489)"
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/clone="yk2269"
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/sex="hermaphrodite, male"
/tissue_type="whole animal"
/dev_stage="varied"
105 a 84 c 87 g 77 t 6 others
BASE COUNT
ORIGIN

alignment_scores
Quality: 50.00 Length: 17
Ratio: 3.571 Gaps: 0

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Percent Similarity: 82.353 Percent Identity: 64.706
alignment_block:
US-08-653-294-29 x D35579 ..
Align seg 1/1 to: D35579 from: 1 to: 360
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||| |||:|||||:|||||:|||||:|||||:|||||:|||||:
24 AGATCCGCGTTAAGGTTGACGGAAGAAGATCCAATCTGAGGATTATTCT 73
18 u 18
74 G 74

seq_name: gb_est17:C69731

seq_documentation_block:
LOCUS C69731 360 bp mRNA EST 23-SEP-1997
DEFINITION Yuji Kohara unpublished cDNA Caenorhabditis elegans cDNA
clone yk368h10 5', mRNA sequence.
ACCESSION C69731
VERSION C69731.1 GI:2431087
KEYWORDS EST.
SOURCE Caenorhabditis elegans.
ORGANISM Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditidae;
Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
Kohara, Y., Mochashi, T., Tabara, H., Watanabe, H., Sugimoto, A.,
Sano, M., Miyata, A. and Nishigaki, A.
Expression map of the C.elegans genome
Unpublished (1996)
On Sep 12, 1996 this sequence version replaced gi:1316439.
Contact: Yuji Kohara
Gene Library Lab
National Institute of Genetics
Yata 1111, Mishima, Shizuoka 411, Japan
Tel: 81-559-81-6854
Fax: 81-559-81-6855
Email: ykohara@lab.nig.ac.jp.
FEATURES
Source
1..360
/organism="Caenorhabditis elegans"
/strain="CB1489 him-8(e1489)"
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18 u 18
94 G 94

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LOCUS C69775
DEFINITION C69775 Yuji Kohara unpublished cDNA Caenorhabditis elegans cDNA
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ACCESSION C69775
VERSION C69775.1 GI:2440300
KEYWORDS EST
SOURCE Caenorhabditis elegans.
ORGANISM Caenorhabditis elegans
Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditidae;
Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
REFERENCE 1 (bases 1 to 360)
AUTHORS Kohara,Y., Motohashi,T., Tabara,H., Watanabe,H., Sugimoto,A.,
Sano,M., Miyata,A. and Nishigaki,A.
TITLE Expression map of the C.elegans genome
JOURNAL Unpublished (1996)
COMMENT Contact: Yuji Kohara
Gene Library Lab
National Institute of Genetics
Yata 1111, Mishima, Shizuoka 411, Japan
Tel: 81-559-81-6854
Fax: 81-559-81-6855
Email: ykohara@lab.nig.ac.jp.
Location/Qualifiers
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TITLE Expression map of the C.elegans genome
JOURNAL Unpublished (1996)
COMMENT On May 18, 1995 this sequence version replaced gi:810965.
Contact: Yuji Kohara
Gene Library Lab
National Institute of Genetics
Yata 1111, Mishima, Shizuoka 411, Japan
Tel: 81-559-81-6854
Fax: 81-559-81-6855
Email: ykohara@lab.nig.ac.jp.
Location/Qualifiers
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Ratio:	3.692	Gaps:	0
Percent Similarity:	92.857	Percent Identity:	57.143

Align seq 1/1 to: AQ655562 from: 1 to: 627

Align seq 1/1 to: AQ655562 from: 1 to: 627

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DEFINITION	nbxb008907f	CUGI Rice BAC Library	Oryza sativa	genomic clone
	nbxb008907f	genomic survey sequence.		

ACCESSION AQ576359
 VERSION AQ576359.1 GI:4976844
 KEYWORDS GSS.
 SOURCE *Oryza sativa*.

REFERENCE
AUTHORS
1 (bases 1 to 693)
Wing, R.A. and Dean, R.A.

TITLE	A BAC End Sequencing Framework to Sequence the Rice Genome
JOURNAL	Unpublished (1998)
COMMENT	Contact: Wing RA

Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 7288
Fax: 864 656 4293

Email: rwing@clemson.edu
Seq primer: TAATACGACTCACTATAGGG
Class: BAC ends
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Location/Qualifiers
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/HindIII=vector: pBeloPAC11; Site.1: HindIII; Site.2: HindIII. Rice is one of two most popular grains in the world. Half of the world population especially those inhabiting highly populated areas of the humid tropics and subtropics, rely on rice as their primary source of carbohydrate. Monocotyledonous rice is a diploid plant (2n=24) with a haploid genome equivalent of 431 Mbp (Arumuganathan and Earle, 1991). The relatively small genome of rice, three times larger than that of Arabidopsis, makes it suitable for genomic studies. In order to facilitate positional cloning, physical mapping and genome sequencing of rice, we have constructed a BAC library from *Oryza sativa*, Nipponbare variety. The library contains 36,864 clones with an average insert size of 128.5 Kb providing 10.9 haploid genome equivalents. The deep coverage allows the isolation a particular sequence with a probability of 99.9 %. Two high density filters, each containing 18,432 clones (doubly spotted), represent the whole library for colony screening.

232 c 219 g 119 t 1 others

122 a	232 c	219 g	119 t	1 others
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BASE COUNT	represent the whole	library	1 others
ORIGIN			
122 a	232 c	219 g	119 t

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run On: February 8, 2000, 04:05:43 ; Search time 133.56 Seconds
(without alignments)
3.547 Million cell updates/sec

Title: US-08-653-294-30

Perfect score: 100

Sequence: 1 YRLATRLNERENLTALRY 20

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 188963 seqs, 23686106 residues

Total number of hits satisfying chosen parameters: 188963

Minimum DB seq length: 0

Maximum DB seq length: 1000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : A_Geneseq_36.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	100	100.0	20	1 R92910	HLA-B*2702 CTL modu
2	100	100.0	20	1 W33793	Peptide B2702.84-7
3	94	94.0	20	1 R92908	HLA-B*2702 CTL modu
4	94	94.0	20	1 R92909	HLA-B*2702 CTL modu
5	94	94.0	20	1 W33791	Peptide B2702.84-7
6	94	94.0	20	1 W33792	Peptide B2702.84-7
7	88	88.0	20	1 R92907	HLA-B*2702 CTL modu
8	88	88.0	20	1 R35428	HLA-B*2702 84-75-84
9	88	88.0	20	1 W33778	Immunomodulating d
10	75	75.0	20	1 R95430	HLA-B*2702 84-75-77
11	50	50.0	10	1 R83095	HLA-B*2702 CTL modu
12	50	50.0	10	1 R95426	HLA-B*2702 75-84(T)
13	50	50.0	10	1 W33788	Peptide B2702.75-8
14	46.5	46.5	20	1 R92911	HLA-B*2702 CTL modu
15	46.5	46.5	20	1 W33779	Immunomodulating d
16	45	45.0	25	1 R48286	Peptide fragment o
17	45	45.0	25	1 R83093	HLA-B*2702 CTL modulat
18	45	45.0	25	1 R95422	HLA-B*2702.84-75-84
19	45	45.0	184	1 Y06801	Peptide Seq ID No:
20	45	45.0	362	1 R31142	Sequence of HLA-B*53
21	45	45.0	362	1 R31144	Sequence of HLA-B*53
22	45	45.0	362	1 R12463	HLA-B*2702 CTL modu
23	44	44.0	10	1 R41208	Peptide fragment o
24	44	44.0	10	1 R83062	HLA-B*2702 CTL modu
25	44	44.0	10	1 R95413	Alpha1-helix of HL
26	44	44.0	10	1 W07512	T-cell modulating
27	44	44.0	10	1 W47265	Immunomodulatory p
28	44	44.0	10	1 W47266	Immunomodulatory p
29	44	44.0	10	1 W33784	Peptide B2702.75-8
30	44	44.0	15	1 R92912	HLA-B*2702 CTL modu
31	44	44.0	15	1 W33795	Peptide B2702.70-8
32	44	44.0	20	1 R92913	HLA-B*7 CTL modulat
33	44	44.0	20	1 R95415	HLA-B*7.84-75-84 Pa
34	44	44.0	20	1 W33790	Peptide B7.84-75/7

35	44	44.0	20	1 W33797	Peptide B7.84-75/7
36	44	44.0	25	1 R41205	Peptide fragment o
37	44	44.0	25	1 R83090	HLA-B*2702 CTL modu
38	44	44.0	25	1 R95416	HLA-B*2702.60-84. C
39	44	44.0	25	1 W33794	Peptide B2702.60-8
40	43	43.0	10	1 W07522	T-cell modulating
41	43	43.0	1228	1 R77673	S-layer protein en
42	43	43.0	1228	1 W22862	Bacillus stearothe
43	42	42.0	580	1 W68402	FelV-A gag protein
44	42	42.0	1784	1 R05898	Gene product of f1
45	42	42.0	1784	1 R94427	FELV F6A provirus

ALIGNMENTS

RESULT 1	
ID R92910	standard; peptide; 20 AA.
AC R92910:	
DT 16-MAY-1996 (first entry)	
DE HLA-B*2702 CTL modulating peptide (B2702.84-75(T)/75-84(T)).	
KW cytotoxic T lymphocyte; CTL; major histocompatibility complex; MHC;	
KW immunosuppressant; graft versus host disorder; transplantation; therapy;	
KW class I MHC; HLA-B*2702.	
OS Synthetic.	
PN W09526979-A1.	
PD 12-OCT-1995.	
PF 05-APR-1995; U04349.	
PR 05-APR-1994; US-222851.	
PA (STRD) UNIV LELAND STANFORD JUNIOR.	
PI Clayberger C, Krensky AM, Parham P;	
DR WPI: 95-358582/46.	
PT Extension of acceptance period of transplants from MHC unmatched	
PT donor hosts - using Class I B75-84 MHC antigen of the recipient	
PT host	
PS Example 15; Page 36; 80pp; English.	
CC R83061-R83085, R83090-R83096 and R92907-R92913 represent fragments of	
CC class I major histocompatibility complex (MHC) antigens. This sequence	
CC is an inverted dimer of residues 75-84 of the alpha-1 domain of the class	
CC I MHC HLA-B*2702. These sequences can be used to extend the period of	
CC acceptance by a recipient of a transplant from an MHC unmatched donor.	
CC The peptides are administered to a patient in conjunction with a	
CC subtherapeutic amount of an immunosuppressant. This is administered to	
CC the patient for a limited period of time (compared to the lifetime	
CC administration for current treatments). The peptides particularly	
CC modulate (or inhibit) the activity of the cytotoxic T lymphocytes (CTLs)	
CC of the patient.	
SQ Sequence 20 AA:	

Query Match 100.0%; Score 100; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 3.6e-10;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1	YRLATRLNERENLTALRY 20
DB 1	YRLATRLNERENLTALRY 20

RESULT 2	
ID W33793	standard; peptide; 20 AA.
AC W33793:	
DT 19-JUN-1998 (first entry)	
DE Peptide B2702.84-75(T)/75-84r tested for immunomodulating activity.	
KW Immunomodulating dimer; immunosuppressant drug; CTL activation;	
KW transplantation; autoimmune disease; Class I HLA-B alpha-1 domain;	
KW rejection.	
OS Synthetic.	
PN Homo sapiens.	
PD W09744351-A1.	
PD 27-NOV-1997.	

PF 22-MAY-1997; U08689.
 PR (STRD) UNIV LELAND STANFORD JUNIOR.
 PI Beulow R, Clayberger C, Krensky AM;
 DR WPI: 98-086530/08.
 PT New immunomodulating dimer peptide(s) - based on a Class I HLA-B
 PT alpha-1 domain, used for preventing rejection of transplants or
 PT treating autoimmune diseases
 PS Example 1; Page 19; 41pp; English.
 CC Peptides W3784-98 and W3778-9 were assayed for their immunomodulating
 CC activity. A peptide-type compound or variant is claimed which has
 CC immunomodulating activity, including the N-terminal acylated and/or
 CC C-terminal amidated or esterified forms of up to 60 amino acids, where
 CC the peptide-type compound comprises the formula: A-B, where A, B =
 CC (R aa76-77L) (aa79-84) or (aa84-79) (Laa77-76R); aa76 = E or V; aa77 =
 CC D, S or N; aa79 = R or G; aa80 = I or N; aa81, aa84 = a hydrophobic or
 CC small amino acid; aa82 = R or L; aa83 = G or R; and aa represents amino
 CC acid. The sequence in the brackets may optionally be absent or truncated
 CC at any peptide type bond within the brackets. The compounds comprise
 CC amino acid sequences related to a Class I HLA-B alpha1 domain (positions
 CC 79-84). They can be used to inhibit cytotoxic T-lymphocytes (CTL) from
 CC undesirably attacking cells in a host or in vitro. They can also be
 CC used in combination with antigenic peptides or proteins of interest to
 CC activate CTLs. They can also inhibit the proliferation of T cells in
 CC response to anti-CD3. The peptide can be used for preventing rejection
 CC of transplants or for treating autoimmune diseases, e.g. diabetes,
 CC rheumatoid arthritis and lupus erythematosus. The products can also be
 CC used for detection and diagnosis.
 SQ Sequence 20 AA;

Query Match 100.0%; Score 100; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 3.6e-10; Indels 0; Gaps 0;
 Matches 20; Conservative 0; Mismatches 0;

OY 1 YRLATRLNERENLTALRY 20
 |||||
 DB 1 YRLATRLNERENLTALRY 20

RESULT 3

R92909 ID R92909 standard; peptide; 20 AA.
 AC R92909;
 DT 16-MAY-1996 (first entry)
 DE HLA-B2702 CTL modulating peptide (B2702.84-75/75-84(T)).
 KW Cytotoxic T lymphocyte; CTL; major histocompatibility complex; MHC;
 KW immunosuppressant; graft versus host disorder; transplantation; therapy;
 KW class I MHC; HLA-B2702.
 OS Synthetic.
 PN W09526979-A1.
 PD 12-OCT-1995.
 PF 05-APR-1995; U04349.
 PR 03-APR-1994; US-222851.
 PA (STRD) UNIV LELAND STANFORD JUNIOR.
 PI Clayberger C, Krensky AM, Parham P;
 DR WPI: 95-358582/46.
 PT Extension of acceptance period of transplants from MHC unmatched
 PT donor hosts - using Class I B75-84 MHC antigen of the recipient
 PT host

PS Example 15; Page 36; 80pp; English.
 CC R3061-R3085, R83090-R83096 and R92907-R92913 represent fragments of
 CC class I major histocompatibility complex (MHC) antigens. This sequence
 CC is an inverted dimer of residues 75-84 of the alpha-1 domain of the class
 CC I MHC HLA-B2702. These sequences can be used to extend the period of
 CC acceptance by a recipient of a transplant from an MHC unmatched donor.
 CC The peptides are administered to a patient in conjunction with a
 CC subtherapeutic amount of an immunosuppressant. This is administered to
 CC the patient for a limited period of time (compared to the lifetime
 CC administration for current treatments). The peptides particularly
 CC modulate (or inhibit) the activity of the cytotoxic T lymphocytes (CTLs)
 CC of the patient.
 SQ Sequence 20 AA;

Query Match 94.0%; Score 94; DB 1; Length 20;
 Best Local Similarity 95.0%; Pred. No. 3.4e-09;
 Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 YRLATRLNERENLTALRY 20
 |||||
 DB 1 YRLATRLNERENLTALRY 20

RESULT 4

R92908 ID R92908 standard; peptide; 20 AA.
 AC R92908;
 DT 16-MAY-1996 (first entry)
 DE HLA-B2702 CTL modulating peptide (B2702.84-75(T)/75-84).
 KW Cytotoxic T lymphocyte; CTL; major histocompatibility complex; MHC;
 KW immunosuppressant; graft versus host disorder; transplantation; therapy;
 KW class I MHC; HLA-B2702.
 OS Synthetic.
 PN W09526979-A1.
 PD 12-OCT-1995.
 PF 05-APR-1995; U04349.
 PR 05-APR-1994; US-222851.
 PA (STRD) UNIV LELAND STANFORD JUNIOR.
 PI Clayberger C, Krensky AM, Parham P;
 DR WPI: 95-358582/46.
 PT Extension of acceptance period of transplants from MHC unmatched
 PT donor hosts - using Class I B75-84 MHC antigen of the recipient
 PT host

PS Example 15; Page 36; 80pp; English.
 CC R3061-R3085, R83090-R83096 and R92907-R92914 represent fragments of
 CC class I major histocompatibility complex (MHC) antigens. This sequence
 CC is an inverted dimer of residues 75-84 of the alpha-1 domain of the class
 CC I MHC HLA-B2702. These sequences can be used to extend the period of
 CC acceptance by a recipient of a transplant from an MHC unmatched donor.
 CC The peptides are administered to a patient in conjunction with a
 CC subtherapeutic amount of an immunosuppressant. This is administered to
 CC the patient for a limited period of time (compared to the lifetime
 CC administration for current treatments). The peptides particularly
 CC modulate (or inhibit) the activity of the cytotoxic T lymphocytes (CTLs)
 CC of the patient.
 SQ Sequence 20 AA;

Query Match 94.0%; Score 94; DB 1; Length 20;
 Best Local Similarity 95.0%; Pred. No. 3.4e-09;
 Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 YRLATRLNERENLTALRY 20
 |||||
 DB 1 YRLATRLNERENLTALRY 20

RESULT 5

R92911 ID W3791 standard; peptide; 20 AA.
 AC W3791;
 DT 19-JUN-1998 (first entry)
 DE Peptide B2702.84-75/75-84 tested for immunomodulating activity.
 KW Immunomodulating dimer; immunosuppressant drug; CTL activation;
 KW transplantation; autoimmune disease; Class I HLA-B alpha-1 domain;
 KW rejection.
 OS Synthetic.
 OS Homo sapiens.
 PN W09744351-A1.
 PD 27-NOV-1997.
 PF 22-MAY-1997; U08689.
 PR 24-MAY-1996; US-653294.
 PA (STRD) UNIV LELAND STANFORD JUNIOR.
 PI Beulow R, Clayberger C, Krensky AM;
 DR WPI: 98-086530/08.

PT New immunomodulating dimer peptide(s) - based on a Class I HLA-B
 PT alpha-1 domain, used for preventing rejection of transplants or
 PT treating autoimmune diseases
 PS Example 1; Page 19; 41pp; English.
 CC Peptides W33784-98 and W33778-9 were assayed for their immunomodulating
 CC activity. A peptide-type compound or variant is claimed which has
 CC immunomodulating activity, including the N-terminal acylated and/or
 CC C-terminal amidated or esterified forms of up to 60 amino acids, where
 CC the peptide-type compound comprises the formula: A-B, where A, B =
 CC (R aa76-77L) (aa79-84) or (aa84-79) (Laa77-76R); aa76 = E or V; aa77 =
 CC D, S or N; aa79 = R or G; aa80 = I or N; aa81, aa84 = a hydrophobic or
 CC small amino acid; aa82 = R or L; aa83 = G or R; and aa represents amino
 CC acid. The sequence in the brackets may optionally be absent or truncated
 CC at any peptide type bond within the brackets. The compounds comprise
 CC amino acid sequences related to a Class I HLA-B alpha1 domain (positions
 CC 79-84). They can be used to inhibit cytotoxic T-lymphocytes (CTL) from
 CC undesirably attacking cells in a host or in vitro. They can also be
 CC used in combination with antigenic peptides or proteins of interest to
 CC activate CTLs. They can also inhibit the proliferation of T cells in
 CC response to anti-CD3. The peptide can be used for preventing rejection
 CC of transplants or for treating autoimmune diseases, e.g. diabetes,
 CC rheumatoid arthritis and lupus erythematosus. The products can also be
 CC used for detection and diagnosis.
 SQ Sequence 20 AA;

Query Match 94.0%; Score 94; DB 1; Length 20;
 Best Local Similarity 95.0%; Pred. No. 3.4e-09;
 Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YRLATRLNERENLRALRY 20
 ||||| ||||| ||||| |||||
 Db 1 YRLATRLNERENLRALRY 20

RESULT 6
 W33792 ID R92907 standard; peptide; 20 AA.
 AC W33792;
 DT 19-JUN-1998 (first entry)
 DE Peptide B2702:84-75/75-84 tested for immunomodulating activity.
 KW Immunomodulating dimer; immunosuppressant drug; CTL activation;
 KW transplantation; autoimmune disease; Class I HLA-B alpha-1 domain;
 KW rejection.
 OS Synthetic.
 OS Homo sapiens.
 PN W09744351-A1.
 PD 27-NOV-1997.
 PF 22-MAY-1997; U08689.
 PR 24-MAY-1996; US-653294.
 PA (STRD) UNIV LELAND STANFORD JUNIOR.
 PI Beulow R, Clayberger C, Krensky AM;
 DR WPI; 98-086530/08.
 PT New immunomodulating dimer peptide(s) - based on a Class I HLA-B
 PT alpha-1 domain, used for preventing rejection of transplants or
 PT treating autoimmune diseases
 PS Example 1; Page 19; 41pp; English.
 CC Peptides W33784-98 and W33778-9 were assayed for their immunomodulating
 CC activity. A peptide-type compound or variant is claimed which has
 CC immunomodulating activity, including the N-terminal acylated and/or
 CC C-terminal amidated or esterified forms of up to 60 amino acids, where
 CC the peptide-type compound comprises the formula: A-B, where A, B =
 CC (R aa76-77L) (aa79-84) or (aa84-79) (Laa77-76R); aa76 = E or V; aa77 =
 CC D, S or N; aa79 = R or G; aa80 = I or N; aa81, aa84 = a hydrophobic or
 CC small amino acid; aa82 = R or L; aa83 = G or R; and aa represents amino
 CC acid. The sequence in the brackets may optionally be absent or truncated
 CC at any peptide type bond within the brackets. The compounds comprise
 CC amino acid sequences related to a Class I HLA-B alpha1 domain (positions
 CC 79-84). They can be used to inhibit cytotoxic T-lymphocytes (CTL) from
 CC undesirably attacking cells in a host or in vitro. They can also be
 CC used in combination with antigenic peptides or proteins of interest to
 CC activate CTLs. They can also inhibit the proliferation of T cells in
 CC response to anti-CD3. The peptide can be used for preventing rejection

CC of transplants or for treating autoimmune diseases, e.g. diabetes,
 CC rheumatoid arthritis and lupus erythematosus. The products can also be
 CC used for detection and diagnosis.
 SQ Sequence 20 AA;

Query Match 94.0%; Score 94; DB 1; Length 20;
 Best Local Similarity 95.0%; Pred. No. 3.4e-09;
 Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YRLATRLNERENLRALRY 20
 ||||| ||||| ||||| |||||
 Db 1 YRLATRLNERENLRALRY 20

RESULT 7
 R92907 ID R92907 standard; peptide; 20 AA.
 AC R92907;
 DT 16-MAY-1996 (first entry)
 DE HLA-B2702 CTL modulating peptide (B2702:84-75/75-84).
 KW Cytotoxic T lymphocyte; CTL; major histocompatibility complex; MHC;
 KW immunosuppressant; graft versus host disorder; transplantation; therapy;
 KW class I MHC; HLA-B2702.
 OS Synthetic.
 OS Homo sapiens.
 PN W09526979-A1.
 PD 12-OCT-1995.
 PF 05-APR-1995; U04349.
 PR 05-APR-1994; US-222851.
 PA (STRD) UNIV LELAND STANFORD JUNIOR.
 PI Clayberger C, Krensky AM, Parham P;
 DR WPI; 95-358582/46.
 PT Extension of acceptance period of transplants from MHC unmatched
 PT donor hosts - using Class I B75-84 MHC antigen of the recipient
 PT host
 PS Example 15; Page 36; 80pp; English.
 CC R83061-R83085, R83090-R83096 and R92907-R92914 represent fragments of
 CC class I major histocompatibility complex (MHC) antigens. This sequence
 CC is an inverted dimer of residues 75-84 of the alpha-1 domain of the class
 CC I MHC HLA-B2702. These sequences can be used to extend the period of
 CC acceptance by a recipient of a transplant from an MHC unmatched donor.
 CC The peptides are administered to a patient in conjunction with a
 CC subtherapeutic amount of an immunosuppressant. This is administered to
 CC the patient for a limited period of time (compared to the lifetime
 CC administration for current treatments). The peptides particularly
 CC modulate (or inhibit) the activity of the cytotoxic T lymphocytes (CTLs)
 CC of the patient.
 SQ Sequence 20 AA;

Query Match 88.0%; Score 88; DB 1; Length 20;
 Best Local Similarity 90.0%; Pred. No. 3.2e-08;
 Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 YRLATRLNERENLRALRY 20
 ||||| ||||| ||||| |||||
 Db 1 YRLATRLNERENLRALRY 20

RESULT 8
 R95428 ID R95428 standard; peptide; 20 AA.
 AC R95428;
 DT 12-NOV-1996 (first entry)
 DE HLA-B2702 84-75-84 palindromic.
 KW HLA; p74; alpha1-helix; human-leucocyte-associated antigen; inhibitor;
 KW T-cell lysate; membrane protein; mammal; heat shock protein; Hsc70; APC;
 KW B cell; calcium influx; cytotoxic T lymphocyte; CTL; differentiation;
 KW cytolysis; antigen presenting cell.
 OS Synthetic.
 PN W09513288-A1.
 PD 18-MAY-1995.
 PF 10-NOV-1994; U12985.

PR 10-NOV-1993; US-150493.
 PA (STRD) UNIV LELAND STANFORD JUNIOR.
 PI Clayberger C, Krensky AM;
 DR WPI; 95-194027/25.
 PT Compens. comprising lymphoid surface membrane proteins - which may
 PT inhibit cytolytic activity and differentiation of CTLs.
 PS Example: Page 12; 29pp; English.
 CC R95413, and R95415-R95431 represent palindromes and fragments of
 CC human-leucocyte-associated antigens. This sequence represents the
 CC HLA-B2702 84-75-84 palindrome. These sequences can be used to isolate
 CC the protein p74 from a T-cell lysate. p74 is a T-cell surface membrane
 CC protein associated with T-cell activation in mammalian T-cells, and is
 CC also immunologically cross reactive with the heat shock protein Hsc70.
 CC p74 is found in a limited number of cell types, but is particularly
 CC expressed on B and T cells. p74 can be isolated by lysis of a suitable
 CC cell with an amphoteric detergent, and then passed through an affinity
 CC column containing a covalently bound HLA-B2702 palindromic peptide.
 CC Compositions comprising the extracellular fragment of p74 combined with
 CC HLA-B2702.60-84 (see R95416), induces calcium influx, and inhibits
 CC cytotoxic T lymphocyte (CTL) differentiation or cytotoxicity. Candidate
 CC compounds can be screened for their effect on the cytolytic activity of
 CC T-cells, by combining them with the extracellular portion of p74 and
 CC determining the amount of binding between the candidate compound and p74.
 CC Modulation of CTL activity can be inhibited in a cellular composition
 CC containing T-cells and antigen presenting cells (APCs), by adding to the
 CC mix the extracellular portion of p74, in an amount sufficient to compete
 CC with p74 for the binding of the p74 ligand.
 SQ Sequence 20 AA;

Query Match 88.0%; Score 88; DB 1; Length 20;
 Best Local Similarity 90.0%; Pred. No. 3.2e-08;
 Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 YRLATRLNERENLRALRY 20
 ||||| ||||| ||||| |||||
 DB 1 YRLAIRELNERENLRALRY 20

RESULT 9
 W33778
 ID W33778 standard; peptide; 20 AA.
 AC W33778;
 DE 19-JUN-1998 (first entry)
 DE Immunomodulating dimer peptide #1.
 KW Immunomodulating dimer; immunosuppressant drug; CTL activation;
 KW transplantation; autoimmune disease; Class I HLA-B alpha-1 domain;
 OS rejection.
 OS Synthetic.
 OS Homo sapiens.
 PN W09744351-A1.
 PD 27-NOV-1997.
 PF 22-MAY-1997; U08689.
 PR 24-MAY-1996; US-653294.
 PA (STRD) UNIV LELAND STANFORD JUNIOR.
 PI Beulow R, Clayberger C, Krensky AM;
 DR WPI; 98-086530/08.
 PT New immunomodulating dimer peptide(s) - based on a Class I HLA-B
 PT alpha-1 domain, used for preventing rejection of transplants or
 PT treating autoimmune diseases
 PT Claim 16; Page 35; 41pp; English.
 CC This sequence represents a specifically claimed immunomodulating
 CC dimer peptide of the invention. A peptide-type compound or variant is
 CC claimed which has immunomodulating activity, including the N-terminal
 CC acylated and/or C-terminal amidated or esterified forms of up to 60
 CC amino acids, where the peptide-type compound comprises the formula: A-B,
 CC where A, B = (R aa76-77L) (aa79-84) or (aa84-79) (Laa77-76R); aa76 = E or
 CC V; aa77 = D, S or N; aa79 = R or G; aa80 = I or N; aa81, aa84 = a
 CC hydrophobic or small amino acid; aa82 = R or L; aa83 = G or R; and aa
 CC represents amino acid. The sequence in the brackets may optionally be
 CC absent or truncated at any peptide type bond within the brackets. The
 CC compounds comprise amino acid sequences related to a Class I HLA-B
 CC alpha1 domain (positions 79-84). They can be used to inhibit cytotoxic

CC T-lymphocytes (CTL) from undesirably attacking cells in a host or in
 CC vitro. They can also be used in combination with antigenic peptides or
 CC proteins of interest to activate CTLs. They can also inhibit the
 CC proliferation of T cells in response to anti-CD3. The peptide can be
 CC used for preventing rejection of transplants or for treating autoimmune
 CC diseases, e.g. diabetes, rheumatoid arthritis and lupus erythematosus.
 CC The products can also be used for detection and diagnosis.
 SQ Sequence 20 AA;

Query Match 88.0%; Score 88; DB 1; Length 20;
 Best Local Similarity 90.0%; Pred. No. 3.2e-08;
 Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 YRLATRLNERENLRALRY 20
 ||||| ||||| ||||| |||||
 DB 1 YRLAIRELNERENLRALRY 20

RESULT 10
 R95430
 ID R95430 standard; peptide; 20 AA.
 AC R95430;
 DT 12-NOV-1996 (first entry)
 DE HLA-B2702 84-75T/75-84T palindrome.
 KW HLA; p74; alpha1-helix; human-leucocyte-associated antigen; inhibitor;
 KW T-cell lysate; membrane protein; mammal; heat shock protein; Hsc70; APC;
 KW B cell; calcium influx; cytotoxic T lymphocyte; CTL; differentiation;
 KW cytotoxicity; antigen presenting cell.
 OS Synthetic.
 PN W09513288-A1.
 PD 18-MAY-1995.
 PF 10-NOV-1994; U12985.
 PR 10-NOV-1993; US-150493.
 PA (STRD) UNIV LELAND STANFORD JUNIOR.
 PI Clayberger C, Krensky AM;
 DR WPI; 95-194027/25.
 PT Compens. comprising lymphoid surface membrane proteins - which may
 PT inhibit cytolytic activity and differentiation of CTLs.
 PS Example: Page 12; 29pp; English.
 CC R95413, and R95415-R95431 represent palindromes and fragments of
 CC human-leucocyte-associated antigens. This sequence represents the
 CC HLA-B2702 84-75T/75-84T palindrome. These sequences can be used to
 CC isolate the protein p74 from a T-cell lysate. p74 is a T-cell surface
 CC membrane protein associated with T-cell activation in mammalian T-cells,
 CC and is also immunologically cross reactive with the heat shock protein
 CC Hsc70. p74 is found in a limited number of cell types, but is
 CC particularly expressed on B and T cells. p74 can be isolated by lysis of
 CC a suitable cell with an amphoteric detergent, and then passed through an
 CC affinity column containing a covalently bound HLA-B2702 palindromic
 CC peptide. Compositions comprising the extracellular fragment of p74
 CC combined with HLA-B2702.60-84 (see R95416), induces calcium influx, and
 CC inhibits cytotoxic T lymphocyte (CTL) differentiation or cytotoxicity.
 CC Candidate compounds can be screened for their effect on the cytolytic
 CC activity of T-cells, by combining them with the extracellular portion of
 CC p74 and determining the amount of binding between the candidate compound
 CC and p74. Modulation of CTL activity can be inhibited in a cellular
 CC composition containing T-cells and antigen presenting cells (APCs), by
 CC adding to the mix the extracellular portion of p74, in an amount
 CC sufficient to compete with p74 for the binding of the p74 ligand.
 SQ Sequence 20 AA;

Query Match 75.0%; Score 75; DB 1; Length 20;
 Best Local Similarity 84.2%; Pred. No. 4.1e-06;
 Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 YRLATRLNERENLRALRY 19
 ||||| ||||| ||||| |||||
 DB 1 YRLAIRELNERENLRALRY 19

RESULT 11

CC dimer peptide of the invention. A peptide-type compound or variant is
 CC claimed which has immunomodulating activity, including the N-terminal
 CC acylated and/or C-terminal amidated or esterified forms of up to 60
 CC amino acids, where the peptide-type compound comprises the formula: A-B,
 CC where A, B = (R aa76-77L) (aa79-84) or (aa84-79) (Laa77-76R); aa76 = E or
 CC V; aa77 = D, S or N; aa79 = R or G; aa80 = I or N; aa81, aa84 = a
 CC hydrophobic or small amino acid; aa82 = R or L; aa83 = G or R; and aa
 CC represents amino acid. The sequence in the brackets may optionally be
 CC absent or truncated at any peptide type bond within the brackets. The
 CC compounds comprise amino acid sequences related to a Class I HLA-B
 CC alphas domain (positions 79-84). They can be used to inhibit cytotoxic
 CC T-lymphocytes (CTL) from undesirably attacking cells in a host or in
 CC vitro. They can also be used in combination with antigenic peptides or
 CC proteins of interest to activate CTLs. They can also inhibit the
 CC proliferation of T cells in response to anti-CD3. The peptide can be
 CC used for preventing rejection of transplants or for treating autoimmune
 CC diseases, e.g. diabetes, rheumatoid arthritis and lupus erythematosus.
 CC The products can also be used for detection and diagnosis.
 SQ Sequence 20 AA;

Query Match 46.5%; Score 46.5; DB 1; Length 20;
 Best Local Similarity 63.2%; Pred. No. 0.17;
 Matches 12; Conservative 1; Mismatches 3; Indels 3; Gaps 1;

QY 1 YRLATRLNERENLTALR 19
 ||||| ||||| | | | |
 Db 1 YRLAIRLNER---YRLAIR 16

Search completed: February 8, 2000, 04:05:43
 Job time: 9360 sec

QY 11 RENLRTALRY 20
 ||||| |||||
 Db 1 RENLRTALRY 10

RESULT 14
 R92911
 ID R92911 standard; peptide: 20 AA.
 AC R92911;
 DE HLA-B2702 CTL modulating peptide (B2702.84-75/84-75).
 KW Cytotoxic T lymphocyte; CTL; major histocompatibility complex; MHC;
 KW immunosuppressant; graft versus host disorder; transplantation; therapy;
 KW class I MHC; HLA-B2702.
 OS Synthetic.
 PN WO9526979-A1.
 PD 12-OCT-1995.
 PF 05-APR-1995; U04349.
 PR 05-APR-1994; US-222851.
 PA (STRD) UNIV LELAND STANFORD JUNIOR.
 PI Clayberger C, Krensky AM, Parham P;
 DR WPI: 95-358582/46.
 PT Extension of acceptance period of transplants from MHC unmatched
 PT donor hosts - using Class I B75-84 MHC antigen of the recipient
 PT host
 PS Example 15: Page 36; 80pp; English.
 CC R83061-R83085, R83090-R83096 and R92907-R92914 represent fragments of
 CC class I major histocompatibility complex (MHC) antigens. This sequence
 CC is a dimer of residues 75-84 of the alpha-1 domain of the class I MHC
 CC HLA-B2702. These sequences can be used to extend the period of
 CC acceptance by a recipient of a transplant from an MHC unmatched donor.
 CC The peptides are administered to a patient in conjunction with a
 CC subtherapeutic amount of an immunosuppressant. This is administered to
 CC the patient for a limited period of time (compared to the lifetime
 CC administration for current treatments). The peptides particularly
 CC modulate (or inhibit) the activity of the cytotoxic T lymphocytes (CTLs)
 CC of the patient.
 SQ Sequence 20 AA;

Query Match 46.5%; Score 46.5; DB 1; Length 20;
 Best Local Similarity 63.2%; Pred. No. 0.17;
 Matches 12; Conservative 1; Mismatches 3; Indels 3; Gaps 1;

QY 1 YRLATRLNERENLTALR 19
 ||||| ||||| | | | |
 Db 1 YRLAIRLNER---YRLAIR 16

RESULT 15
 W33779
 ID W33779 standard; peptide: 20 AA.
 AC W33779;
 DT 19-JUN-1998 (first entry)
 DE Immunomodulating dimer peptide #2.
 KW Immunomodulating dimer; immunosuppressant drug; CTL activation;
 KW transplantation; autoimmune disease; Class I HLA-B alpha-1 domain;
 KW rejection.
 OS Synthetic.
 OS Homo sapiens.
 PN WO9744351-A1.
 PD 27-NOV-1997.
 PF 22-MAY-1997; U08689.
 PR 24-MAY-1996; US-653294.
 PA (STRD) UNIV LELAND STANFORD JUNIOR.
 PI Beulow R, Clayberger C, Krensky AM;
 DR WPI: 98-086530/08.
 PT New immunomodulating dimer peptide(s) - based on a Class I HLA-B
 PT alpha-1 domain, used for preventing rejection of transplants or
 PT treating autoimmune diseases
 PS Claim 16; Page 35; 41pp; English.
 CC This sequence represents a specifically claimed immunomodulating

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OM protein - protein search, using sw model

Run on: February 7, 2000, 18:04:39 ; Search time 111.22 Seconds
(without alignments)
8.482 Million cell updates/sec

Title: US-08-653-294-30

Perfect score: 100

Sequence: 1 YRLATRLNERENLTALRY 20

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 142080 seqs, 47169319 residues

Total number of hits satisfying chosen parameters: 142080

Minimum DB seq length: 0

Maximum DB seq length: 1000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

PIR_62:*

1: p1r1:*

2: p1r2:*

3: p1r3:*

4: p1r4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	51	51.0	355	137516	HLA-B alpha-chain
2	51	51.0	362	S25415	class I histocompa
3	51	51.0	362	A45850	MHC class I histoc
4	51	51.0	362	I61861	MHC HLA-B*44.2 cha
5	51	51.0	362	I54442	MHC class I histoc
6	48	48.0	137	I80174	class I histocompa
7	46	46.0	359	HLHUB4	MHC class I histoc
8	46	46.0	362	I54457	MHC class I lympho
9	45	45.0	273	I38509	MHC class I histoc
10	45	45.0	274	I54463	MHC HLA-B*38 chain
11	45	45.0	362	B30345	MHC class I histoc
12	45	45.0	362	A45834	MHC class I histoc
13	45	45.0	362	I84486	transmembrane glyc
14	45	45.0	362	A30345	MHC class I histoc
15	45	45.0	362	I59633	MHC HLA-B transmem
16	45	45.0	362	S24434	class I histocompa
17	45	45.0	362	I37120	MHC class I histoc
18	45	45.0	483	S25606	bleomycin hydrolas
19	44	44.0	292	I57806	MHC H-2K-kml mRNA
20	44	44.0	354	I59308	class I histocompa
21	44	44.0	354	I80168	class I histocompa
22	44	44.0	354	I80167	class I histocompa
23	44	44.0	355	I80169	class I histocompa
24	44	44.0	355	I80171	class I histocompa
25	44	44.0	359	1 HLH012	MHC class I histoc
26	44	44.0	362	1 HLHUB8	MHC class I histoc
27	44	44.0	362	B45876	class I histocompa
28	44	44.0	362	2 JH0341	class I histocompa
29	44	44.0	362	2 JH0339	class I histocompa
30	44	44.0	362	2 JH0540	class I histocompa

31 44 44.0 362 2 I62045 gene HLA B-1517 pr
32 44 44.0 362 2 I84490 lymphocyte antigen
33 44 44.0 362 2 I37521 HLA-B*57.2 antigen
34 44 44.0 363 2 S07113 class I histocompa
35 44 44.0 383 2 S03537 class I histocompa
36 44 44.0 384 2 D35997 MHC class I histoc
37 44 44.0 365 2 S77963 HLA-AW24 protein -
38 44 44.0 365 2 I54416 HLA class I histoc
39 44 44.0 365 2 I54493 MHC class I histoc
40 44 44.0 369 1 HLMSKK MHC class I histoc
41 43 43.0 388 2 A60854 MHC class I histoc
42 43 43.0 368 2 I49712 H-2K-s - mouse
43 43 43.0 368 2 I49713 H-2K-sml - mouse
44 43 43.0 1228 2 I40468 surface layer prot
45 43 43.0 2077 1 WZBE24 240K tegument prot

ALIGNMENTS

RESULT 1

I37516

HLA-B alpha-chain - human (fragment)

C:Species: Homo sapiens (man)

C:Date: 04-Oct-1996 #sequence_revision 04-Oct-1996 #text_change 23-Jul-1999

C:Accession: I37516

R:Gauchat-Feiss, D.; Breur-Vriesendorp, B.S.; Rufer, N.; Jeannet, M.; Roosnek, E.; T1

Tissue Antigens 44, 261-264, 1994

A:Title: Sequencing of a novel functional HLA-B*44 subtype differing in two residues 1

A:Reference number: I37516; MUID:95176328

A:Accession: I37516

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-355 <RES>

A:Cross-references: EMBL:X75953; NID:g791007; PIDN:CRAA53566.1; PID:g791008

C:Superfamily: class I histocompatibility antigen; immunoglobulin homology

Query Match 51.0%; Score 51; DB 2; Length 355;

Best Local Similarity 68.8%; Pred. No. 1-2;

Matches 11; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 5 TRLNERENLTALRY 20

| | | | | | | | | |

Db 93 TMTOTYRENLRTALRY 108

RESULT 2

S25415

class I histocompatibility antigen HLA-B*4403 alpha chain - human

C:Species: Homo sapiens (man)

C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 23-Jul-1999

C:Accession: S25415

R:Fleischhauer, K.; Kernan, N.A.; Dupont, B.; Yang, S.Y.

Tissue Antigens 37, 133-137, 1991

A:Title: The two major subtypes of HLA-B*44 differ for a single amino acid in codon 15

A:Reference number: S25415; MUID:91335451

A:Accession: S25415

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-362 <FIE>

A:Cross-references: EMBL:X64366; NID:g32178; PIDN:CRAA45718.1; PID:g32179

C:Genetics:

A:Gene: GDB:HLA-B

A:Cross-references: GDB:120048; OMIM:142830

A:Map position: 6p21.3-6p21.3

C:Superfamily: class I histocompatibility antigen; immunoglobulin homology

C:Keywords: transmembrane protein

F:220-285/Domain: Immunoglobulin homology <IMM>

Query Match 51.0%; Score 51; DB 2; Length 362;

Best Local Similarity 68.8%; Pred. No. 1-2;

A:Cross-references: GB:M15470; NID:g187680; PIDN:AAA59619.1; PID:g386883
C:Genetics:

A:Gene: GDB:HLA-B
A:Cross-references: GDB:120048; OMIM:142830
A:Map position: 6p21.3-6p21.3
C:Superfamily: class I histocompatibility antigen; immunoglobulin homology
C:Keywords: duplication; glycoprotein; heterodimer; transmembrane protein; transplantati
F:1-21/Domain: signal sequence (fragment) #status predicted <SIG>
F:22-359/Product: class I histocompatibility antigen HLA-B44 alpha chain #status predict
F:22-304/Domain: extracellular #status predicted <EXT>
F:22-111/Domain: alpha-1 <EX1>
F:112-203/Domain: alpha-2 <EX2>
F:217-282/Domain: immunoglobulin homology <IMM>
F:305-328/Domain: transmembrane #status predicted <TMN>
F:329-359/Domain: intracellular #status predicted <INT>
F:107/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 46.0%; Score 46; DB 1; Length 359;
Best Local Similarity 62.5%; Pred. No. 7.3;
Matches 10; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 5 TRLNERENLRALRY 20
| | | | | | | |
Db 90 TNTQTYRENLRALRY 105

RESULT 8
154457

MHC class I lymphocyte antigen - human
C:Species: Homo sapiens (man)
C:Date: 07-Jun-1996 #sequence_revision 07-Jun-1996 #text_change 23-Jul-1999
C:Accession: I54457
R:Pohla, H.; Kuon, W.; Tabaczewski, P.; Doerner, C.; Weiss, E.H.
Immunogenetics 29, 297-307, 1989
A:Title: Allelic variation in HLA-B and HLA-C sequences and the evolution of the HLA-B a
A:Reference number: I54457; MUID:89233295
A:Accession: I54457
A:Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: mRNA
A:Residues: 1-362 <RES>
A:Cross-references: GB:M20205; NID:g576470; PIDN:AAA57145.1; PID:g576471
C:Superfamily: class I histocompatibility antigen; immunoglobulin homology

Query Match 46.0%; Score 46; DB 2; Length 362;
Best Local Similarity 62.5%; Pred. No. 7.3;
Matches 10; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 5 TRLNERENLRALRY 20
| | | | | | | |
Db 93 TNTQTYRENLRALRY 108

RESULT 9
138509

MHC class I histocompatibility antigen - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 06-Sep-1996 #sequence_revision 06-Sep-1996 #text_change 23-Jul-1999
C:Accession: I38509
R:Cereb, N.; Choi, J.W.; Riu, K.Z.; Yang, S.Y.
Tissue Antigens 44, 271-273, 1994
A:Title: HLA-B*5105, a newly identified B51 IEF variant.
A:Reference number: I38509; MUID:95176331
A:Accession: I38509
A:Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: mRNA
A:Residues: 1-273 <RES>
A:Cross-references: EMBL:U06697; NID:g469544; PIDN:AAA92997.1; PID:g469545

C:Genetics:
A:Gene: GDB:HLA-B
A:Cross-references: GDB:120048; OMIM:142830
A:Map position: 6p21.3-6p21.3

C:Superfamily: class I histocompatibility antigen; immunoglobulin homology

Query Match 45.0%; Score 45; DB 2; Length 273;
Best Local Similarity 62.5%; Pred. No. 7.8;
Matches 10; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 5 TRLNERENLRALRY 20
| | | | | | | |
Db 68 TNTQTYRENLRALRY 83

RESULT 10
154463

MHC HLA-B38 chain - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 07-Jun-1996 #sequence_revision 07-Jun-1996 #text_change 23-Jul-1999
C:Accession: I54463
R:Mueller, C.A.; Engler-Blum, G.; Gekeler, V.; Steiert, I.; Weiss, E.; Schmidt, H.
Immunogenetics 30, 200-207, 1989
A:Title: Genetic and serological heterogeneity of the supertypic HLA-B locus specific
A:Reference number: I54463; MUID:89379286
A:Accession: I54463
A:Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: DNA
A:Residues: 1-274 <RES>
A:Cross-references: GB:M29864; NID:g187674; PIDN:AAA36222.1; PID:g187675
C:Superfamily: class I histocompatibility antigen; immunoglobulin homology

Query Match 45.0%; Score 45; DB 2; Length 274;
Best Local Similarity 62.5%; Pred. No. 7.8;
Matches 10; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 5 TRLNERENLRALRY 20
| | | | | | | |
Db 69 TNTQTYRENLRALRY 84

RESULT 11
B30345

MHC class I histocompatibility antigen HLA-Bw52 precursor - human
C:Species: Homo sapiens (man)
C:Date: 29-Jan-1990 #sequence_revision 29-Jan-1990 #text_change 16-Feb-1997
C:Accession: B30345
R:Hayashi, H.; Ennis, P.D.; Ariga, H.; Salter, R.D.; Parham, P.; Kano, K.; Takiguchi, J.
Immunol. 142, 306-311, 1989
A:Title: HLA-B51 and HLA-Bw52 differ by only two amino acids which are in the helical
A:Reference number: A30345; MUID:89080265
A:Accession: B30345
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-362 <HAY>
C:Superfamily: class I histocompatibility antigen; immunoglobulin homology
C:Keywords: transmembrane protein
F:220-285/Domain: immunoglobulin homology <IMM>

Query Match 45.0%; Score 45; DB 2; Length 362;
Best Local Similarity 62.5%; Pred. No. 11;
Matches 10; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 5 TRLNERENLRALRY 20
| | | | | | | |
Db 93 TNTQTYRENLRALRY 108

RESULT 12
A45834

MHC class I histocompatibility antigen HLA-B53 alpha chain precursor - human
C:Species: Homo sapiens (man)
C:Date: 03-Jun-1993 #sequence_revision 03-Jun-1993 #text_change 23-Jul-1999
C:Accession: A45834

R:Hayashi, H.; Ooba, T.; Nakayama, S.; Sekimata, M.; Kano, K.; Takiguchi, M.
Immunogenetics 32, 195-199, 1990
A:Title: Allelopecificities between HLA-B*53 and HLA-B*35 are generated by substitution of
A:Reference number: A45834; MUID:91033941
A:Accession: A45834
A:Molecule type: DNA
A:Residues: 1-362 <HAY>
A:Cross-references: GB:M58636; NID:q187756; PIDN:AAA36228.1; PID:q187757; GB:M33574
A:Note: this allele is designated B*5301
C:Genetics:
A:Gene: GDB:HLA-B
A:Cross-references: GDB:I20048; OMIM:142830
A:Map position: 6p21.3-6p21.3
C:Superfamily: class I histocompatibility antigen; immunoglobulin homology
C:Keywords: glycoprotein; heterodimer; transmembrane protein
F:1-24/Domain: signal sequence #status predicted <SIG>
F:220-285/Domain: immunoglobulin homology <IMM>
F:110/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 45.08; Score 45; DB 2; Length 362;
Best Local Similarity 62.5%; Pred. NO. 11;
Matches 10; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 5 TRLNERENLRALRY 20
| | | | | | | | | |
DB 93 TQTQTYRENLRALRY 108

RESULT 13
184486
transmembrane glycoprotein - human
C:Species: Homo sapiens (man)
C:Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 23-Jul-1999
C:Accession: 184486
R:Hildebrand, W.H.; Domene, J.D.; Shen, S.Y.; Lau, M.; Terasaki, P.I.; Bunce, M.; Marsh,
Tissue Antigens 43, 209-218, 1994
A:Title: HLA-B*51: a widespread and diverse family of HLA-B alleles.
A:Reference number: 138421; MUID:94367483
A:Accession: 184486
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-362 <RES>
A:Cross-references: GB:L15005; NID:g493154; PIDN:AAA56832.1; PID:g493155
C:Genetics:
A:Gene: HLA-B*1513
C:Superfamily: class I histocompatibility antigen; immunoglobulin homology
C:Keywords: glycoprotein

Query Match 45.08; Score 45; DB 2; Length 362;
Best Local Similarity 62.5%; Pred. NO. 11;
Matches 10; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 5 TRLNERENLRALRY 20
| | | | | | | | | |
DB 93 TQTQTYRENLRALRY 108

RESULT 14
A30345
MHC class I histocompatibility antigen HLA-B*51 precursor - human
C:Species: Homo sapiens (man)
C:Date: 29-Jan-1990 #sequence_revision 29-Jan-1990 #text_change 23-Jul-1999
C:Accession: A30345; 168746; 137499
R:Hayashi, H.; Ennis, P.D.; Ariga, H.; Salter, R.D.; Parham, P.; Kano, K.; Takiguchi, M.
J. Immunol. 142, 306-311, 1989
A:Title: HLA-B*51 and HLA-B*52 differ by only two amino acids which are in the helical re
A:Reference number: A30345; MUID:89080265
A:Accession: A30345
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-362 <HAY>

R:Pohla, H.; Kuon, W.; Tabaczewski, P.; Doerner, C.; Weiss, E.H.
Immunogenetics 29, 297-307, 1989
A:Title: Allelic variation in HLA-B and HLA-C sequences and the evolution of the HLA-
A:Reference number: 154457; MUID:89233295
A:Accession: 168746
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-362 <RES>
A:Cross-references: GB:L41087; NID:g735900; PIDN:AAA64513.1; PID:g735902
R:Steinle, A.; Schendel, D.J.
Tissue Antigens 44, 268-270, 1994
A:Title: HLA class I alleles of ICL 721 and 174 x CEM.T2 (T2).
A:Reference number: 137499; MUID:95176330
A:Accession: 137499
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-206 <RE2>
A:Cross-references: EMBL:z46808; NID:g599783; PIDN:CAA86838.1; PID:g599784
C:Genetics:
A:Gene: GDB:HLA-B
A:Cross-references: GDB:I20048; OMIM:142830
A:Map position: 6p21.3-6p21.3
C:Superfamily: class I histocompatibility antigen; immunoglobulin homology
C:Keywords: transmembrane protein
F:220-285/Domain: immunoglobulin homology <IMM>

Query Match 45.08; Score 45; DB 2; Length 362;
Best Local Similarity 62.5%; Pred. NO. 11;
Matches 10; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 5 TRLNERENLRALRY 20
| | | | | | | | | |
DB 93 TQTQTYRENLRALRY 108

RESULT 15
159633
MHC HLA-B transmembrane glycoprotein - human
C:Species: Homo sapiens (man)
C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 23-Jul-1999
C:Accession: 159633
R:Hildebrand, W.H.; Domene, J.D.; Parham, P.
Tissue Antigens 41, 190-195, 1993
A:Title: Primary structure shows HLA-B*59 to be a hybrid of HLA-B*55 and HLA-B*51, and n
A:Reference number: 159633; MUID:93369833
A:Accession: 159633
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-362 <RES>
A:Cross-references: GB:L07743; NID:g388314; PIDN:AAA59621.1; PID:g388315
C:Genetics:
A:Gene: GDB:HLA-B
A:Cross-references: GDB:I20048; OMIM:142830
A:Map position: 6p21.3-6p21.3
C:Superfamily: class I histocompatibility antigen; immunoglobulin homology
C:Keywords: glycoprotein

Query Match 45.08; Score 45; DB 2; Length 362;
Best Local Similarity 62.5%; Pred. NO. 11;
Matches 10; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 5 TRLNERENLRALRY 20
| | | | | | | | | |
DB 93 TQTQTYRENLRALRY 108

Search completed: February 7, 2000, 18:04:39
Job time: 22205 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: February 8, 2000, 01:26:00 ; Search time 68.63 Seconds
(without alignments)
8.703 Million cell updates/sec

Title: US-08-653-294-30

Perfect score: 100

Sequence: 1 YRLATRLNERENLTALRY 20

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 82229 seqs, 29864865 residues

Total number of hits satisfying chosen parameters: 82229

Minimum DB seq length: 0

Maximum DB seq length: 1000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : SwissProt_38.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	51	51.0	362	1	P30461 homo sapien
2	51	51.0	362	1	P30481 homo sapien
3	51	51.0	362	1	P30482 homo sapien
4	46	46.0	359	1	P10320 homo sapien
5	45	45.0	362	1	P30487 homo sapien
6	45	45.0	362	1	P18464 homo sapien
7	45	45.0	362	1	P30489 homo sapien
8	45	45.0	362	1	P30490 homo sapien
9	45	45.0	362	1	P30491 homo sapien
10	45	45.0	454	1	Q01532 saccharomyc
11	44	44.0	359	1	P13750 pan troglod
12	44	44.0	362	1	P30379 gorilla gor
13	44	44.0	362	1	P30380 gorilla gor
14	44	44.0	362	1	P30381 gorilla gor
15	44	44.0	362	1	P18465 homo sapien
16	44	44.0	362	1	P30497 homo sapien
17	44	44.0	362	1	P10319 homo sapien
18	44	44.0	362	1	P01893 homo sapien
19	44	44.0	362	1	P30447 homo sapien
20	44	44.0	365	1	P05534 homo sapien
21	44	44.0	365	1	P04223 mus musculus
22	44	44.0	369	1	P35825 bacillus st
23	43	43.0	1228	1	P30002 herpes simp
24	43	43.0	2077	1	P52340 herpes simp
25	43	43.0	2077	1	P12407 anabaena sp
26	42	42.0	187	1	Q05631 salmonella
27	42	42.0	351	1	P04322 feline sarc
28	42	42.0	414	1	P03337 feline sarc
29	42	42.0	425	1	P03340 feline sarc
30	42	42.0	536	1	P10262 feline leuk
31	42	42.0	580	1	P40850 saccharomyc
32	41.5	41.5	630	1	P12044 bacillus su
33	41	41.0	162	1	PUR6_BACSU
34	41	41.0	281	1	O42364 brachydanio

RESULT 1

ID	1B05_HUMAN	STANDARD;	PRT;	362 AA.
AC	P30461;			
DT	01-APR-1993 (Rel. 25, Created)			
DT	01-APR-1993 (Rel. 25, Last sequence update)			
DT	15-JUL-1998 (Rel. 36, Last annotation update)			
DE	HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B*1301 ALPHA CHAIN			
DE	PRECURSOR (B13.1).			
GN	HLA-B OR HLAB.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;			
OC	Eutheria; Primates; Catarrhini; Hominidae; Homo.			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE; 89235215.			
RA	PARHAM P., LAWOR D.A., LOMEN C.E., ENNIS P.D.;			
RT	"Diversity and diversification of HLA-A,B,C alleles.";			
RL	J. Immunol. 142:3937-3950(1989).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE; 88152906.			
RA	ZEMMOUR J., ENNIS P.D., PARHAM P., DUPONT B.;			
RT	"Comparison of the structure of HLA-B*47 to HLA-B13 and its			
RL	relationship to 21-hydroxylase deficiency.";			
RN	[3]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE= BLOOD;			
RX	MEDLINE; 96053518.			
RA	LIN L., TOKUNAGA K., NAKAJIMA F., ISHIKAWA Y., KASHIWAKE K.,			
RA	TANAKA H., KUWATA S., SIDENTSEVA E., AKAZA T., TADOKORO K.,			
RA	SHIBATA Y., CHANDANAYONG D., JUJI T.;			
RT	"Both HLA-B*1301 and B*1302 exist in Asian populations and are			
RL	associated with different haplotypes.";			
Hum. Immunol.	43:51-56(1995).			
CC	- - FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO			
CC	THE IMMUNE SYSTEM.			
CC	- - SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-			
CC	MICROGLOBULIN).			
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CC	or send an email to license@isb-sib.ch).			
CC	EMBL; M24041; AAA59660.1; -			
DR	EMBL; M19757; AAA52657.1; -			
DR	EMBL; D50291; BAA08822.1; -			
DR	HSSP; P30491; 1A1M.			
DR	MIM; 142830; -			
DR	PROSITE; PS00290; IG_MHC; 1.			
DR	PFAM; PF00047; ig; 1.			
DR	PFAM; PF00129; MHC_I; 1.			

ALIGNMENTS

35	41	41.0	362	1	1B29_HUMAN	P18463 homo sapien
36	41	41.0	362	1	1B45_HUMAN	P30485 homo sapien
37	41	41.0	380	1	LEU3_PHACH	O59330 phanerochaete
38	41	41.0	3210	1	CENF_HUMAN	P49454 homo sapien
39	40	40.0	137	1	YG4V_YEAST	P50084 saccharomyc
40	40	40.0	205	1	Y967_METJA	O58377 methanococc
41	40	40.0	338	1	1B20_HUMAN	P30467 homo sapien
42	40	40.0	361	1	1B14_HUMAN	P03989 homo sapien
43	40	40.0	362	1	1B16_HUMAN	P19373 homo sapien
44	40	40.0	362	1	1B18_HUMAN	P10318 homo sapien
45	40	40.0	362	1	1B19_HUMAN	O08136 homo sapien

```

KW  MHC I; Transmembrane; Glycoprotein; Signal.
FT  SIGNAL      1 24
FT  CHAIN       25 362
FT
FT  DOMAIN      25 114
FT  DOMAIN      115 206
FT  DOMAIN      207 298
FT  DOMAIN      299 309
FT  TRANSMEM    310 333
FT  DOMAIN      334 362
FT  CARBOHYD    110 110
FT  DISULFID    125 188
FT  DISULFID    227 283
FT  SEQUENCE    362 AA; 40474 MW; 28B67875 CRC32;

Query Match      51.0%; Score 51; DB 1; Length 362;
Best Local Similarity 68.8%; Pred. No. 0.47;
Matches 11; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY  5  TRLNERENLTALRY 20
    |  |||||
DB  93  TINTQTYRENLTALRY 108

RESULT 2
1B41_HUMAN
ID  1B41_HUMAN STANDARD; PRT; 362 AA.
AC  P30481;
DT  01-APR-1993 (Rel. 25, Created)
DT  01-APR-1993 (Rel. 25, Last sequence update)
DT  15-JUL-1999 (Rel. 38, Last annotation update)
DE  HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, BW-44(B-12) B*4402 ALPHA CHAIN
DE  PRECURSOR (B44.2).
DE  HLA-B OR HLAB.
GN  Homo sapiens (Human).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC  Eutheria; Primates; Catarrhini; Hominiidae; Homo.
RN  [1]
RP  SEQUENCE FROM N.A.
RX  MEDLINE; 89235215.
RT  FARHAM P., LAWOR D.A., LOMEN C.E., ENNIS P.D.;
RT  "Diversity and diversification of HLA-A,B,C alleles.";
RL  J. Immunol. 142:3937-3950(1989).
CC  -!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
CC  THE IMMUNE SYSTEM.
CC  -!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
CC  MICROGLOBULIN).
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CC  or send an email to license@isb-sib.ch).
CC
CC  EMBL; M24038; AAA59663.1; -.
CC  HSSP; P30491; IALM.
CC  MIM; 142830; -.
CC  PROSITE; PS00250; IG_MHC; 1.
CC  PFAM; PF00047; Ig; 1.
CC  PFAM; PF00129; MHC_I; 1.
CC  MHC I; Transmembrane; Glycoprotein; Signal.
FT  SIGNAL      1 24
FT  CHAIN       25 362
FT
FT  DOMAIN      25 114
FT  DOMAIN      115 206
FT  DOMAIN      207 298
FT  DOMAIN      299 309
FT  TRANSMEM    310 333
FT  DOMAIN      334 362
FT  CARBOHYD    110 110
FT  DISULFID    125 188
FT  DISULFID    227 283
FT  SEQUENCE    362 AA; 40474 MW; 28B67875 CRC32;

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FT DOMAIN 334 362 CYTOPLASMIC TAIL.
 FT CARBOHYD 110 110 BY SIMILARITY.
 FT DISULFID 125 188 BY SIMILARITY.
 FT DISULFID 227 283 BY SIMILARITY.
 SQ SEQUENCE 362 AA; 40479 MW; E72CE669 CRC32;

Query Match 51.0%; Score 51; DB 1; Length 362;

Best Local Similarity 68.8%; Pred. No. 0.47; Length 362;
 Matches 11; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Oy 5 TRLNERENLTALRY 20
 Db 93 TMTQTYRENLTALRY 108

RESULT 4
 1B40_HUMAN STANDARD; PRT; 359 AA.
 AC P10320;
 DT 01-MAR-1989 (Rel. 10, Created)
 DT 01-MAR-1989 (Rel. 10, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, BW-44(B-12) B*4401 ALPHA CHAIN
 DE PRECURSOR (B44.1) (FRAGMENT).
 GN HLA-B OR HLAB.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Eutheria; Primates; Catarrhini; Hominidae; Homo.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 86249389.
 RA KOTTMANN A.H., SEEMANN G.H.A., GUESOW H.D., ROOS M.H.;
 RT "DNA sequence of the coding region of the HLA-B44 gene.";
 RL Immunogenetics 23:396-400(1986).

CC -1- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
 CC THE IMMUNE SYSTEM.
 CC -1- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
 CC MICROGLOBULIN).
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CC EMBL; M15470; AAA59619.1; -
 CC PTR; A25295; HLHUB4.
 CC HSP; P30491; IALM.
 CC MIM; 142830;
 CC PROSITE; PS00290; IG_MHC; 1.
 CC PFAM; PF00047; ig; 1.
 CC PFAM; PF00129; MHC.I; 1.
 CC MHC I; Transmembrane; Glycoprotein; Signal.
 CC NON_TER 1 1
 CC SIGNAL <1 21
 CC CHAIN 22 359

FT FT HLA CLASS I HISTOCOMPATIBILITY ANTIGEN,
 FT BW-44(B-12) B*4401 ALPHA CHAIN.
 FT DOMAIN 22 111
 FT DOMAIN 112 203
 FT DOMAIN 204 295
 FT DOMAIN 296 305
 FT TRANSMEM 306 329
 FT DOMAIN 330 359
 FT CARBOHYD 107 107
 FT DISULFID 122 185
 FT DISULFID 224 280
 SQ SEQUENCE 359 AA; 40040 MW; 7C0DB32E CRC32;

Query Match

46.0%; Score 46; DB 1; Length 359;

Best Local Similarity 62.5%; Pred. No. 3;
 Matches 10; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Oy 5 TRLNERENLTALRY 20
 Db 90 TMTQTYRENLTALRY 105

RESULT 5
 1B47_HUMAN STANDARD; PRT; 362 AA.
 AC P30487;
 DT 01-APR-1993 (Rel. 25, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 01-FEB-1996 (Rel. 33, Last annotation update)
 DE HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B*49(B-21) B*4901 ALPHA CHAIN
 DE PRECURSOR.
 GN HLA-B OR HLAB.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Eutheria; Primates; Catarrhini; Hominidae; Homo.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 89235215.
 RA PARHAM P., LAWLER D.A., LOMEN C.E., ENNIS P.D.;
 RT "Diversity and diversification of HLA-A,B,C alleles.";
 RL J. Immunol. 142:3937-3950(1989).
 RN [2]
 RP REVISION TO 78.
 RX MEDLINE; 93056529.
 RA HILDEBRAND W.H., MADRIGAL J.A., BELICH M.P., ZEMMOUR J., WARD F.E.,
 RA WILLIAMS R.C., PARHAM P.;
 RT "Serologic cross-reactivities poorly reflect allelic relationships in
 RT the HLA-B*2 and HLA-B*21 groups. Dominant epitopes of the alpha 2
 RT helix.";
 RL J. Immunol. 149:3563-3568(1992).

CC -1- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
 CC THE IMMUNE SYSTEM.
 CC -1- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
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CC EMBL; M24037; AAA02950.1; -
 CC HSP; P30491; IALM.
 CC MIM; 142830;
 CC PROSITE; PS00290; IG_MHC; 1.
 CC PFAM; PF00047; ig; 1.
 CC PFAM; PF00129; MHC.I; 1.
 CC MHC I; Transmembrane; Glycoprotein; Signal.
 CC NON_TER 1 24
 CC SIGNAL 25 362

FT FT HLA CLASS I HISTOCOMPATIBILITY ANTIGEN,
 FT B*49(B-21) B*4901 ALPHA CHAIN.
 FT DOMAIN 25 114
 FT DOMAIN 115 206
 FT DOMAIN 207 298
 FT DOMAIN 299 309
 FT TRANSMEM 310 333
 FT DOMAIN 334 362
 FT CARBOHYD 110 110
 FT DISULFID 125 188
 FT DISULFID 227 283
 SQ SEQUENCE 362 AA; 40581 MW; E996F82F CRC32;

Query Match

45.0%; Score 45; DB 1; Length 362;
 Best Local Similarity 62.5%; Pred. No. 4.3;

Matches 10; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 5 TRLNERENLRALRY 20
 DB 93 TNTQTYENLRALRY 108

RESULT 6
 ID 1B49 HUMAN STANDARD; PRT; 362 AA.
 AC P18464;
 DT 01-NOV-1990 (Rel. 16, Created)
 DT 01-NOV-1990 (Rel. 16, Last sequence update)
 DT 01-FEB-1996 (Rel. 33, Last annotation update)
 DE HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B*51(B-5) B*5101 ALPHA CHAIN
 DE PRECURSOR.
 GN HLA-B OR HLAB.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Eutheria; Primates; Catarrhini; Hominidae; Homo.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 90207291.
 RA ENNIS P.D., ZEMMOUR J., SALTER R.D., PARHAM P.;
 RT "Rapid cloning of HLA-A, B cDNA by using the polymerase chain
 RT reaction: frequency and nature of errors produced in amplification.";
 RN Proc. Natl. Acad. Sci. U.S.A. 87:2833-2837(1990).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 89080265.
 RA HAYASHI H., ENNIS P.D., ARIGA H., SALTER R.D., PARHAM P., KANO K.,
 RA TAKIGUCHI M.;
 RT "HLA-B*51 and HLA-B*52 differ by only two amino acids which are in the
 RT helical region of the alpha 1 domain";
 RN J. Immunol. 142:306-311(1989).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 89233295.
 RA POHLA H., KUON W., TABACZEWSKI P., DOERNER C., WEISS E.H.;
 RT "Allelic variation in HLA-B and HLA-C sequences and the evolution of
 RT the HLA-B alleles";
 RN Immunogenetics 29:297-307(1989).
 CC -!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
 CC THE IMMUNE SYSTEM.
 CC -!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
 CC MICROGLOBULIN).
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 CC -----
 CC EMBL; M32319; AAA36232.1;
 CC EMBL; M22792; AAA59620.1; ALT_SEQ.
 CC EMBL; M22786; AAA59620.1; JOINED.
 CC EMBL; M22787; AAA59620.1; JOINED.
 CC EMBL; M22788; AAA59620.1; JOINED.
 CC EMBL; M22789; AAA59620.1; JOINED.
 CC EMBL; M22790; AAA59620.1; JOINED.
 CC EMBL; M22791; AAA59620.1; JOINED.
 CC EMBL; L41087; AAA64513.1;
 CC EMBL; L41086; AAA64513.1; JOINED.
 CC PIR; A30345; A30345.
 CC PIR; A30548; A30548.
 CC HSSP; P30491; IALM.
 CC MIM; 142830;
 CC PROSITE; PS00290; IG_MHC; 1.
 CC PFAM; PF00047; ig; 1.
 CC PFAM; PF00129; MHC_I; 1.
 CC MHC I; Transmembrane; Glycoprotein; Signal.
 CC -----

FT SIGNAL 1 24
 FT CHAIN 25 362
 FT
 FT DOMAIN 25 114
 FT DOMAIN 115 206
 FT DOMAIN 207 298
 FT DOMAIN 299 308
 FT TRANSMEM 309 332
 FT DOMAIN 333 362
 FT CARBOHYD 110 110
 FT DISULFID 125 188
 FT DISULFID 227 283
 SQ SEQUENCE 362 AA; 40566 MW; 4D846F30 CRC32;

Query Match 45.0%; Score 45; DB 1; Length 362;
 Best Local Similarity 62.5%; Pred. No. 4.3;
 Matches 10; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 5 TRLNERENLRALRY 20
 DB 93 TNTQTYENLRALRY 108

RESULT 7
 ID 1B52 HUMAN STANDARD; PRT; 362 AA.
 AC P30489;
 DT 01-APR-1993 (Rel. 25, Created)
 DT 01-APR-1993 (Rel. 25, Last sequence update)
 DT 01-APR-1993 (Rel. 25, Last annotation update)
 DE HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B*51(B-5) B*5104 ALPHA CHAIN
 DE PRECURSOR.
 GN HLA-B OR HLAB.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Eutheria; Primates; Catarrhini; Hominidae; Homo.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 92265955.
 RA BELICH M.P., MADRIGAL J.A., HILDEBRAND W.H., ZEMMOUR J.,
 RA WILLIAMS R.C., LUZ R., PETZL-ERLER M.L., PARHAM P.;
 RT "Unusual HLA-B alleles in two tribes of Brazilian Indians.";
 RN Nature 357:326-329(1992).
 CC -!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
 CC THE IMMUNE SYSTEM.
 CC -!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
 CC MICROGLOBULIN).
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 CC -----
 CC EMBL; Z15143; CAA78849.1;
 CC HSSP; P30491; IALM.
 CC MIM; 142830;
 CC PROSITE; PS00290; IG_MHC; 1.
 CC PFAM; PF00047; ig; 1.
 CC PFAM; PF00129; MHC_I; 1.
 CC MHC I; Transmembrane; Glycoprotein; Signal.
 CC -----

FT CARBOHYD 110 110 BY SIMILARITY.
 FT DISULFID 125 188 BY SIMILARITY.
 FT DISULFID 227 283 BY SIMILARITY.
 SQ SEQUENCE 362 AA; 40560 MW; F22F08AB CRC32;

Query Match 45.08; Score 45; DB 1; Length 362;
 Best Local Similarity 62.58; Pred. No. 4.3;
 Matches 10; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 5 TRLNERRENLTALRY 20
 I | | | | | | | |
 Db 93 TINTOTYRENLTALRY 108

RESULT 8
 1B53_HUMAN
 ID 1B53_HUMAN STANDARD; PRT; 362 AA.
 AC P30490;
 DT 01-APR-1993 (Rel. 25, Created)
 DT 01-APR-1993 (Rel. 25, Last sequence update)
 DT 01-APR-1993 (Rel. 25, Last annotation update)
 DE HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, BW-52(B-5) B*5201 ALPHA CHAIN
 DE PRECURSOR.
 GN HLA-B OR HLAB.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Eutheria; Primates; Catarrhini; Homnidae; Homo.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 89080265.
 RA HAYASHI H., ENNIS P.D., ARIGA H., SALTER R.D., PARHAM P., KANO K.,
 RA TAKIGUCHI M.
 RT "HLA-B51 and HLA-Bw52 differ by only two amino acids which are in the
 RT helical region of the alpha 1 domain."
 RL J. Immunol. 142:306-311(1989).
 CC -1- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
 CC THE IMMUNE SYSTEM.
 CC -1- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
 CC MICROGLOBULIN).

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 CC EMBL; M22799; AAA59645.1; ALT SEQ.
 CC EMBL; M22793; AAA59645.1; JOINED.
 CC EMBL; M22794; AAA59645.1; JOINED.
 CC EMBL; M22795; AAA59645.1; JOINED.
 CC EMBL; M22796; AAA59645.1; JOINED.
 CC EMBL; M22797; AAA59645.1; JOINED.
 CC EMBL; M22798; AAA59645.1; JOINED.
 CC PIR; B30345; B30345.
 CC PIR; B30348; B30548.
 CC HSP; P30491; IAIM.
 CC MIM; 142830; -
 CC PFAM; PF00047; Ig; 1.
 CC PROSITE; PS00290; IG_MHC; 1.
 CC PFAM; PF00129; MHC.I; 1.
 CC PFAM; PF00129; MHC.I; 1.
 CC MHC I; Transmembrane; Glycoprotein; Signal.
 CC SIGNAL 1 24
 CC CHAIN 25 362
 CC HLA CLASS I HISTOCOMPATIBILITY ANTIGEN,
 CC BW-52(B-5) B*5201 ALPHA CHAIN.
 CC FT DOMAIN 25 114
 CC FT DOMAIN 115 206
 CC FT DOMAIN 207 298
 CC FT DOMAIN 299 308
 CC FT :TRANSMEM 309 332
 CC FT DOMAIN 333 362
 CC CYTOPLASMIC TAIL.

FT CARBOHYD 110 110 BY SIMILARITY.
 FT DISULFID 125 188 BY SIMILARITY.
 FT DISULFID 227 283 BY SIMILARITY.
 SQ SEQUENCE 362 AA; 40521 MW; 3B436FEB CRC32;

Query Match 45.08; Score 45; DB 1; Length 362;
 Best Local Similarity 62.58; Pred. No. 4.3;
 Matches 10; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 5 TRLNERRENLTALRY 20
 I | | | | | | | |
 Db 93 TINTOTYRENLTALRY 108

RESULT 9
 1B54_HUMAN
 ID 1B54_HUMAN STANDARD; PRT; 362 AA.
 AC P30491;
 DT 01-APR-1993 (Rel. 25, Created)
 DT 01-APR-1993 (Rel. 25, Last sequence update)
 DT 15-JUL-1998 (Rel. 36, Last annotation update)
 DE HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, BW-53 B*5301 ALPHA CHAIN
 DE PRECURSOR.
 GN HLA-B OR HLAB.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Eutheria; Primates; Catarrhini; Homnidae; Homo.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 91033941.
 RA HAYASHI H., Ooba T., NAKAYAMA S., SEKIMATA M., KANO K.,
 RA TAKIGUCHI M.
 RT "Allospecificities between HLA-Bw53 and HLA-B35 are generated by
 RT substitution of the residues associated with HLA-Bw4/Bw6 public
 RT epitopes."
 RL Immunogenetics 32:195-199(1990).
 CC -1- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
 CC THE IMMUNE SYSTEM.
 CC -1- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
 CC MICROGLOBULIN).

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 CC EMBL; M58636; AAA36228.1; -
 CC PIR; A45834; A45834.
 CC PDB; 1AIM; 08-APR-98.
 CC PDB; 1AIO; 08-APR-98.
 CC MIM; 142830; -
 CC PROSITE; PS00290; IG_MHC; 1.
 CC PFAM; PF00047; Ig; 1.
 CC PFAM; PF00129; MHC.I; 1.
 CC MHC I; Transmembrane; Glycoprotein; Signal; 3D-structure.
 CC SIGNAL 1 24
 CC CHAIN 25 362
 CC HLA CLASS I HISTOCOMPATIBILITY ANTIGEN,
 CC BW-53 B*5301 ALPHA CHAIN.
 CC FT DOMAIN 25 114
 CC FT DOMAIN 115 206
 CC FT DOMAIN 207 298
 CC EXTRACELLULAR ALPHA-1.
 CC EXTRACELLULAR ALPHA-2.
 CC EXTRACELLULAR ALPHA-3.

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FT DOMAIN 299 308 CONNECTING PEPTIDE.
FT TRANSMEM 309 332
FT DOMAIN 333 362 CYTOPLASMIC TAIL.
FT CARBOHYD 110 110 BY SIMILARITY.
FT DISULFID 125 188
FT DISULFID 227 283
SQ SEQUENCE 362 AA: 40495 MW: 2BDC746E CRC32:

Query Match 45.0%; Score 45; DB 1; Length 362;
Best Local Similarity 62.5%; Pred. No. 4.3;
Matches 10; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 5 TRLNERENLRALRY 20
DB 93 TMTQTYRENRURIALRY 108

RESULT 10
BLH1_YEAST STANDARD; PRT: 454 AA.
ID BLH1_YEAST
AC Q01532;
DT 01-APR-1993 (Rel. 25, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 15-DEC-1999 (Rel. 39, Last annotation update)
DE CYSTEINE PROTEINASE 1 (EC 3.4.22.-) (Y3) (BLEOMYCIN HYDROLASE) (BLM
DE HYDROLASE).
GN BLH1 OR YCP1 OR LAP3 OR GAL6 OR YNL239W OR N1118.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Hemiascomycetes; Saccharomycetales;
OC Saccharomycetaceae; Saccharomyces.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE: 93016103.
RA KAMBOURIS N.G., BURKE D.J., CREUTZ C.E.;
RT "Cloning and characterization of a cysteine proteinase from
RT Saccharomyces cerevisiae."
RL J. Biol. Chem. 267:21570-21576(1992).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE: 9314342.
RA MAGDOLEN U., MUELLER G., MAGDOLEN V., BANDLOW W.;
RT "A yeast gene (BLH1) encodes a polypeptide with high homology to
RT vertebrate bleomycin hydrolase, a family member of thiol
RT proteinases."
RL Biochim. Biophys. Acta 1171:299-303(1993).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE: 93216638.
RA ENENKEL C., WOLF D.H.;
RT "BLH1 codes for a yeast thiol aminopeptidase, the equivalent of
RT mammalian bleomycin hydrolase."
RL J. Biol. Chem. 268:7036-7043(1993).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE: 97051596.
RA PANDOLFO D., DE ANTONI A., LANFRANCHI G., VALLE G.;
RT "The DNA sequence of cosmid 14-5 from chromosome XIV reveals 21 open
RT reading frames including a novel gene encoding a globin-like
RT domain."
RL Yeast 12:1071-1076(1996).
RN [5]
RP SEQUENCE OF 199-222 AND 338-358.
RX MEDLINE: 91353077.
RA CREUTZ C.E., SNYDER S.L., KAMBOURIS N.G.;
RT "Calcium-dependent secretory vesicle-binding and lipid-binding
RT proteins of Saccharomyces cerevisiae."
RL Yeast 7:229-244(1991).
RN [6]
RP PARTIAL SEQUENCE FROM N.A., AND X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).
RX MEDLINE: 95365811.
RA JOSHUA-TOR L., XU H.E., JOHNSTON S.A., REES D.C.;
RT "Crystal structure of a conserved protease that binds DNA: the
```

```
RT bleomycin hydrolase, Gal6."
RL Science 269:945-950(1995).
RN [7]
RP X-RAY CRYSTALLOGRAPHY (2.05 ANGSTROMS).
RX MEDLINE: 98206472.
RA ZHENG W., JOHNSTON S.A., JOSHUA-TOR L.;
RT "The unusual active site of Gal6/bleomycin hydrolase can act as a
RT carboxypeptidase, aminopeptidase, and peptide ligase."
RL Cell 93:103-109(1998).
RN [8]
RP DNA-BINDING, AND CHARACTERIZATION.
RX MEDLINE: 94342285.
RA XU H.E., JOHNSTON S.A.;
RT "Yeast bleomycin hydrolase is a DNA-binding cysteine protease.
RT Identification, purification, biochemical characterization."
RL J. Biol. Chem. 269:21177-21183(1994).
CC -!- FUNCTION: NON ESSENTIAL TO THE VIABILITY OF YEAST CELLS. CAN
CC PROTECT YEAST FROM THE TOXIC EFFECTS OF BLEOMYCIN. ACTS AS A
CC REPRESSOR IN THE GAL4 REGULATORY SYSTEM. BINDS SINGLE-STRANDED DNA
CC WITH HIGHER AFFINITY THAN DOUBLE-STRANDED DNA.
CC -!- COFACTOR: CALCIUM.
CC -!- SUBUNIT: HOMODIMER.
CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY C1; ALSO KNOWN AS THE
CC PAPAIN FAMILY OF THIOL PROTEASES.
CC -!- CAUTION: IT IS UNCERTAIN WHETHER MET-1 OR MET-30 IS THE INITIATOR,
CC ALTHOUGH FLANKING SEQUENCES POINT TO THE SECOND.
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CC -----
CC EMBL: M97910; AAA35231.1; -
CC EMBL: X69124; CAA48878.1; -
CC EMBL: X68228; CAA48309.1; -
CC EMBL: 271515; CAA96144.1; -
CC EMBL: 269381; CAA93359.1; -
CC EMBL: U74299; AAB18260.1; -
CC PIR: S25606; S25606.
CC PIR: S28224; S28224.
CC PDB: 1GCB; 15-OCT-95.
CC PDB: 3GCB; 21-OCT-98.
CC PDB: 1A6R; 21-OCT-98.
CC SGD: L0000929; LAP3.
CC PROSITE: PS00139; THIOL_PROTEASE_CYS; 1.
CC PROSITE: PS00639; THIOL_PROTEASE_HIS; 1.
CC PROSITE: PS00640; THIOL_PROTEASE_ASN; FALSE NEG.
KW Hydrolase; Thiol protease; DNA-binding; 3D-structure.
FT ACT_SITE 73 73
FT ACT_SITE 369 369
FT ACT_SITE 392 392
FT REPEAT 28 48
FT REPEAT 193 213
FT CONFLICT 158 158 I -> M (IN REF. 2).
SQ SEQUENCE 454 AA: 52088 MW: B90FB48E CRC32:

Query Match 45.0%; Score 45; DB 1; Length 454;
Best Local Similarity 58.8%; Pred. No. 5.7;
Matches 10; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 3 LATRLNERENLRALRY 19
DB 180 LTTKLREFAETLRALK 196

RESULT 11
1B01_PANTR
ID 1B01_PANTR STANDARD; PRT: 359 AA.
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CC -----

DR EMBL; X03664; CAA27301.1; -
DR EMBL; X03667; CAA27301.1; JOINED.
DR EMBL; L38504; AAM69724.1; -
DR PIR; B25092; HLHUBK.
DR HSP; P03989; IHSA.
DR MIM; I42830; -
DR PROSITE; PS00290; IG_MHC; 1.
DR PFAM; PF00047; Ig; 1.
DR PFAM; PF00129; MHC.I; 1.
KW MHC I; Transmembrane; Glycoprotein; Signal.
FT SIGNAL 1 24
FT CHAIN 25 362 HLA CLASS I HISTOCOMPATIBILITY ANTIGEN,
B-27 B*2702 ALPHA CHAIN.
FT DOMAIN 25 114 EXTRACELLULAR ALPHA-1.
FT DOMAIN 115 206 EXTRACELLULAR ALPHA-2.
FT DOMAIN 207 298 EXTRACELLULAR ALPHA-3.
FT DOMAIN 299 308 CONNECTING PEPTIDE.
FT TRANSMEM 309 332 CYTOPLASMIC TAIL.
FT DOMAIN 333 362 BY SIMILARITY.
FT CARBOHYD 110 110 BY SIMILARITY.
FT DISULFID 125 188 BY SIMILARITY.
FT DISULFID 227 283 BY SIMILARITY.
SQ SEQUENCE 362 AA; 40397 MW; 9798F0BB CRC32;

Query Match 44.0%; Score 44; DB 1; Length 362;
Best Local Similarity 90.0%; Pred. No. 6.3;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 11 RENTLALRY 20
 |||||
Db 99 RENTLALRY 108

Search completed: February 8, 2000, 01:26:00
Job time: 1560 sec

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: February 8, 2000, 19:16:14 : Search time 176.54 Seconds
(without alignments)
7.855 Million cell updates/sec

Title: US-08-653-294-30
Perfect score: 100
Sequence: 1 YRLATLNERENLTALRY 20

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 225878 seqs, 69334122 residues

Total number of hits satisfying chosen parameters: 225878

Minimum DB seq length: 0

Maximum DB seq length: 1000000

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database : SPTREMBL12.*
1: sp_archaea.*
2: sp_bacteria.*
3: sp_fungi.*
4: sp_human.*
5: sp_invertebrate.*
6: sp_mammal.*
7: sp_mmc.*
8: sp_organelle.*
9: sp_phage.*
10: sp_plant.*
11: sp_rodent.*
12: sp_virus.*
13: sp_vertebrate.*
14: sp_unclassified.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	51	51.0	89	019674	019674 homo sapien
2	51	51.0	89	019565	019565 homo sapien
3	51	51.0	131	097998	097998 homo sapien
4	51	51.0	131	097999	097999 homo sapien
5	51	51.0	181	019779	019779 homo sapien
6	51	51.0	181	030197	030197 homo sapien
7	51	51.0	181	019669	019669 homo sapien
8	51	51.0	181	078028	078028 homo sapien
9	51	51.0	355	029853	029853 homo sapien
10	51	51.0	362	029637	029637 homo sapien
11	51	51.0	362	029935	029935 homo sapien
12	51	51.0	362	079524	079524 homo sapien
13	51	51.0	362	029850	029850 homo sapien
14	51	51.0	362	029661	029661 homo sapien
15	51	51.0	362	078180	078180 homo sapien
16	51	51.0	362	029933	029933 homo sapien
17	50	50.0	361	09XRY0	09XRY0 pongo pygma
18	48	48.0	137	095533	095533 pan troglod
19	46.5	46.5	346	095459	095459 rattus norv
20	46.5	46.5	346	078088	078088 rattus norv

21	46.5	46.5	348	7	046875	046875 rattus norv
22	46.5	46.5	362	7	030721	030721 macaca mula
23	46	46.0	89	4	095956	095956 homo sapien
24	46	46.0	89	7	077959	077959 homo sapien
25	46	46.0	181	7	077934	077934 homo sapien
26	46	46.0	330	7	019356	019356 macaca mula
27	46	46.0	331	7	002944	002944 macaca mula
28	46	46.0	331	7	002945	002945 macaca mula
29	46	46.0	362	7	029938	029938 homo sapien
30	46	46.0	368	7	061895	061895 mus musculus
31	45	45.0	89	7	019569	019569 homo sapien
32	45	45.0	172	7	019770	019770 homo sapien
33	45	45.0	172	7	019774	019774 homo sapien
34	45	45.0	172	7	019775	019775 homo sapien
35	45	45.0	172	7	019780	019780 homo sapien
36	45	45.0	172	7	095364	095364 homo sapien
37	45	45.0	172	7	019771	019771 homo sapien
38	45	45.0	172	7	019772	019772 homo sapien
39	45	45.0	172	7	019773	019773 homo sapien
40	45	45.0	175	7	029694	029694 homo sapien
41	45	45.0	181	7	046703	046703 homo sapien
42	45	45.0	181	7	062899	062899 homo sapien
43	45	45.0	181	7	062922	062922 homo sapien
44	45	45.0	181	7	019623	019623 homo sapien
45	45	45.0	181	7	019747	019747 homo sapien

ALIGNMENTS

RESULT 1
019674 PRELIMINARY; PRT; 89 AA.
AC 019674;
DT 01-JAN-1998 (TREMREL. 05, Created)
DT 01-JAN-1998 (TREMREL. 05, Last sequence update)
DT 01-NOV-1998 (TREMREL. 08, Last annotation update)
DE HLA-B*13 (FRAGMENT).
GN HLA-B*13.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Primates; Catarrhini; Hominidae; Homo.
RN [1]
RP SEQUENCE FROM N.A.
RA MAERTENS R., DE CANCK I.;
RL Submitted (APR-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; Y12378; CAA73021.1; -.
DR PFAM; PF00129; MHC_I; 1.
KW MHC.
FT NON_TER 1
FT NON_TER 89
SQ SEQUENCE 89 AA; 10581 MW; 9AC7631C CRC32;
Query Match 51.0%; Score 51; DB 7; Length 89;
Best Local Similarity 68.8%; Pred. No. 0.59;
Matches 11; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
QY 5 TRLNERENLTALRY 20
DB 68 TNTQTYRENLTALRY 83
RESULT 2
019565 PRELIMINARY; PRT; 89 AA.
ID 019565;
AC 019565;
DT 01-JAN-1998 (TREMREL. 05, Created)
DT 01-MAY-1999 (TREMREL. 10, Last sequence update)
DT 01-MAY-1999 (TREMREL. 10, Last annotation update)
DE MHC CLASS I ANTIGEN (FRAGMENT).
GN HLA-B.
OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Eutheria; Primates; Catarrhini; Hominidae; Homo.
 RN [1]
 RP SEQUENCE FROM N.A.
 RA CAO K., BURDETT L., ZHANG G., FERNANDEZ-VINA M.;
 RL Submitted (AUG-1997) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF017316; AAB70282.2; -
 KW MHC
 FT NON_TER 1 1
 FT NON_TER 89 89
 SQ SEQUENCE 89 AA; 10581 MW; 9AC7631C CRC32;

Query Match 51.0%; Score 51; DB 7; Length 89;
 Best Local Similarity 68.8%; Pred. No. 0.59;
 Matches 11; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY 5 TRLNERRENLTALRY 20
 DB 68 TNTQTYRENLTALRY 83

RESULT 3
 O97998
 ID O97998 PRELIMINARY; PRT; 131 AA.
 AC O97998;
 DT 01-MAY-1999 (TREMBlrel. 10, Created)
 DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)
 DT 01-MAY-1999 (TREMBlrel. 10, Last annotation update)
 DE MHC CLASS I ANTIGEN (FRAGMENT).
 GN HLA-B.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Eutheria; Primates; Catarrhini; Hominidae; Homo.
 RN [1]
 RP SEQUENCE FROM N.A.
 RA HOLDSWORTH R.;
 RL Submitted (NOV-1997) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF035648; AAD02035.1; -
 KW MHC
 FT NON_TER 1 1
 FT NON_TER 131 131
 SQ SEQUENCE 131 AA; 15134 MW; 931C8D27 CRC32;

Query Match 51.0%; Score 51; DB 7; Length 131;
 Best Local Similarity 68.8%; Pred. No. 0.87;
 Matches 11; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY 5 TRLNERRENLTALRY 20
 DB 34 TNTQTYRENLTALRY 49

RESULT 4
 O97999
 ID O97999 PRELIMINARY; PRT; 131 AA.
 AC O97999;
 DT 01-MAY-1999 (TREMBlrel. 10, Created)
 DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)
 DT 01-MAY-1999 (TREMBlrel. 10, Last annotation update)
 DE MHC CLASS I ANTIGEN (FRAGMENT).
 GN HLA-B.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Eutheria; Primates; Catarrhini; Hominidae; Homo.
 RN [1]
 RP SEQUENCE FROM N.A.
 RA HOLDSWORTH R.;
 RL Submitted (NOV-1997) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF035649; AAD02036.1; -
 KW MHC
 FT NON_TER 1 1

FT NON_TER 131 131
 SQ SEQUENCE 131 AA; 15057 MW; 32C865A3 CRC32;

Query Match 51.0%; Score 51; DB 7; Length 131;
 Best Local Similarity 68.8%; Pred. No. 0.87;
 Matches 11; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY 5 TRLNERRENLTALRY 20
 DB 34 TNTQTYRENLTALRY 49

RESULT 5
 O19779
 ID O19779 PRELIMINARY; PRT; 181 AA.
 AC O19779;
 DT 01-JAN-1998 (TREMBlrel. 05, Created)
 DT 01-JAN-1998 (TREMBlrel. 05, Last sequence update)
 DT 01-NOV-1999 (TREMBlrel. 12, Last annotation update)
 DE MHC CLASS I ANTIGEN (FRAGMENT).
 GN HLA-B.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Eutheria; Primates; Catarrhini; Hominidae; Homo.
 RN [1]
 RP SEQUENCE FROM N.A.
 RA STRINER N.K., NG J., BUSH J., HARTZMAN R.J., JOHNSON-DOW L.,
 RA HURLEY C.K.;
 RL Hum. Immunol. 56:0-0(1997).
 DR EMBL; U90241; AAB82305.1; -
 DR EMBL; U90240; AAB82305.1; JOINED.
 DR HSSP; P10318; 1ROG.
 DR PFAM; PF00129; MHC_I; 1.
 KW MHC.
 FT NON_TER 1 1
 FT NON_TER 181 181
 SQ SEQUENCE 181 AA; 21095 MW; 97EC3597 CRC32;

Query Match 51.0%; Score 51; DB 7; Length 181;
 Best Local Similarity 68.8%; Pred. No. 1.2;
 Matches 11; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY 5 TRLNERRENLTALRY 20
 DB 68 TNTQTYRENLTALRY 83

RESULT 6
 O30197
 ID O30197 PRELIMINARY; PRT; 181 AA.
 AC O30197;
 DT 01-NOV-1996 (TREMBlrel. 01, Created)
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
 DT 01-NOV-1999 (TREMBlrel. 12, Last annotation update)
 DE MHC CLASS I ANTIGEN (FRAGMENT).
 GN HLA-B.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Eutheria; Primates; Catarrhini; Hominidae; Homo.
 RN [1]
 RP SEQUENCE FROM N.A.
 RA HURLEY C.K., HOYER R.J.;
 RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
 DR EMBL; U63560; AAB05925.1; -
 DR EMBL; U63559; AAB05925.1; JOINED.
 DR HSSP; P10318; 1ROG.
 DR PFAM; PF00129; MHC_I; 1.
 KW MHC.
 FT NON_TER 1 1
 FT NON_TER 181 181
 SQ SEQUENCE 181 AA; 20997 MW; 70FABE37 CRC32;

Query Match 51.0%; Score 51; DB 7; Length 181;
 Best Local Similarity 68.8%; Pred. No. 1.2;
 Matches 11; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 5 TRLNERENLRTALRY 20
 | | | | | | | | | |
 DB 68 TNTQTYENLRTALRY 83

RESULT 7
 ID 019669 PRELIMINARY; PRT; 181 AA.
 AC 019669;
 DT 01-JAN-1998 (TEMBLrel. 05, Created)
 DT 01-JAN-1998 (TEMBLrel. 05, Last sequence update)
 DT 01-NOV-1999 (TEMBLrel. 12, Last annotation update)
 DE MHC CLASS I ANTIGEN SHCHA (FRAGMENT).
 GN HLA-B
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Eutheria; Primates; Catarrhini; Hominidae; Homo.
 RN [1]
 RP SEQUENCE FROM N.A.
 RA HURLEY C.K., STEINER N.K.;
 RL Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.
 DR EMBL; U58470; AAB02607.1; -;
 DR EMBL; U58469; AAB02607.1; JOINED.
 DR HSSP; P10318; 1ROG.
 DR PFAM; PF00129; MHC_I; 1.
 KW MHC.
 FT NON_TER 1
 FT NON_TER 181
 SQ SEQUENCE 181 AA; 21028 MW; EC872642 CRC32;

Query Match 51.0%; Score 51; DB 7; Length 181;
 Best Local Similarity 68.8%; Pred. No. 1.2;
 Matches 11; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 5 TRLNERENLRTALRY 20
 | | | | | | | | | |
 DB 68 TNTQTYENLRTALRY 83

RESULT 8
 ID 078028 PRELIMINARY; PRT; 181 AA.
 AC 078028;
 DT 01-NOV-1998 (TEMBLrel. 08, Created)
 DT 01-NOV-1998 (TEMBLrel. 08, Last sequence update)
 DT 01-NOV-1999 (TEMBLrel. 12, Last annotation update)
 DE HLA-B*15MD (FRAGMENT).
 GN HLA-B*15MD.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Eutheria; Primates; Catarrhini; Hominidae; Homo.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-BLOOD;
 RA GAO X., MATHESON B.;
 RL Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.
 DR EMBL; U58316; AAB87723.1; -;
 DR EMBL; U58315; AAB87723.1; JOINED.
 DR HSSP; P10318; 1ROG.
 DR PFAM; PF00129; MHC_I; 1.
 KW MHC.
 FT NON_TER 1
 FT NON_TER 181
 SQ SEQUENCE 181 AA; 21029 MW; C35A18BE CRC32;

Query Match 51.0%; Score 51; DB 7; Length 181;
 Best Local Similarity 68.8%; Pred. No. 1.2;
 Matches 11; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 5 TRLNERENLRTALRY 20
 | | | | | | | | | |
 DB 68 TNTQTYENLRTALRY 83

RESULT 9
 ID 029853 PRELIMINARY; PRT; 355 AA.
 AC 029853;
 DT 01-NOV-1996 (TEMBLrel. 01, Created)
 DT 01-NOV-1996 (TEMBLrel. 01, Last sequence update)
 DT 01-NOV-1999 (TEMBLrel. 12, Last annotation update)
 DE HLA-B ALPHA-CHAIN (FRAGMENT).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Eutheria; Primates; Catarrhini; Hominidae; Homo.
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE; 95176328.
 RA GAUCHAT-FEISS D., BREUR-VRIESENDORP B.S., RUFER N., JEANNET M.,
 RA ROOSNEK E., TIERCY J.M.;
 RT "Sequencing of a novel functional HLA-B*44 subtype differing in two
 RT residues in the alpha 2 domain";
 RL Tissue Antigens 44:261-264(1994).
 DR EMBL; X75953; CAA53566.1; -;
 DR HSSP; P30491; 1ALM.
 DR PROSITE; PS00290; IG_MHC; 1.
 DR PFAM; PF00047; Ig; 1.
 DR PFAM; PF00129; MHC_I; 1.
 KW MHC.
 FT NON_TER 355
 FT NON_TER 355
 SQ SEQUENCE 355 AA; 39845 MW; EF81934E CRC32;

Query Match 51.0%; Score 51; DB 7; Length 355;
 Best Local Similarity 68.8%; Pred. No. 2.4;
 Matches 11; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 5 TRLNERENLRTALRY 20
 | | | | | | | | | |
 DB 93 TNTQTYENLRTALRY 108

RESULT 10
 ID 029637 PRELIMINARY; PRT; 362 AA.
 AC 029637;
 DT 01-NOV-1996 (TEMBLrel. 01, Created)
 DT 01-NOV-1996 (TEMBLrel. 01, Last sequence update)
 DT 01-NOV-1999 (TEMBLrel. 12, Last annotation update)
 DE MHC CLASS I ANTIGEN.
 GN HLA-B
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Eutheria; Primates; Catarrhini; Hominidae; Homo.
 RN [1]
 RP SEQUENCE FROM N.A.
 RA DOMENA J.D., PARHAM P.;
 RL Submitted (DEC-1993) to the EMBL/GenBank/DBJ databases.
 DR EMBL; U04244; AAB87397.1; -;
 DR HSSP; P30460; 1AGE.
 DR PROSITE; PS00290; IG_MHC; 1.
 DR PFAM; PF00047; Ig; 1.
 DR PFAM; PF00129; MHC_I; 1.
 KW MHC.
 FT NON_TER 362
 FT NON_TER 362
 SQ SEQUENCE 362 AA; 40359 MW; EEAB95D7 CRC32;

Query Match 51.0%; Score 51; DB 7; Length 362;

QY 5 TRLNERNLRTALRY 20
| |||||
|||||

RESULT	14
ID	Q29661
ID	PRELIMINARY; PRT; 362 AA.
AC	Q29661;
DT	01-NOV-1996 (TREMBLrel. 01, Created)
DT	01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT	01-NOV-1999 (TREMBLrel. 12, Last annotation update)
DE	MHC ANTIGEN HLA-B*1303 PRECURSOR.
DE	HLA-B*1303.
OS	Homo sapiens (Human).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC	Eutheria; Primates; Catarrhini; Homnidae; Homo.
RN	[1]
RP	SEQUENCE FROM N.A.
RC	TISSUE=BLOOD;
RA	MEDLINE; 96232969.
RX	BALAS A., GARCIA-SANCHEZ F., VICARIO J.L.;
RT	"HLA-B*1303: a new example of poor correlation between serology and structure.";
RL	Hum. Immunol. 45:32-36(1996).
DR	EMBL; U14943; AAB06829.1; -
DR	HSSP; P30491; 1ALM.
DR	PROSITE; PS00290; IG_MHC; 1.
DR	PFAM; PF00047; Ig_1.
DR	PFAM; PF00129; MHC_1; 1.
KW	Signal; MHC.
FT	SIGNAL
FT	POTENTIAL.
CHAIN	25 362
SEQUENCE	362 AA: 40501 MW: 9277DEFB CRC32:
SO	POTENTIAL. MHC ANTIGEN HLA-B*1303 .

Query Match 51.0%; Score 51; DB 7; Length 362;
 Best Local Similarity 68.8%; Pred. No. 2.4;
 Matches 11; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 5 TRLNERRENLTALRY 20
 |
 Db 93 TNTQTYRENLTALRY 108
 |

RESULT 15

O78180
 ID O78180 PRELIMINARY; PRT; 362 AA.
 AC O78180;
 DT 01-NOV-1998 (TREMELrel. 08, Created)
 DT 01-NOV-1998 (TREMELrel. 08, Last sequence update)
 DT 01-NOV-1999 (TREMELrel. 12, Last annotation update)
 DE HLA CLASS I ANTIGEN HLA-B.
 GN HLA-B.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Eutheria; Primates; Catarrhini; Hominidae; Homo.
 RN [1]
 RP SEQUENCE FROM N.A.
 RA ELLEXSON M.E., HILDEBRAND W.H.;
 RT "Molecular characterization of HLA-B*1303new."
 RL Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.
 DR EMBL; U75533; AAC31793.1;
 DR HSSP; P30491; IAHM.
 DR PROSITE; PS00290; IG_MHC; 1.
 DR PFAM; PF00047; Ig; 1.
 DR PFAM; PF00129; MHC_I; 1.
 KW MHC.
 SQ SEQUENCE 362 AA; 40476 MW; 8BA369FA CRC32;

Query Match 51.0%; Score 51; DB 7; Length 362;
 Best Local Similarity 68.8%; Pred. No. 2.4;
 Matches 11; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 5 TRLNERRENLTALRY 20
 |
 Db 93 TNTQTYRENLTALRY 108
 |

Search completed: February 8, 2000, 19:16:14
 Job time: 21501 sec

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OM of: US-08-653-294-30 to: GenEmbl.* out_format : pfs

Date: Feb 8, 2000 10:23 PM

About: Results were produced by the GenCore software, version 4.5,
Copyright (c) 1993-2000 CompuGen Ltd.

Command line parameters:

-MODEL=frame model p2n model -DEV=xlp
-Q=/cgn11/USPTO_spool/US08653294/runat_04022000_160701_15779/app_query.fasta.2
-DB=GenEmbl -QMT=fastcap -SUFFIX=rge -GAPOP=12.000 -GAPEXT=4.000
-MINMATCH=0.000 -LOOPEXT=0.000 -QGAPOP=4.500
-QGAPEXT=0.050 -XGAPOP=10.000 -XGAPEXT=0.500 -FGAPOP=6.000
-FGAPEXT=7.000 -YGAPOP=10.000 -YGAPEXT=0.500 -DELOP=6.000
-DELEXT=7.000 -START=1 -MATRIX=blossum62 -TRANS-human40.cdi
-LIST=45 -LOCALIGN=200 -THR_SCORE=pct -ALIGN=15 -MODE=LOCAL
-OUTMT=pfs -NORM=ext -MINLEN=0 -MAXLEN=1000000 -USER=US08653294
-NCPU=6 -ICPU=3 -NO_XLPXY -WAIT -THREADS=1

Search information block:

Query: US-08-653-294-30

Query length: 20

Database: GenEmbl.*

Database sequences: 821193

Database length: 1518192014

Search time (sec): 10176.920000

score_list:

Sequence	Strd Orig	zscore	Escore	Len	Documentation
gb_hhg3:AC010413	+	52.00	113.93	253.22	25949 ! AC010413 Homo sapiens chromos
gb_hhg5:AC015865	+	52.00	100.35	1.4e+03	123347 ! AC015865 Homo sapiens clone
gb_hhg4:AC011290	+	52.00	98.73	1.8e+03	148409 ! AC011290 Homo sapiens clone
gb_hhg4:AC010352	+	52.00	98.47	1.8e+03	135027 ! AC010352 Homo sapiens chrom
gb_pr1:HSG44HLA2	+	51.00	155.00	1.31	163 ! X78849 H.sapiens HLA-B gene, ex
gb_pr1:HSHLAB2	+	51.00	153.80	1.52	187 ! X78426 H.sapiens HLA-B gene, ex
gb_pr1:HSGA18648	+	51.00	150.60	2.30	270 ! Y18648 Homo sapiens HLA-B gene,
gb_pr1:HSAL132659	+	51.00	150.60	2.30	270 ! A132659 Homo sapiens HLA-B gene,
gb_pr1:HSHLAB132	+	51.00	150.60	2.30	270 ! Y12378 H.sapiens HLA-B*13 gene,
gb_pr2:HSAL249724	+	51.00	150.60	2.30	270 ! A249724 Homo sapiens partial H
gb_pr2:HSCHAO1	+	51.00	150.60	2.30	270 ! U58469 Human MHC class I antige
gb_pr3:HSGLAB15M1	+	51.00	150.60	2.30	270 ! U58315 Human HLA-B*15MD gene, e
gb_pr3:HSGLABSH1	+	51.00	150.60	2.30	270 ! U90240 Human MHC class I antige
gb_pr4:AS017316	+	51.00	150.60	2.30	270 ! AF017316 Homo sapiens MHC class
gb_pr4:HB38021G1	+	51.00	150.60	2.30	270 ! AF181857 Homo sapiens HLA-B MHC
gb_pr4:HS44032S1	+	51.00	150.60	2.30	270 ! U63559 Human MHC class I antige
gb_pr4:AF035649	+	51.00	147.29	3.51	395 ! AF035648 Homo sapiens MHC class
gb_pr4:AF035649	+	51.00	147.29	3.51	395 ! AF035649 Homo sapiens MHC class
gb_pr2:HDMB44HLA	+	51.00	147.09	3.60	404 ! L31798 Homo sapiens HLA-B*44 va
gb_pr2:AS032598	+	51.00	144.71	4.89	531 ! AB032598 Homo sapiens MHC class
gb_pr2:HSAL13267	+	51.00	144.47	5.04	546 ! A132667 Homo sapiens mRNA for
gb_pr2:HSAL238702	+	51.00	139.94	9.01	918 ! A238702 Homo sapiens MHC class
gb_pr4:AF056981	+	51.00	139.67	9.33	947 ! AF056981 Homo sapiens MHC class
gb_pr4:U90561	+	51.00	139.67	9.33	947 ! U90561 Homo sapiens MHC class
gb_pr1:HSHLABAB	+	51.00	138.65	10.63	1064 ! X75953 H.sapiens HLA-B mRNA. 4
gb_pr1:HSHLAB44	+	51.00	138.45	10.91	1089 ! X64366 H.sapiens HLA-B*4403 mR
gb_pr1:HSHLAB44G	+	51.00	138.45	10.91	1089 ! X90391 H.sapiens mRNA for HLA-
gb_pr1:HDMB1301A	+	51.00	138.45	10.91	1089 ! D50290 Human mRNA for HLA-B*13
gb_pr1:HDMB1302B	+	51.00	138.45	10.91	1089 ! D50291 Human mRNA for HLA-B*13
gb_pr1:HDMHB38A	+	51.00	138.45	10.91	1089 ! L22028 Human MHC class I HLA-B
gb_pr1:HDMHCB13A	+	51.00	138.45	10.91	1089 ! M24041 Human MHC class I HLA-B
gb_pr1:HDMHCB44A	+	51.00	138.45	10.91	1089 ! M24038 Human MHC class I HLA-B
gb_pr2:HSAL13118	+	51.00	138.45	10.91	1089 ! AJ131118 Homo sapiens mRNA for
gb_pr2:HSU04244	+	51.00	138.45	10.91	1089 ! U04244 Human MHC class I antige
gb_pr2:HSU64801	+	51.00	138.45	10.91	1089 ! U64801 Human MHC class I HLA-B
gb_pr2:HDMHLABK	+	51.00	138.45	10.91	1089 ! L42282 Homo sapiens (clone 18)
gb_pr2:HDMHLABL	+	51.00	138.45	10.91	1089 ! L42283 Homo sapiens major hist
gb_pr3:HSU75533	+	51.00	138.45	10.91	1089 ! U75533 Homo sapiens HLA class
gb_pr1:HDMHLAB13	+	51.00	138.42	10.95	1093 ! M19757 Human MHC class I HLA-B
gb_pr1:HDMHBA13A	+	51.00	138.42	10.95	1093 ! M24075 Human MHC class I HLA-B
gb_pr2:HSU14943	+	51.00	136.90	13.31	1301 ! U14943 Human MHC antigen (HLA-
gb_pr3:AC004182	+	51.00	106.77	633.95	41275 ! AC004182 Homo sapiens clone U

gb_pr2:HDMB270 + 50.00 141.35 7.52 546 ! L76935 Homo sapiens MHC clas
gb_pr4:AF118895 + 50.00 135.35 16.24 1088 ! AF118895 Pongo pygmaeus MHC
gb_ro:AF109166 - 50.00 127.09 46.80 2805 ! AF109166 Rattus norvegicus

seq_name: gb_hhg3:AC010413

seq_documentation_block:

LOCUS AC010413 25949 bp DNA HTG 15-SEP-1999
DEFINITION Homo sapiens chromosome 5 clone CITB-H1_216BD21, *** SEQUENCING IN
PROGRESS ***, 32 unordered pieces.

ACCESSION AC010413.1 GI:5882523

KEYWORDS HTG; HTGS_PHASE1.

SOURCE human.

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;

Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 25949)

Sequencing of Human Chromosome 5

Unpublished

2 (bases 1 to 25949)

DOE Joint Genome Institute.

Direct Submission

Submitted (15-SEP-1999) Production Sequencing Facility, DOE Joint

Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA

www.jgi.doe.gov.

COMMENT

* NOTE: This is a 'working draft' sequence. It currently
* consists of 32 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved. 780: contig of 780 bp in length
* 1
* 781: contig of 270 bp in length
* 1051: contig of 665 bp in length
* 1716: contig of 704 bp in length
* 2420: contig of 735 bp in length
* 3155: contig of 727 bp in length
* 3882: contig of 311 bp in length
* 4193: contig of 381 bp in length
* 4574: contig of 1058 bp in length
* 5632: contig of 828 bp in length
* 6460: contig of 272 bp in length
* 6732: contig of 814 bp in length
* 7546: contig of 510 bp in length
* 8056: contig of 828 bp in length
* 8884: contig of 769 bp in length
* 9653: contig of 222 bp in length
* 9875: contig of 241 bp in length
* 10116: contig of 992 bp in length
* 11108: contig of 1060 bp in length
* 12167: gap of unknown length

```

* 12168 13182: contig of 1015 bp in length
*      gap of unknown length
* 13183 14040: contig of 858 bp in length
*      gap of unknown length
* 14041 15296: contig of 1256 bp in length
*      gap of unknown length
* 15297 16215: contig of 919 bp in length
*      gap of unknown length
* 16216 17301: contig of 1086 bp in length
*      gap of unknown length
* 17302 18060: contig of 759 bp in length
*      gap of unknown length
* 18061 18903: contig of 843 bp in length
*      gap of unknown length
* 18904 19771: contig of 868 bp in length
*      gap of unknown length
* 19772 20568: contig of 797 bp in length
*      gap of unknown length
* 20569 21622: contig of 1054 bp in length
*      gap of unknown length
* 21623 22449: contig of 827 bp in length
*      gap of unknown length
* 22450 23873: contig of 1424 bp in length
*      gap of unknown length
* 23874 25949: contig of 2076 bp in length.
FEATURES          Location/Qualifiers
Source            1..25949
                  /organism="Homo sapiens"
                  /db_xref="taxon:9606"
                  /chromosome="5"
                  /clone="CITB-H1.2168D21"
BASE COUNT       7182 a 5843 c 5600 g 7316 t      8 others
ORIGIN

```

```

alignment_scores:
  Quality: 52.00      Length: 15
  Ratio: 4.000        Gaps: 0
Percent Similarity: 86.667 Percent Identity: 73.333

```

```

alignment_block:
US-08-653-294-30 x AC010413

```

```

Align seg 1/1 to: AC010413 from: 1 to: 25949

```

```

2 ArgLeuAlaThrArgLeuAsnGluArgGluAsnLeuArgThr 16
||||| ||||||||| ||||||| ||||||| |||||||
8826 AAATCCCAACACGCTGCAACATCAGAAGGAACACCTCCGGACA 8870

```

```

seq_name: gb_htg5:AC015865

```

```

seq_documentation_block:
LOCUS      AC015865 123347 bp    DNA             HTG             17-NOV-1999
DEFINITION Homo sapiens clone RP11-55A1, LOW-PASS SEQUENCE SAMPLING.
ACCESSION  AC015865
VERSION    AC015865.1 GI:6446803
KEYWORDS   HTG: HTGS_PHASE0; NULL.
SOURCE     human.

```

```

ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1 (bases 1 to 123347)
AUTHORS   Birren,B., Linton,L., Nusbaum,C. and Lander,E.
TITLE     Homo sapiens, clone RP11-55A1
JOURNAL   Unpublished
REFERENCE  2 (bases 1 to 123347)
AUTHORS   Birren,B., Linton,L., Nusbaum,C., Lander,E., Allen,N., Anderson,M.,
            Baldwin,J., Barna,N., Beckerly,R., Boguslavsky,L., Boukhgalter,B.,
            Brown,A., Castle,A., Colangelo,M., Collins,S., Collymore,A.,
            Cooke,P., DeArelano,K., Dewar,K., Domino,M., Donelan,L., Doyle,M.,
            Ferreira,P., FitzHugh,W., Forrest,C., Funke,R., Gage,D., Horton,L.,
            Galagan,J., Gardyna,S., Grant,G., Hagos,B., Heaford,A., Horton,L.,
            Howland,J.C., Johnson,R., Jones,C., Kann,L., Karatas,A., Klein,J.,

```

Lehoczkzy, J., Lieu, C., Locke, K., Macdonald, P., Marquis, N., McEwan, P., McGurk, A., McKernan, K., McLaughlin, J., Meldrim, J., Morrow, J., Naylor, J., Norman, C.H., O'Connor, T., O'Donnell, P., Peterson, K., Pollara, V., Riley, R., Roy, A., Santos, R., Severy, P., Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J., Testaye, S., Tirrell, A., Vassiliev, H., Vo, A., Wheeler, J., Wu, X., Wyman, D., Ye, W.J., Zimmer, A. and Zody, M.

Direct Submission
Submitted (17-NOV-1999) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
<http://ftp.genome.washington.edu/RM/RepeatMasker.html>

----- Project Information
Center project name: L626
Center clone name: 55_A_1

* NOTE: This record contains 140 individual
* sequencing reads that have not been assembled into
* contigs. Runs of N are used to separate the reads
* and the order in which they appear is completely
* arbitrary. Low-pass sequence sampling is useful for
* identifying clones that may be gene-rich and allows
* overlap relationships among clones to be deduced.
* However, it should not be assumed that this clone
* will be sequenced to completion. In the event that
* the record is updated, the accession number will
* be preserved.

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* 1      868: contig of 868 bp in length
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* 869    1706: contig of 838 bp in length
*      gap of unknown length
* 1707   2529: contig of 823 bp in length
*      gap of unknown length
* 2530   3392: contig of 863 bp in length
*      gap of unknown length
* 3393   4216: contig of 824 bp in length
*      gap of unknown length
* 4217   5052: contig of 836 bp in length
*      gap of unknown length
* 5053   5879: contig of 827 bp in length
*      gap of unknown length
* 5880   6713: contig of 834 bp in length
*      gap of unknown length
* 6714   7550: contig of 837 bp in length
*      gap of unknown length
* 7551   8392: contig of 842 bp in length
*      gap of unknown length
* 8393   9234: contig of 842 bp in length
*      gap of unknown length
* 9235   10079: contig of 845 bp in length
*      gap of unknown length
* 10080  10934: contig of 855 bp in length
*      gap of unknown length
* 10935  11767: contig of 833 bp in length
*      gap of unknown length
* 11768  12598: contig of 831 bp in length
*      gap of unknown length
* 12599  13443: contig of 845 bp in length
*      gap of unknown length
* 13444  14281: contig of 838 bp in length
*      gap of unknown length
* 14282  15101: contig of 820 bp in length
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* 15102  15950: contig of 849 bp in length
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* 15951  16782: contig of 832 bp in length
*      gap of unknown length
* 16783  17627: contig of 845 bp in length
*      gap of unknown length
* 17628  18473: contig of 846 bp in length
*      gap of unknown length
* 18474  19302: contig of 829 bp in length

```

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* * gap of unknown length
* 19303 20156: contig of 854 bp in length
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* 20157 20994: contig of 838 bp in length
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* 20995 21914: contig of 820 bp in length
* * gap of unknown length
* 21815 22644: contig of 830 bp in length
* * gap of unknown length
* 22645 23466: contig of 822 bp in length
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* 23467 24313: contig of 847 bp in length
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* 24314 25156: contig of 843 bp in length
* * gap of unknown length
* 25157 25981: contig of 825 bp in length
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* 25982 26819: contig of 838 bp in length
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* 26820 27671: contig of 852 bp in length
* * gap of unknown length
* 27672 28514: contig of 843 bp in length
* * gap of unknown length
* 28515 29448: contig of 934 bp in length
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* 29449 30281: contig of 833 bp in length
* * gap of unknown length
* 30282 31107: contig of 826 bp in length
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* 31108 31948: contig of 841 bp in length
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* 31949 32786: contig of 838 bp in length
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* 32787 33641: contig of 855 bp in length
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* 33642 34485: contig of 844 bp in length
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* 34486 35305: contig of 820 bp in length
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* 35306 36153: contig of 848 bp in length
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* 36154 36993: contig of 840 bp in length
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* 36994 37824: contig of 831 bp in length
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* 37825 38653: contig of 829 bp in length
* * gap of unknown length
* 38654 39490: contig of 837 bp in length
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* 39491 40345: contig of 855 bp in length
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* 40346 41178: contig of 833 bp in length
* * gap of unknown length
* 41179 42015: contig of 837 bp in length
* * gap of unknown length
* 42016 42860: contig of 845 bp in length
* * gap of unknown length
* 42861 43696: contig of 836 bp in length
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* 43697 44524: contig of 828 bp in length
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* 44525 45347: contig of 823 bp in length
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* 45348 46177: contig of 830 bp in length
* * gap of unknown length
* 46178 47013: contig of 836 bp in length
* * gap of unknown length
* 47014 47836: contig of 823 bp in length
* * gap of unknown length
* 47837 48670: contig of 834 bp in length
* * gap of unknown length
* 48671 49502: contig of 832 bp in length
* * gap of unknown length
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* 49503 50363: contig of 861 bp in length
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* 50364 51194: contig of 831 bp in length
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* 51195 52027: contig of 833 bp in length
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* 52028 52875: contig of 848 bp in length
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* 52876 53712: contig of 837 bp in length
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* 53713 54539: contig of 827 bp in length
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* 54540 55376: contig of 837 bp in length
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* 56208 57066: contig of 859 bp in length
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* 57067 57881: contig of 815 bp in length
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* 57882 58715: contig of 834 bp in length
* * gap of unknown length
* 58716 59549: contig of 834 bp in length
* * gap of unknown length
* 59550 60371: contig of 822 bp in length
* * gap of unknown length
* 60372 61213: contig of 842 bp in length
* * gap of unknown length
* 61214 62061: contig of 848 bp in length
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* 62062 62993: contig of 932 bp in length
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* 62994 63913: contig of 920 bp in length
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alignment_scores:

```
Quality: 52.00 Length: 15
Ratio: 4.000 Gaps: 0
Percent Similarity: 86.667 Percent Identity: 73.333
```

alignment_block:

```
US-08-653-294-30 x AC015865 ..
```

```
Align seg 1/1 to: AC015865 from: 1 to: 123347
```

```
2 ArgLeuAlaThrArgLeuAsnGluArgGluAsnLeuArgThr 16
:::||||| ||||| ||||| ||||| ::||| ||||| |||||
47640 AAATCCGACACGCTGTGAATATCAGAGGACACCTCCGGACA 47684
```

```
seq_name: gb_htg4:AC011290
```

seq_documentation_block:

```
LOCUS AC011290 148409 bp DNA HTG 15-OCT-1999
DEFINITION Homo sapiens clone NH0064102, *** SEQUENCING IN PROGRESS ***, 3
```

```
unordered pieces.
```

```
ACCESSION AC011290
```

```
VERSION AC011290.2 GI:6042094
```

```
KEYWORDS HTG: HTGS_PHASE1.
```

```
SOURCE human.
```

ORGANISM

```
Homo sapiens
```

```
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
```

```
Eutheria; Primates; Catarrhini; Hominidae; Homo.
```

```
REFERENCE 1 (bases 1 to 148409)
```

```
AUTHORS Waterston,R.H.
```

```
TITLE The sequence of Homo sapiens clone
```

```
JOURNAL Unpublished
```

```
REFERENCE 2 (bases 1 to 148409)
```

```
AUTHORS Waterston,R.H.
```

```
TITLE Direct Submission
```

```
JOURNAL Submitted (05-OCT-1999) Genome Sequencing Center, Washington
```

```
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
```

```
MO 63108, USA
```

```
COMMENT On Oct 15, 1999 this sequence version replaced gi:6012159.
```

```
* NOTE: This is a 'working draft' sequence. It currently
```

* consists of 3 contigs. The true order of the pieces
 * is not known and their order in this sequence record is
 * arbitrary. Gaps between the contigs are represented as
 * runs of N, but the exact sizes of the gaps are unknown.
 * This record will be updated with the finished sequence
 * as soon as it is available and the accession number will
 * be preserved.

* 1 1991: contig of 1991 bp in length
 * 1992 2009: gap of unknown length
 * 2010 64050: contig of 62041 bp in length
 * 64051 64088: gap of unknown length
 * 64069 148409: contig of 84341 bp in length.

FEATURES

Location/Qualifiers
 1..148409
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="NH0064102"

BASE COUNT 44805 a 31502 c 29724 g 42342 t 36 others
 ORIGIN

alignment_scores:

Quality: 52.00 Length: 15
 Ratio: 4.000 Gaps: 0
 Percent Similarity: 86.667 Percent Identity: 73.333

alignment_block:

US-08-653-294-30 x AC011290 ..

Align seg 1/1 to: AC011290 from: 1 to: 148409

2 ArgLeuAlaThrArgLeuAsnGluArgGluAsnLeuArgThr 16

33983 AAACCTCCGACACGCTGTAATATCATGAGAGACACCTCCGGACA 34027

seq_name: gb_htg4:AC010352

seq_documentation_block:

LOCUS AC010352 153027 bp DNA HTG 31-OCT-1999
 DEFINITION Homo sapiens chromosome 5 clone C17B-H1_2022F20, *** SEQUENCING IN
 PROGRESS ***, 77 unordered pieces.

ACCESSION AC010352
 VERSION AC010352.2 GI:6165069
 KEYWORDS HTG; HTGS_PHASE1.
 SOURCE human.

ORGANISM

Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 153027)

DOE Joint Genome Institute.

TITLE Sequencing of Human Chromosome 5

JOURNAL Unpublished

REFERENCE 2 (bases 1 to 153027)

DOE Joint Genome Institute.

Direct Submission

Submitted (15-SEP-1999), Production Sequencing Facility, DOE Joint

Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA

On Oct 31, 1999 this sequence version replaced gi:5882582.

* NOTE: This is a 'working draft' sequence. It currently

* consists of 77 contigs. The true order of the pieces

* is not known and their order in this sequence record is

* arbitrary. Gaps between the contigs are represented as

* runs of N, but the exact sizes of the gaps are unknown.

* This record will be updated with the finished sequence

* as soon as it is available and the accession number will

* be preserved.

* 1 675: contig of 675 bp in length

* 676 1399: contig of 724 bp in length

* 1400 2124: contig of 725 bp in length

* 2125 2891: contig of 767 bp in length

* 2892 3576: contig of 685 bp in length
 * 3577 4442: contig of 866 bp in length
 * 4443 5226: contig of 784 bp in length
 * 5227 5881: contig of 655 bp in length
 * 5882 6591: contig of 710 bp in length
 * 6592 7225: contig of 634 bp in length
 * 7226 7780: contig of 555 bp in length
 * 7781 8459: contig of 679 bp in length
 * 8460 9189: contig of 730 bp in length
 * 9190 9894: contig of 705 bp in length
 * 9895 10528: contig of 634 bp in length
 * 10529 11169: contig of 641 bp in length
 * 11170 11816: contig of 647 bp in length
 * 11817 12641: contig of 825 bp in length
 * 12642 13127: contig of 486 bp in length
 * 13128 13960: contig of 833 bp in length
 * 13961 14620: contig of 660 bp in length
 * 14621 15321: contig of 701 bp in length
 * 15322 16382: contig of 1061 bp in length
 * 16383 16563: contig of 181 bp in length
 * 16564 17592: contig of 1029 bp in length
 * 17593 18581: contig of 989 bp in length
 * 18582 19292: contig of 711 bp in length
 * 19293 20208: contig of 916 bp in length
 * 20209 21122: contig of 914 bp in length
 * 21123 21499: contig of 377 bp in length
 * 21500 22611: contig of 1112 bp in length
 * 22612 23418: contig of 807 bp in length
 * 23419 24584: contig of 1166 bp in length
 * 24585 25024: contig of 440 bp in length
 * 25025 25800: contig of 776 bp in length
 * 25801 26106: contig of 306 bp in length
 * 26107 26994: contig of 888 bp in length
 * 26995 27627: contig of 633 bp in length
 * 27628 28281: contig of 654 bp in length
 * 28282 29585: contig of 1304 bp in length
 * gap of unknown length

```
* 29586 30424: contig of 839 bp in length
*      gap of unknown length
* 30425 31385: contig of 961 bp in length
*      gap of unknown length
* 31386 31815: contig of 430 bp in length
*      gap of unknown length
* 31816 32488: contig of 673 bp in length
*      gap of unknown length
* 32489 33843: contig of 1355 bp in length
*      gap of unknown length
* 33844 34640: contig of 797 bp in length
*      gap of unknown length
* 34641 35604: contig of 964 bp in length
*      gap of unknown length
* 35605 36604: contig of 1000 bp in length
*      gap of unknown length
* 36605 37233: contig of 629 bp in length
*      gap of unknown length
* 37234 38551: contig of 1318 bp in length
*      gap of unknown length
* 38552 40124: contig of 1573 bp in length
*      gap of unknown length
* 40125 41518: contig of 1394 bp in length
*      gap of unknown length
* 41519 43017: contig of 1499 bp in length
*      gap of unknown length
* 43018 44900: contig of 1883 bp in length
*      gap of unknown length
* 44901 46617: contig of 1717 bp in length
*      gap of unknown length
* 46618 49303: contig of 2686 bp in length
*      gap of unknown length
* 49304 51254: contig of 1951 bp in length
*      gap of unknown length
* 51255 54500: contig of 3246 bp in length
*      gap of unknown length
* 54501 55630: contig of 1130 bp in length
*      gap of unknown length
* 55631 57502: contig of 1872 bp in length
*      gap of unknown length
* 57503 59256: contig of 1754 bp in length
*      gap of unknown length
* 59257 61561: contig of 2305 bp in length
*      gap of unknown length
* 61562 65095: contig of 3534 bp in length
*      gap of unknown length
* 65096 67286: contig of 2191 bp in length
*      gap of unknown length
* 67287 71068: contig of 3782 bp in length
*      gap of unknown length
* 71069 76255: contig of 5187 bp in length
*      gap of unknown length
* 76256 81531: contig of 5276 bp in length
*      gap of unknown length
* 81532 87291: contig of 5760 bp in length
*      gap of unknown length
* 87292 92814: contig of 5523 bp in length
*      gap of unknown length
* 92815 98788: contig of 5974 bp in length
*      gap of unknown length
* 98789 107107: contig of 8319 bp in length
*      gap of unknown length
* 107108 115470: contig of 8363 bp in length
*      gap of unknown length
* 115471 121604: contig of 6134 bp in length
*      gap of unknown length
* 121605 129121: contig of 7517 bp in length
*      gap of unknown length
* 129122 135498: contig of 6377 bp in length
*      gap of unknown length
* 135499 143045: contig of 7547 bp in length
*      gap of unknown length
* 143046 153027: contig of 9982 bp in length.
```

```
FEATURES             Location/Qualifiers
     source            1..153027
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /chromosome="5"
                     /clone="CIT8-H1-2022F20"
BASE COUNT      43128 a 33071 c 33103 g 43621 t    104 others
ORIGIN

alignment_scores:
  Quality:      52.00      Length:      15
  Ratio:        4.000      Gaps:        0
  Percent Similarity: 86.667      Percent Identity: 73.333

alignment_block:
US-08-653-294-30 x AC010352/rev ..
Align seg 1/1 to reverse of: AC010352 from: 1 to: 153027

      2 ArgLeuAlaThrArgLeuAsnGluArgGluAsnLeuArgThr 16
      ::::| | | | | | | | | | | | | | | | | | | | | |
135173 AAACTCGAACACGCTGTGACATCATGAGGACACACCTCGGACA 135129

seq_name: gb_pri:HSB44HLA2

seq_documentation_block:
LOCUS      HSB44HLA2      163 bp      DNA      PRI      16-DEC-1994
DEFINITION H.sapiens HLA-B gene, exon 2.
ACCESSION      X78849
VERSION      X78849.1 GI:602874
KEYWORDS      heavy chain; MHC class I; MHC class I HLA-B44.
SOURCE      human.
ORGANISM      Homo sapiens
               Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
               Primates; Catarrhini; Hominoidea; Homo.
REFERENCE      1 (bases 1 to 163)
AUTHORS      Yao, Z., Volgger, A., Scholz, S., Bonisch, J. and Albert, E.D.
TITLE      Nucleotide sequence of a novel HLA-B44 subtype B*4405
JOURNAL      Immunogenetics 40 (4), 310 (1994)
MEDLINE      94364642
REFERENCE      2 (bases 1 to 163)
AUTHORS      Albert, E.
TITLE      Direct Submission
JOURNAL      Submitted (11-APR-1994) E. Albert, Labor fuer Immunogenetik,
               Kinderpoliklinik der LMU Muenchen, Pettenhoferstr. 8a, 80336
               Muenchen, FRG

FEATURES             Location/Qualifiers
     source            1..163
                     /organism="Homo sapiens"
                     /isolate="WJG"
                     /db_xref="taxon:9606"
                     /chromosome="6"
                     /germline
                     /note="MHC"
     exon              1..163
                     /note="MHC Class I heavy chain HLA-B44 variant"
                     /number=2
BASE COUNT      45 a 50 c 54 g 14 t
ORIGIN

alignment_scores:
  Quality:      51.00      Length:      16
  Ratio:        3.923      Gaps:        0
  Percent Similarity: 81.250      Percent Identity: 68.750

alignment_block:
US-08-653-294-30 x HSB44HLA2 ..
Align seg 1/1 to: HSB44HLA2 from: 1 to: 163

      5 ThrArgLeuAsnGluArgGluAsnLeuArgThrAlaLeuArgTyr 20
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40


```

TITLE      HLA-B Alleles Associated with the B15 Serologically Defined
JOURNAL    Antigen
REFERENCE   Hum. Immunol. 56 (1997) In press
AUTHORS    2 (bases 1 to 270)
TITLE      Steiner,N.K. and Hurley,C.K.
JOURNAL    Direct Submission
SUBMITTED  (20-FEB-1997) Microbiology & Immunology, Georgetown
UNIVERSITY, 3970 Reservoir Rd. NW, Washington, DC 20007, USA
FEATURES   Location/Qualifiers
            source
            1..270
            /organism="Homo sapiens"
            /isolate="GN00155"
            /db_xref="taxon:9606"
            exon
            1..270
            /gene="HLA-B"
            /number=2
BASE COUNT 60 a 88 c 85 g 37 t
ORIGIN
alignment_scores:
    Quality: 51.00      Length: 16
    Ratio: 3.923       Gaps: 0
Percent Similarity: 81.250 Percent Identity: 68.750
alignment_block:
US-08-653-294-30 x HSHLABSH1 ..
Align seg 1/1 to: HSHLABSH1 from: 1 to: 270
5 ThrArgLeuAsnGluArgGluAsnLeuArgThrAlaLeuArgTyr 20
||||: ::|||
204 ACCAACACACAGACTTACCGAGAGACCTGCGCAGCGCTCGCTAC 251
seq_name: gb_pr4:AF017316
seq_documentation_block:
LOCUS      AF017316      270 bp      DNA      PRI      26-MAR-1999
DEFINITION Homo sapiens HLA-B MHC class I antigen (HLA-B) gene, partial cds.
ACCESSION  AF017316
VERSION    AF017316.1 GI:2394335
KEYWORDS   human.
SOURCE     Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1 (bases 1 to 270)
AUTHORS    Cao,K., Burdett,L., Zhang,G. and Fernandez-Vina,M.
TITLE      Direct Submission
JOURNAL    Submitted (07-AUG-1997) Nat. Histocompatibility Lab, Am Red Cross,
            box 173, 22 S. Greene St., Baltimore, MD 21201, USA
FEATURES   Location/Qualifiers
            source
            1..270
            /organism="Homo sapiens"
            /db_xref="taxon:9606"
            /clone="27B"
            /chromosome="6"
            <1..>270
            /gene="HLA-B"
            /note="novel allele"
            <1..>270
            /gene="HLA-B"
            /codon_start=3
            /product="MHC class I antigen"
            /protein_id="AAB70282.2"
            /db_xref="GI:4521330"
            /translation="SHSMRVFYTAMSRPGRPFITGVYVDDTFQVRFSDATSPRM
            APRAPWIEQEGPEVMDRETQISKTNTQTYRENTALRYNQSEA"
BASE COUNT 59 a 92 c 83 g 36 t
ORIGIN
alignment_scores:
    Quality: 51.00      Length: 16
    Ratio: 3.923       Gaps: 0
Percent Similarity: 81.250 Percent Identity: 68.750
alignment_block:
US-08-653-294-30 x HB38021G1 ..
Align seg 1/1 to: HB38021G1 from: 1 to: 270
5 ThrArgLeuAsnGluArgGluAsnLeuArgThrAlaLeuArgTyr 20
||||: ::|||
204 ACCAACACACAGACTTACCGAGAGACCTGCGCAGCGCTCGCTAC 251
seq_name: gb_pr4:AF017316
seq_documentation_block:
LOCUS      AF017316      270 bp      DNA      PRI      23-SEP-1999
DEFINITION Homo sapiens HLA-B MHC class I antigen (HLA-B) gene, HLA-B-*38021
ACCESSION  AF181857
VERSION    AF181857.1 GI:5919134
KEYWORDS   human.
SOURCE     Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1 (bases 1 to 270)
AUTHORS    Pimtanothai,N. and Hurley,C.K.
TITLE      Novel HLA-B allele
JOURNAL    Unpublished
REFERENCE  2 (bases 1 to 270)
AUTHORS    Pimtanothai,N. and Hurley,C.K.
TITLE      Direct Submission
JOURNAL    Submitted (30-AUG-1999) Microbiology & Immunology, Georgetown
            University, 3970 Reservoir Rd. N.W., Washington, D.C. 20007, USA
FEATURES   Location/Qualifiers
            source
            1..270
            /organism="Homo sapiens"
            /db_xref="taxon:9606"
            /clone="49N-TA"
            <1..>270
            /gene="HLA-B"
            /number=2
            exon
            1..270
BASE COUNT 58 a 87 c 88 g 37 t
ORIGIN
alignment_scores:
    Quality: 51.00      Length: 16
    Ratio: 3.923       Gaps: 0
Percent Similarity: 81.250 Percent Identity: 68.750
alignment_block:
US-08-653-294-30 x HB38021G1 ..
Align seg 1/1 to: HB38021G1 from: 1 to: 270
5 ThrArgLeuAsnGluArgGluAsnLeuArgThrAlaLeuArgTyr 20
||||: ::|||
204 ACCAACACACAGACTTACCGAGAGACCTGCGCAGCGCTCGCTAC 251

```

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OM of: US-08-653-294-30 to: N_Geneseq_36:* out_format : pfs

Date: Feb 8, 2000 7:31 PM

About: Results were produced by the GenCore software, version 4.5,
Copyright (c) 1993-2000 CompuGen Ltd.

Command line parameters:

-MODEL=frame+p2n.model -DEV=xlp
-O=/cgn1.1/USPTO_spool/US08653294/runat_04022000.160701.15807/app_query.fasta.2
-DB=N_Geneseq_36 -QFMT=fastap -SUFFIX=mg -GAPOP=12.000
-GAPEXT=4.000 -MINMATCH=0.100 -LOOPEXT=0.000 -LOOPEXT=0.000
-GAPOP=4.500 -GAPEXT=0.050 -XGAPOP=10.000 -XGAPEXT=0.500
-GAPOP=6.000 -GAPEXT=7.000 -XGAPOP=10.000 -XGAPEXT=0.500
-DELOP=6.000 -DELEXT=7.000 -START=1 -MATRIX=blossum62
-TRANS=human40.cdi -LIST=45 -DOCALLIGN=200 -THR_SCORE=pct
-ALIGN=15 -MODE=LOCAL -OUTFMT=pfs -NORM=ext -MINLEN=0
-MAXLEN=100000 -USER=US08653294 -NCPU=6 -ICPU=3 -NO_XLPXY -WAIT
-THREADS=1

Search information block:

Query: US-08-653-294-30
Query length: 20
Database: N_Geneseq_36:*
Database sequences: 311585
Database length: 125096042
Search time (sec): 873.190000

score_list:

Sequence	Strd	Orig	zScore	EScore	Len	Documentation
N_Geneseq_36:T42608	+	46.00	137.82	4.47	285	! Synthetic gene, LqhIV encoding
N_Geneseq_36:Q29167	+	45.00	135.21	6.25	270	! HLA-Bw 52 exon 2 alpha-1 domain
N_Geneseq_36:Q01834	+	45.00	122.32	32.65	1086	! Sequence encoding HLA-Bw51 anti
N_Geneseq_36:Q01822	+	45.00	122.32	32.65	1086	! Sequence encoding HLA-Bw52 anti
N_Geneseq_36:Q05693	+	45.00	122.29	32.75	1089	! HLA-Bw51 gene for production of
N_Geneseq_36:Q05701	+	45.00	122.29	32.75	1089	! HLA-Bw52 gene for production of
N_Geneseq_36:Q12114	+	45.00	122.29	32.75	1089	! HLA-Bw53 exon. HLA-Bw53 gene,
N_Geneseq_36:Q02045	+	45.00	111.64	128.49	3442	! Encodes KEX2 endopeptidase wit
N_Geneseq_36:Q09896	+	45.00	110.00	158.44	4106	! Yeast KEX2 gene. Yeast with re
N_Geneseq_36:V52236	+	44.00	104.08	338.44	5558	! Streptococcus pneumoniae genom
N_Geneseq_36:Q62429	+	44.00	100.12	562.75	8528	! Construct PC2L (Contains catr
N_Geneseq_36:Q41225	+	43.50	111.15	136.71	2190	! Clone PC14 encoding major sur
N_Geneseq_36:T07447	+	43.00	126.26	19.68	362	! B. subtilis aprE target DNA. De
N_Geneseq_36:N80745	+	43.00	115.01	83.32	1220	! Coding region of the aprE gene
N_Geneseq_36:Q06587	+	43.00	115.01	83.32	1220	! aprA gene encoding subtilisin.
N_Geneseq_36:N70890	+	43.00	115.01	83.32	1220	! Thermotable Bacillus subtilis
N_Geneseq_36:Q03536	+	43.00	113.11	105.41	1499	! Subtilisin gene. Mutant prokar
N_Geneseq_36:N71241	+	43.00	113.10	106.49	1500	! Subtilisin gene from Bacillus
N_Geneseq_36:Q05058	+	43.00	113.10	106.49	1500	! Bacillus subtilis subtilisin g
N_Geneseq_36:Q90042	+	43.00	113.10	106.49	1500	! B. subtilis subtilisin gene. Re
N_Geneseq_36:N60475	+	43.00	112.95	108.52	1524	! Sequence of the apr [bsu] gene
N_Geneseq_36:X25097	+	43.00	107.45	219.71	2760	! Bacillus subtilis metalloprote
N_Geneseq_36:T75487	+	43.00	104.77	309.90	3687	! DNA for Bacillus steatothermo
N_Geneseq_36:T08695	+	43.00	104.41	324.43	3832	! sbsA gene encoding S-layer pro
N_Geneseq_36:Q28344	+	42.00	111.00	139.35	1344	! pBULI core sequence from Lacto
N_Geneseq_36:V49262	+	42.00	103.50	364.95	3023	! FelV-B gag/pol gene. Multi-val
N_Geneseq_36:N82261	+	42.00	102.85	396.71	3243	! Enkephalinase gene (rat). Deox
N_Geneseq_36:Q62679	+	42.00	102.85	396.71	3243	! Rat enkephalinase cDNA. Method
N_Geneseq_36:Q29114	+	42.00	101.69	460.09	3674	! FelV-A gag/pol fragment. Vacci
N_Geneseq_36:T13265	+	42.00	93.99	1.2e+03	8440	! FelV F6A provirus clone 61E ga
N_Geneseq_36:X20550	+	42.00	93.76	1.3e+03	8648	! Polynucleotide sequence from t
N_Geneseq_36:T60544	+	41.50	122.04	33.84	345	! (Pro33-Lys33)delAsn37-ile-134) t
N_Geneseq_36:T60542	+	41.50	120.28	42.38	417	! MetGDNF degenerate DNA sequence
N_Geneseq_36:T39144	+	41.00	136.23	5.48	63	! FKBP 3' sequence/Influenza epit
N_Geneseq_36:V45091	+	41.00	136.23	5.48	63	! pBJS/NFIE expression vector 3' e
N_Geneseq_36:T13522	+	41.00	111.79	125.97	882	! Sequence proximal to Xp/Yp PAR1
N_Geneseq_36:T84985	+	41.00	107.83	209.41	1353	! Burkholderia cepacia ET12 stra
N_Geneseq_36:X14387	+	41.00	104.52	320.10	1934	! H. pylori GHP0 504 gene. New
N_Geneseq_36:T84986	+	41.00	102.67	405.68	2361	! Burkholderia cepacia insertion
N_Geneseq_36:T42791	+	41.00	101.11	495.50	2794	! Scytalidium catalase gene. New
N_Geneseq_36:Q78276	+	41.00	97.85	752.73	3973	! T. niveum alanine-racemase. Ne

N_Geneseq_36:Q78281 - 41.00 97.85 752.73 3973 ! T. niveum alanine-racemase.
N_Geneseq_36:V74362 + 41.00 92.97 1.4e+03 6730 ! Staphylococcus aureus conti
N_Geneseq_36:Q86851 + 41.00 90.50 1.9e+03 8789 ! Human mitosis gene. Purifie
N_Geneseq_36:V09076 + 41.00 90.50 1.9e+03 8789 ! Mitosis nucleic acid sequen

seq_name: N_Geneseq_36:T42608

seq_documentation_block:

ID T42608 standard; DNA; 285 BP.

AC T42608.

DT 07-AUG-1997 (first entry)

DE Synthetic gene, LqhIV encoding scorpion neurotoxin.

KW neurotoxin; pest control; insect; acarid; nematode; LqhIV; LqhVI;

KW venom; Leiurus quinquestratus hebraeus; scorpion; lepidoptera;

OS baculovirus; arthropod; ds.

OS Synthetic.

FH Key Location/Qualifiers

FT cds 70..267

FT /*tag= a

FT /note= "no start codon given"

PN WO9636221-A2.

PD 21-NOV-1996.

PF 30-APR-1996; U06076.

PR 08-MAY-1995; US-435040.

PA (REGC) UNIV CALIFORNIA.

PI Hammock BD, Herrmann R, Moskowitz H;

DR WPI: 97-011744/01.

DR P-PSDB: W06339.

PT Control of insects, acarids and nematodes - using novel scorpion

PT toxins or a combination of 2 or more insect toxins

PS Claim 1; Fig 1; 35pp; English.

CC A novel method for controlling pests selected from insects, acarids, and

CC nematodes, comprises treating the pests or their loci with at least two

CC different insect toxins, the source of the toxins being at least one

CC recombinant microbe, the toxins having non-overlapping binding sites at

CC an insect cellular membrane channel. The present sequence is a synthetic

CC gene for LqhIV toxin, derived from the venom of Leiurus quinquestratus

CC hebraeus (Scorpion). LqhIV is the most potent lepidopterous toxin

CC isolated from scorpion venom to date, whilst LqhVI (W06340) has weak

CC mammal toxicity. In particular the insect toxin genes are expressed

CC by baculovirus vectors, as the baculoviruses infect only arthropods,

CC therefore pose little or no risk to humans, plants or the environment.

SQ Sequence 285 BP; 67 A; 92 C; 70 G; 56 T;

alignment_scores:

Quality: 46.00 Length: 19

Ratio: 2.875 Gaps: 0

Percent Similarity: 84.211 Percent Identity: 52.632

alignment_block:

US-08-653-294-30 x T42608 ..

Align seg 1/1 to: T42608 from: 1 to: 285

1 TyrArgLeuAlaThrArgLeuAsnGluArgArgGluAsnLeuArgThrAl 17

66 CACCGCGTGGCGGACGCTCATCGCCGACGACAGACTCGGTGTACA 115

17 aLeuArg 19

116 CTTGCGG 122

seq_name: N_Geneseq_36:Q29167

seq_documentation_block:

ID Q29167 standard; DNA; 270 BP.

AC Q29167.

DT 09-MAR-1993 (first entry)

DE HLA-Bw 52 exon 2 alpha-1 domain.

KW Human leukocyte antigen; transgenic; germ cells; somatic cells;

KW expression; ss.

PN J04091731-A.

5 ThrArgLeuAsnGluArgArgGluAsnLeuArgThrAlaLeuArgTyr 20
||||| :: ||||| ||||| ||||| |||||
276 ACCAACACAGACTTACCGAGAGAACCCTGGGATCGCGGTCCGGCTAC 323

CC native promoter of the gene was removed and replaced with the
CC *Aspergillus gluconylase* promoter gene. This modification allows
CC increased expression of the *carE* gene without the need to supply
CC hydrogen peroxide to induce expression. Cells into which this
CC construct is inserted preferably have the glucose oxidase gene
CC (*gox*) deleted. This deletion minimises the generation of
CC gluconate waste material and the use of waste treatment processes
SQ Sequence 8528 BP; 1951 A; 2321 C; 2209 G; 2047 T;

alignment_scores:		
Quality:	44.00	Length:
Ratio:	3.143	Gaps:
Percent Similarity:	82.353	Percent Identity:
		52.941
		17
		0

alignment_block:
US-08-653-294-30 x Q46249/rev

Align seg 1/1 to reverse of: Q46249 from: 1 to: 8528

1 TyrArgLeuAlaThrArgLeuAsnGluArgArgGluAsnLeuArgThrAl 17
|||||
1776 TATCGTTTAGCATCTAGCTTGAATTCCTGCAGAGACCATCTCGCCACTTC 1727

17 a 17

name: N_Geneseq_36:04

seq_name: N_Geneseq_36:Q41225

documentation_block: Q41225 standard; DNA; 2190 BP.

DE 02-SEP-1993 (first entry)
DT Clone PC14 encoding major surface gp of rat P. carini.
DE Major surface glycoprotein; gp16; rat; Pneumocystis carinii.
DE vaccine; HIV; human immunodeficiency virus; diagnostic; PCR;
OS Rat Pneumocystis carinii.

```
FT misc_feature 1. .8
```

FT 5'utr 9. .1957

ET cds
ET cds
1958: .4370
/ Traction - Grain Promoter

```
FT = catR coding region
```

FT	misc	feature	4433	4440
FT			/*Eg=	d

FT /label= Linker sequence.

```

E1 / *tag= I
E2 /label= c|a| n|v|adenv|at
E3

```

FT	cds	6094.	.8510
----	-----	-------	-------

```

FT      misc feature      9511  9520
      /label= pyrG gene.

```

```

FT
/label= Linker sequence.

```

PD 16-SEP-1993.

PR 04-MAR-1992: US-846181.
PR 04-MAR-1992: US-846181.

PI Berka RM, Fowler T, Rey MW;

PI Aspergillus niger catK gene sequence - II
PT has been deleted and Aspergillus glaucus myc

PS - Disclosure; Figure 3; 43pp; English.

Quality:	43.50	Length:	20
Ratio:	2.719	Gaps:	1
Percent Similarity:	80.000	Percent Identity:	50.000

alignment_block:

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US-08-653-294-30 x Q41225
Align seg 1/1 to: Q41225 from: 1 to: 2190

2 ArgLeuAlaThrArgLeuAsnGluArgGlu...AsnLeuArgThrAl 17
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
1178 AGACTGAGTACGAAATGCTAAAGAGCGGAGAGAAATCTACAAACAA 1227

17 ArgLeuArgTyr 20
||| |||
1228 GCTAGCTTAT 1237

seq_name: N_Geneseq_36:T07447

seq_documentation_block:
ID T07447 standard; DNA; 362 BP.
AC T07447;
DT 27-APR-1996 (first entry)
DE B. subtilis aprE target DNA.
KW DNA; nucleic acid; analyte; lateral flow detection; PCR;
KW polymerase chain reaction; capture probe; hybridisation; aprE gene;
KW ss.
OS Bacillus subtilis.
PN WO9527081-A1.
PF 12-OCT-1995.
PR 30-MAR-1995; U03773.
PR 31-MAR-1994; US-221769.
PR (DUPO) DU PONT DE NEMOURS & CO E I.
PA Ebersole RC, Fitzpatrick-McElligott S, Hendrickson ER;
PI Majarian WR, Payne MS, Rafalski JA;
DR WPI; 95-358650/46.
PT Detecting the presence of a nucleic acid analyte - by contact with a
PT test strip having immobilised capture moieties.
PS Example 1; Page 43; 82pp; English.
CC A specific segment (T07447) of the B. subtilis aprE gene was amplified
CC by PCR using primers 3 (T07448) and 4 (T07449) in the presence of
CC biotin-14-dATP and digoxigenin-11-dUTP. Detection of the PCR product
CC was performed using a lateral flow nucleic acid detection system in
CC which anti-digoxigenin coupled to alkaline phosphatase was
CC deposited on the 'application zone' of a nitrocellulose membrane,
CC and avidin on the 'capture zone'. Amplified aprE target DNA was
CC applied to the application zone and allowed to wick to the capture
CC zone, where it was detected by colorimetry. In another method,
CC target aprE DNA amplified in the presence of biotin-labeled dNTP
CC was hybridised in solution with aprE DNA amplified in the presence
CC of digoxigenin-labeled dNTP to demonstrate lateral flow detection of a
CC bifunctional nucleic acid hybrid.
SQ Sequence 362 BP; 99 A; 89 C; 82 G; 92 T;

alignment_scores:
Quality: 43.00 Length: 17
Ratio: 2.867 Gaps: 0
Percent Similarity: 88.235 Percent Identity: 52.941

alignment_block:
US-08-653-294-30 x T07447/rev
Align seg 1/1 to reverse of: T07447 from: 1 to: 362

3 LeuAlaThrArgLeuAsnGluArgGluAsnLeuArgThrAlaLeuAr 19
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
111 GTAGCCTTGAGAGTGAAGAGCGGCGCTTTAATTGAGAAATGCCATAAG 62

19 g 19
61 G 61

seq_name: N_Geneseq_36:N80745

seq_documentation_block:
ID N80745 standard; DNA; 1220 BP.
AC N80745;
DT 18-FEB-1991 (first entry)
DE aprA gene encoding subtilisin.

```

```

DT 14-SEP-1990 (first entry)
DE Coding region of the aprA gene encoding subtilisin in Bacillus subtilis
KW Bacillus subtilis strain Q8127 (trpC2 leuA8 sacuH200); subtilisin;
KW thermal stability; pH stability; specific activity;
KW substrate specificity; detergency; ss.
OS Bacillus subtilis strain Q8127 (trpC2 leuA8 sacuH200).
FH Key Location/Qualifiers
FT mat_peptide 1..1143
FT /tag- a
FT WO8808033-A.
FT 20-OCT-1988.
PF 28-MAR-1988; U01038.
PR 10-APR-1988; US-036872.
PA (AMGE-) Amgen Inc.
PI Zurowski MM, Stabinsky Y, Levitt M;
DR WPI; 88-307568/43.
DR P-PSDB; P80744.
PT New subtilisin analogues -
PT have aminoacid(s) present in calcium binding site replaced by
PT negatively charged aminoacid(s)
PS Example 2; Table 1, Pages 22-24; 60pp; English.
CC Genomic DNA was isolated from cells of B. subtilis strain Q8127 (trpC2
CC leuA8 sacuH200). The coding region of the aprA gene was sequenced and
CC the results of the sequence are given in N80745. The specific identity
CC of the initial 5 codons of the leader region is attributable to the
CC report of Stahl, et al., J. Bacteriol., 158, 411-418, (1984) and Wong,
CC et al. P.N.A.S. 81, 1184-1188 (1984). There exist codon sequence
CC differences from Stahl, et al., at amino acid positions 84 and 85.
CC Specifically, Stahl, et al., reports a codon GTC (coding for valine) at
CC amino acid position 84 while the codon GTC (also coding for valine)
CC appears in N80745. Stahl, et al., also reports a codon AGC (coding for
CC serine) at amino acid position 85 as opposed to the codon GGC (coding for
CC alanine) in N80745. The patent concerns a novel subtilisin analogue
CC which has an amino acid sequence of a naturally occurring Bacillus
CC subtilisin which has been modified by having: one or more of the amino
CC acids present in a calcium binding site of the naturally occurring
CC Bacillus subtilisin replaced by a negatively charged amino acid, and
CC one or more of any Asn-Gly sequence of the naturally occurring Bacillus
CC subtilisin deleted or replaced by a different amino acid. Pref. it is
CC an analogue of subtilisin Carlsberg, subtilisin DY, subtilisin BPN', an
CC aprA subtilisin of B. subtilis or subtilisin from B. mesentericus. The
CC subtilisin analogues exhibit improved thermal and pH stability,
CC increased specific activity and broad substrate specificity thereby
CC increasing the detergency of detergent formulations contg. such
CC analogues.
SQ Sequence 1220 BP; 355 A; 281 C; 283 G; 301 T;

```

```

alignment_scores:
Quality: 43.00 Length: 17
Ratio: 2.867 Gaps: 0
Percent Similarity: 88.235 Percent Identity: 52.941

alignment_block:
US-08-653-294-30 x N80745/rev
Align seg 1/1 to reverse of: N80745 from: 1 to: 1220

3 LeuAlaThrArgLeuAsnGluArgGluAsnLeuArgThrAlaLeuAr 19
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
381 GTAGCCTTGAGAGTGAAGAGCGGCGCTTTAATTGAGAAATGCCATAAG 332

19 g 19
331 G 331

seq_name: N_Geneseq_36:Q06587

seq_documentation_block:
ID Q06587 standard; DNA; 1220 BP.
AC Q06587;
DT 18-FEB-1991 (first entry)
DE aprA gene encoding subtilisin.

```

KW Detergents; depilatory tanning; serology; ds.
OS Bacillus subtilis.
FH Key Location/Qualifiers
FT conflict 568..573
FT /tag= a
FT /label= gtagc
FT /note= "Stahl et al. J.Bacteriol.,158,411-418 (1984)"
FT cds 1..1143
FT /tag= b
FT mat_peptide 319..1143
FT /tag= c
PN EP-398539-A.
PD 22-NOV-1990.
PF 01-MAY-1990: 304715.
PR 17-MAY-1989: US-353124.
PA (AMGE-) AMGEN INC.
PI Zukowski MM, Narhi LO, Levitt M;
DR WPI: 90-350298/47.
DR P-PSDB: R07970.
PT Bacillus subtilin analogues - with improved pH thermal and oxidn.
PT stability useful in cleaning compns.
PS Claim 20; Table 1; 39pp; English.
CC Modified analogues of subtilisin are useful in cleaning fabrics, and
CC have an improved resistance to oxidation, heat and pH extremes.
CC Analogues have one or more negative AAs present in the calcium
CC binding site (CBS) and may also be used in manufacture of protein
CC hydrolsates and detection of incomplete Abs in serology.
SQ Sequence 1220 BP; 355 A; 281 C; 283 G; 301 T;

alignment_scores:
Quality: 43.00 Length: 17
Ratio: 2.867 Gaps: 0
Percent Similarity: 88.235 Percent Identity: 52.941

alignment_block:
US-08-653-294-30 x Q06587/rev ...
Align seg 1/1 to reverse of: Q06587 from: 1 to: 1220

3 LeuAlaThrArgLeuAsnGluArgArgGluAsnLeuArgThrAlaLeuAr 19
::: ||| :::::::::::::: ||| :::::::::::::: |||
381 GTAGCCTTGAGAGTGAAGCGCGCTTTATTGAGAAATGCCATAAG 332
19 q 19
331 G 331

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OM of: US-08-653-294-30 to: EST:* out_format : pfs
Date: Feb 8, 2000 5:23 AM

About: Results were produced by the GenCore software, version 4.5,
Copyright (c) 1993-2000 CompuGen Ltd.

Command line parameters:
-MODEL=frame+P2n.model -DEV=xlp
-Q/cgn1_l/USPFO-spool/US08653294/runat_04022000_160700_15770/app_query.fasta.2
-DB=EST -QFWT=fastap -SUFFIX=rst -GAPOP=12.000 -GAPEXT=4.000
-MINWAT=0.100 -LOOPEXT=0.000 -LOOPEXT=0.000 -GAPOP=4.500
-GAPEXT=0.050 -GAPOP=10.000 -GAPEXT=0.500 -GAPOP=6.000
-GAPEXT=7.000 -GAPOP=10.000 -GAPEXT=0.500 -DELOP=6.000
-DELEX=7.000 -START=1 -MATRIX=blomsum62 -TRANS=human40.cdi
-LIST=45 -DOALIGN=200 -THR_SCORE=pct -ALIGN=15 -MODE=LOCAL
-OUTFWT=pfs -NORM=ext -MINLEN=0 -MAXLEN=1000000 -USER=US08653294
-NCPU=6 -ICPU=3 -NO_XLPXY -WAIT -THREADS=1

Search information block:

Query: US-08-653-294-30

Query length: 20

Database: EST*

Database sequences: 4538634

Database length: 1887831982

Search time (sec): 7600.090000

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gb_gss4:AQ720034	+	50.00	142.11	37.75	532	AQ720034 HS_5541_A2_G07_SF6E RP
gb_gss15:AQ625497	+	48.00	136.87	73.89	485	AQ625497 CIBR-EI-2653022.TF CI
gb_est1:P35316	+	47.00	136.69	75.59	360	D35316 CELK019GZF Yuji Kohara u
gb_est1:P35321	+	47.00	136.69	75.59	360	D35321 CELK019GZF Yuji Kohara u
gb_est1:P35579	+	47.00	136.69	75.59	360	D35579 CELK022GZF Yuji Kohara u
gb_est1:P69731	+	47.00	136.69	75.59	360	C69731 C69731 Yuji Kohara unpub
gb_est1:P69775	+	47.00	136.69	75.59	360	C69775 C69775 Yuji Kohara unpub
gb_est1:P69958	+	47.00	136.69	75.59	360	C69958 C69958 Yuji Kohara unpub
gb_est1:P37592	+	47.00	135.65	85.90	399	D37592 CELK004C4F Yuji Kohara u
gb_est31:AI676428	+	47.00	133.52	113.45	647	AI676428 EST247158 Eth1 Bimer1
gb_est28:AI488819	+	47.00	131.01	156.72	499	AI488819 EST247158 tomato ovary
gb_est36:AI186046	-	46.00	133.62	112.02	360	AI186046 AV186046 Yuji Kohara u
gb_est33:AI77709	-	46.00	132.77	124.93	393	AI77709 EST258504 tomato suscep
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gb_est34:AI808160	+	46.00	130.10	176.13	518	AI808160 wif5h09.xl Soares_NFL
gb_gss4:AQ713859	+	46.00	129.00	202.72	580	AQ713859 HS_2129_B1_E05_T7C CIT
gb_est32:AI738072	+	46.00	127.18	256.14	700	AI738072 BS8ML33248N4SK Brugla
gb_est8:C03945	+	45.00	134.82	96.11	232	C03945 C03945 Human heart cDNA
gb_est11:AA263158	+	45.00	132.89	123.06	283	AA263158 PMV0534 KGI-a Lambda Z
gb_est40:AW43668	+	45.00	130.91	158.58	347	AW43668 EST239364 Human pancrea
gb_est6:P82221	+	45.00	130.16	174.65	375	P82221 HUMHBC4626 Normalized r
gb_gss15:AQ640208	+	45.00	129.32	194.56	409	N83040 TGE257595b10.r1 TGRH Tac
gb_gss6:AQ849043	-	45.00	127.61	242.35	488	AQ849043 LMAJFV1.Lm4506.xl Lei
gb_gss3:P22809	+	45.00	127.45	247.30	496	B22809 F22FTR IGF Arabidopsis
gb_gss14:AQ572791	+	45.00	126.81	268.56	530	AQ572791 HS_2096_B1_E05_T7C CIT
gb_est20:AU001511	+	45.00	126.17	291.44	566	AU001511 AU001511 Bombyx mori P
gb_est20:AA881004	+	45.00	126.03	296.57	574	AA881004 vx35b04.r1 Stratagene
gb_est38:AW092336	+	45.00	125.29	326.41	620	AW092336 EST285516 tomato mixed
gb_gss15:AQ655562	+	45.00	125.18	331.00	627	AQ655562 Sheared DNA-9C11.TF SH
gb_est9:AA106132	+	45.00	125.08	334.95	633	AA106132 mm20f05.r1 Stratagene
gb_gss10:AQ254983	+	45.00	124.56	358.14	668	AQ254983 mgxb0007C33r CUGI Rice
gb_gss9:AQ083696	+	45.00	124.36	367.50	682	AQ083696 CpG0581B CpIOWAGDNAL C
gb_est31:AI696864	+	45.00	123.47	412.24	748	AI696864 wc74h11.xl NCI CGAP.Pa
gb_gss3:BI2131	+	45.00	119.85	655.48	1086	BI2131 FL3C15-77 IGF Arabidops
gb_est21:AA980664	-	44.00	136.72	75.32	139	AA980664 ua44b04.r1 Soares mous
gb_est20:AA957217	-	44.00	132.76	125.09	209	AA957217 am06d05.s1 Soares_NFL
gb_est15:AA522865	-	44.00	130.87	159.43	254	AA522865 n17if08.s1 NCI CGAP.PH
gb_est10:AA151891	+	44.00	130.63	160.21	255	AA151891 zo01f06.r1 Stratagene
gb_est33:AI776145	+	44.00	130.85	164.12	260	AI776145 EST257233 tomato suscep
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gb_est42:AV307628 - 44.00 129.00 202.62 308 ! AV307628 AV307628 RIKEN full
gb_est27:AI466429 + 44.00 127.33 251.12 365 ! AI466429 vx35b04.yl Stratage
gb_gss9:AQ168853 - 44.00 126.84 267.44 385 ! AQ168853 HS_3149.AL_D10_MR C

seq_name: gb_est23:AI124815

seq_documentation_block:

LOCUS AI124815 414 bp mRNA EST 11-SEP-1998
DEFINITION am56e06.xl Johnston frontal cortex Homo sapiens cDNA clone
IMAGE:1539586 3' similar to gb:M24038.cds1 HLA CLASS I
HISTOCOMPATIBILITY ANTIGEN, BW-44(B-12) B*4402 (HUMAN); contains
MER22.T3 TAR1 repetitive element ;, mRNA sequence.

ACCESSION AI124815

VERSION AI124815.1 GI:35933329

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 414)

AUTHORS

Hillier, L., Allen, M., Bowles, L., Dubuque, T., Geisel, G., Jost, S.,
Krizman, D., Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M.,
Martin, J., Moore, B., Schellenberg, K., Steptoe, M., Tan, F.,
Theising, B., White, Y., Wyllie, T., Waterston, R. and Wilson, R.
WashU-NCI human EST project

Unpublished (1997)

TITLE

JOURNAL

COMMENT

On Jan 17, 1998 this sequence version replaced gi:1899887.

Contact: Wilson RK

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800

Fax: 314 286 1810

Email: est@watson.wustl.edu

This clone is available royalty-free through LINDL : contact the

IMAGE Consortium (info@image.llnl.gov) for further information.

Seq primer: -40m13 fwd. ET from Amersham.

FEATURES

Location/Qualifiers
1..414
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:1539586"
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/lab_host="SOLR (kanamycin resistant)"
/note="Organ: brain; Vector: Bluescript SK-; Site:1:
ECORI; Stanley Neuropathology Consortium
(www.stanleylab.org) brains S-58, S-65, S-67, S-78.
Random + oligo-dT primed into EORI site of ZAP II Vector.
Mass excised. Avg insert length 1.9kb. Custom library
provided by Dr. Nancy Johnston [(410) 614-3918,
ni@wchlink.welch.jhu.edu].
BASE COUNT 80 a 140 c 136 g 58 t
ORIGIN

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Quality: 51.00 Length: 16
Ratio: 3.923 Gaps: 0
Percent Similarity: 81.250 Percent Identity: 68.750

alignment_block:

US-08-653-294-30 x AI124815

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5 ThrArgLeuAsnGluArgArgGluAsnLeuArgThrAlaLeuArgTyr 20
||||| :
266 ACCAACACACAGACTTACCGAGAGAACCTCGCACCCTCCGCTAC 313

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DEFINITION HS_5541_A2_G07_SP6E_RPCI-11 Human Male BAC Library Homo sapiens
            genomic clone Plate-1117 Col-14 Row-W, genomic survey sequence.
ACCESSION  A0720034
VERSION    A0720034.1 GI:5479703
KEYWORDS   GSS.
SOURCE     human.
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1 (bases 1 to 532)
AUTHORS   Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,
            Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and
            Hood,L.
TITLE     Sequence-tagged connectors: A sequence approach to mapping and
            scanning the human genome
JOURNAL    Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999)
MEDLINE    99380589
COMMENT    On Feb 19, 1999 this sequence version replaced gi:4142976.
            Contact: Mahairas GG, Wallace JC, Hood L
            High throughput Sequencing Center
            University of Washington
            401 Queen Anne Avenue North, Seattle, WA 98109, USA
            Tel: (206) 616-3618
            Fax: (206) 616-3887
            Email: jwallace@u.washington.edu
            Clones are derived from the human BAC library RPCI-11. For BAC
            library availability, please contact Pieter de Jong
            (pieter@dejong.med.buffalo.edu). Clones may be purchased from
            BACPAC Resources (http://bacpac.med.buffalo.edu/ordering_bac.htm)
            or from Resear h Genetics (info@resgen.com). BAC end web Server:
            http://www.htsc.washington.edu
            Plate: 1117 row: M column: 14
            Seq primer: SP6
            Class: BAC ends
            High quality sequence stop: 532.
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                /clone_lib="RPCI-11 Human Male BAC Library"
                /sex="male"
                /note="vector: pBACE3.6; Genomic sequence of BAC ends"
BASE COUNT 145 a 119 c 104 g 158 t 6 others
ORIGIN

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            Ratio: 3.571      Gaps: 0
            Percent Similarity: 87.500      Percent Identity: 62.500

alignment_block:
US-08-653-294-30 x A0720034      ..
Align seg 1/1 to: A0720034      from: 1 to: 532
1 TyArgLeuAlaThrArgLeuAsnGluArgGluAsnLeuArgThr 16
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
433 TATAAAGTGGCTTTTACTCAATGCTAGCGAGAGAGGTTGCATACA 480

seq_name: gb_gss15:A0625497

seq_documentation_block:
LOCUS      A0625497      485 bp      DNA      GSS      16-JUN-1999
DEFINITION CITBI-EI-2653J22.TF CITBI-EI Homo sapiens genomic clone 2653J22,
            genomic survey sequence.
ACCESSION  A0625497
VERSION    A0625497.1 GI:5087889
KEYWORDS   GSS.
SOURCE     human.
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1 (bases 1 to 485)
AUTHORS   Zhao,S., Adams,M.D., Nierman,W., Malek,J., Shizuya,H., Simon,M. and
            Venter,J.C.
TITLE     Use of BAC End Sequences from CalTech Libraries for Sequence-Ready
            Map Building
JOURNAL    Unpublished (1997)
COMMENT    Other_GSSs: CITBI-EI-2653J22.TR
            Contact: Shaying Zhao, William Nierman, Mark Adams
            Department of Eukaryotic Genomics
            The Institute for Genomic Research
            9712 Medical Center Dr., Rockville, MD 20850
            Tel: 301 838 0200
            Fax: 301 838 0208
            Email: hbe@tigr.org
            Clones are available from Research Genetics (info@resgen.com). BAC
            end search page:
            http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
            Seq primer: M13-21
            Class: BAC ends.
FEATURES   Location/Qualifiers
            source
            1..485
                /organism="Homo sapiens"
                /db_xref="taxon:9606"
                /clone="2653J22"
                /clone_lib="CITBI-EI"
                /sex="male"
                /cell_type="sperm"
                /note="vector: pBelOBAC11; Site_1: EcoRI; Site_2: EcoRI;
                Caltech Human BAC Library D"
BASE COUNT 181 a 76 c 80 g 148 t
ORIGIN

alignment_scores:
            Quality: 48.00      Length: 19
            Ratio: 3.200      Gaps: 0
            Percent Similarity: 78.947      Percent Identity: 52.632

alignment_block:
US-08-653-294-30 x A0625497      ..
Align seg 1/1 to: A0625497      from: 1 to: 485
2 ArgLeuAlaThrArgLeuAsnGluArgGluAsnLeuArgThrAlaLe 18
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
108 AGATGCTCAACATTACTAAATGTTAGGGAATGAAATCAAAATCGCACT 157

18 uArgTyr 20
|||||
158 TAGATAT 164

seq_name: gb_est1:D35316

seq_documentation_block:
LOCUS      D35316      360 bp      mRNA      EST      08-AUG-1994
DEFINITION CELK019GZF Yuji Kohara unpublished cDNA Caenorhabditis elegans cdNA
            clone yk19g12 5', mRNA sequence.
ACCESSION  D35316
VERSION    D35316.1 GI:526832
KEYWORDS   EST.
SOURCE     Caenorhabditis elegans.
            Caenorhabditis elegans.
            Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida;
            Rhabditina; Rhabditidae; Pelodierinae; Caenorhabditis.
REFERENCE  1 (bases 1 to 360)
AUTHORS   Kohara,Y., Mitsuki,H., Nishigaki,A., Motohashi,T., Sugimoto,A. and
            Tabara,H.
TITLE     Toward an expression map of the C.elegans genome
JOURNAL    Unpublished (1994)
COMMENT    Contact: Yuji Kohara

```

```

BASE COUNT      116 a      85 c      79 g      80 t
ORIGIN

alignment_scores:
  Quality: 47.00
  Ratio: 3.615
  Percent Similarity: 76.471
  Percent Identity: 64.706

alignment_block:
  US-08-6553-294-30 x D35321 ..

Align seg 1/1 to: D35321 from: 1 to: 360

2 ArgLeuAlaThrArgLeuAsnGluArgGluAsnLeuArgThrAlaLe 18
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
79 AGATCCGGGTTAAGGTGTGACGGAAGAAGATCCCAATCTGAGGATTATCT 128

```

129 G 129

seq_name: gb_est1:D35579

seq_documentation_block:

LOCUS D35579 360 bp mRNA EST 08-AUG-1994

DEFINITION CELR02209F Yuji Kohara unpublished cDNA *Caenorhabditis elegans* CDNA clone YK2299 5', mRNA sequence.

ACCESSION D35579

VERSION D35579.1 GI:527030

KEYWORDS EST.

SOURCE *Caenorhabditis elegans*.

ORGANISM *Caenorhabditis elegans*

Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida; Rhabditina; Rhabditidae; Rhabditinae; Peloderinae; *Caenorhabditis*.

REFERENCE 1 (bases 1 to 360)

AUTHORS Kohara, Y., Mitsuki, H., Nishigaki, A., Motohashi, T., Sugimoto, A. and

```

title: Toward an expression map of the C.elegans genome
journal: Unpublished (1994)
comment: Contact: Yuji Kohara
        Gene Library Lab
        National Institute of Genetics
        Yata 1111, Mishima, Shizuoka 411, Japan
        Tel: 81-559-81-6854
        Fax: 81-559-81-6855
        Email: ykohara@lab.nig.ac.jp.

features:
  source:
    1..360
    /organism="Caenorhabditis elegans"
    /strain="CB1489 him-8(e1489)"
    /db_xref="taxon:6239"
    /clone="yk22q9"
    /clone_lib="Yuji Kohara unpublished cDNA"
    /sex="hermaphrodite, male"
    /tissue_type="whole animal"
    /dev_stage="varied"
    106 a 84 c 87 g 77 t 6 others

alignment_scores:
  quality: 47.00 Length: 17
  ratio: 3.615 Gaps: 0
  percent similarity: 76.471 Percent Identity: 64.706

alignment_block:
  US-08-653-294-30 x D35579 ..

  Align seg 1/1 to: D35579 from: 1 to: 360

```

```

24 AGATCCGCGTTAAGGTTGACGGAAGAAGATCAATCTGAGGATTATTCT 73
18 u 18
|
74 G 74

seq_name: gb_est17:C69731

seq_documentation_block:
LOCUS C69731 360 bp mRNA EST 23-SEP-1997
DEFINITION C69731 Yuji Kohara unpublished cDNA Caenorhabditis elegans cDNA
clone yk368h10 5', mRNA sequence.
ACCESSION C69731
VERSION C69731.1 GI:2431087
KEYWORDS EST.
SOURCE Caenorhabditis elegans.
ORGANISM Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditidae;
Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
REFERENCE 1 (bases 1 to 360)
AUTHORS Kohara,Y., Mochizashi,T., Tabara,H., Watanabe,H., Sugimoto,A.,
Sano,M., Miyata,A. and Nishigaki,A.
TITLE Expression map of the C.elegans genome
JOURNAL Unpublished (1996)
COMMENT Contact: Yuji Kohara
National Institute of Genetics
Yata 1111, Mishima, Shizuoka 411, Japan
Tel: 81-559-81-6854
Fax: 81-559-81-6855
Email: ykohara@lab.nig.ac.jp.

FEATURES
source
1..360
/organism="Caenorhabditis elegans"
/strain="CB1489 him-8(e1489)"
/db_xref="taxon:6239"
/clone_lib="Yuji Kohara unpublished cDNA"
/sex="hermaphrodite, male"
/tissue_type="whole animal"
/dev_stage="varied"
BASE COUNT 109 a 90 c 85 g 76 t
ORIGIN
1
|
18 u 18
74 G 74

alignment_scores:
Quality: 47.00 Length: 17
Ratio: 3.615 Gaps: 0
Percent Similarity: 76.471 Percent Identity: 64.706

alignment_block:
US-08-653-294-30 x C69731 ..
Align seg 1/1 to: C69731 from: 1 to: 360
2 ArgLeuAlaThrArgLeuAsnGluArgGluAsnLeuArgThrAlaLe 18
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
44 AGATCCGCGTTAAGGTTGACGGAAGAAGATCAATCTGAGGATTATTCT 93
18 u 18
|
94 G 94

seq_name: gb_est17:C69775

seq_documentation_block:
LOCUS C69775 360 bp mRNA EST 29-SEP-1997
DEFINITION C69775 Yuji Kohara unpublished cDNA Caenorhabditis elegans cDNA
clone yk366d11 5', mRNA sequence.
ACCESSION C69775
VERSION C69775.1 GI:2440300
KEYWORDS EST.

```

```

SOURCE Caenorhabditis elegans.
ORGANISM Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditidae;
Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
REFERENCE 1 (bases 1 to 360)
AUTHORS Kohara,Y., Mochizashi,T., Tabara,H., Watanabe,H., Sugimoto,A.,
Sano,M., Miyata,A. and Nishigaki,A.
TITLE Expression map of the C.elegans genome
JOURNAL Unpublished (1996)
COMMENT Contact: Yuji Kohara
National Institute of Genetics
Yata 1111, Mishima, Shizuoka 411, Japan
Tel: 81-559-81-6854
Fax: 81-559-81-6855
Email: ykohara@lab.nig.ac.jp.

FEATURES
source
1..360
/organism="Caenorhabditis elegans"
/strain="CB1489 him-8(e1489)"
/db_xref="taxon:6239"
/clone_lib="Yuji Kohara unpublished cDNA"
/sex="hermaphrodite, male"
/tissue_type="whole animal"
/dev_stage="varied"
BASE COUNT 112 a 88 c 85 g 75 t
ORIGIN
1
|
18 u 18
75 G 75

seq_name: gb_est17:C69958

seq_documentation_block:
LOCUS C69958 360 bp mRNA EST 29-SEP-1997
DEFINITION C69958 Yuji Kohara unpublished cDNA Caenorhabditis elegans cDNA
clone yk370d10 5', mRNA sequence.
ACCESSION C69958
VERSION C69958.1 GI:2440483
KEYWORDS EST.
SOURCE Caenorhabditis elegans.
ORGANISM Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditidae;
Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
REFERENCE 1 (bases 1 to 360)
AUTHORS Kohara,Y., Mochizashi,T., Tabara,H., Watanabe,H., Sugimoto,A.,
Sano,M., Miyata,A. and Nishigaki,A.
TITLE Expression map of the C.elegans genome
JOURNAL Unpublished (1996)
COMMENT On May 18, 1995 this sequence version replaced gi:810965.
Contact: Yuji Kohara
National Institute of Genetics
Yata 1111, Mishima, Shizuoka 411, Japan
Tel: 81-559-81-6854
Fax: 81-559-81-6855

```


alignment_scores:

US-08-653-294-30 x AI676428

Align seg 1/1 to: AI676428 from: 1 to: 499

1 TyrArgLeuAlaThrArgLeuAsnGluArgGluAsnLeuArgThr 16
|||||
1 TATCGACTTCCACGATGGGATCCAGGAGGAAGATATGAGGACT 48

seq_name: gb_est28:AI488819

seq_documentation_block: 647 bp mRNA EST 29-JUN-1999
LOCUS AI488819
DEFINITION EST247158 tomato ovary, TAMU Lycopersicon esculentum CDNA clone
CLES1818L, mRNA sequence.
ACCESSION AI488819
VERSION AI488819.1 GI:4384190
KEYWORDS EST.
SOURCE tomato.
ORGANISM Lycopersicon esculentum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons; core
eudicots; Asteridae; euasterids I; Solanales; Solanaceae; Solanum;
Potatoe; Lycopersicon.
REFERENCE 1 (bases 1 to 647)
AUTHORS Alcala,J., Vrebalov,J., White,R., Matern,A.L., Vision,T.,
Holt,I.E., Liang,F., Upton,J., Ronning,C.M., Craven,M.B.,
Fuji,C.Y., Bowman,C.L., Niernan,W., Fraser,C.M., Venter,J.C.,
Martin,G.B., Tanksley,S.D. and Giovannoni,J.
Generation of ESTs from tomato carpel tissue
Unpublished (1999)
On May 18, 1998 this sequence version replaced gi:3138293.
COMMENT
TITLE David Frisch
JOURNAL Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 4366
Fax: 864 656 4293
Email: dfrisch@CLEMSON.EDU.

FEATURES
source
1..647
Location/Qualifiers
/organism="Lycopersicon esculentum"
/cultivar="TA496"
/db_xref="taxon:4081"
/clone="cLED1818L"
/clone_lib="tomato ovary, TAMU"
/tissue_type="carpel"
/dev_stage="5.days pre-anthesis to 5 days post-anthesis"
/lab_host="XL1-Blue MRF"
/note="Vector: pBlueScript SK(-); Site_1: EcoRI; Site_2:
XhoI; cLED - Tomato Carpel EST Library. OligodT-primed and
directionally cloned cDNA in vector Lambda ZAP II with 5'
and 3' ends located at the EcoRI and XhoI sites,
respectively."

BASE COUNT 198 a 116 c 148 g 185 t
ORIGIN

alignment_scores:
Quality: 47.00 Length: 20
Ratio: 3.615 Gaps: 0
Percent Similarity: 65.000 Percent Identity: 55.000

alignment_block:

US-08-653-294-30 x AI488819/rev ..

Align seg 1/1 to reverse of: AI488819 from: 1 to: 647

1 TyrArgLeuAlaThrArgLeuAsnGluArgGluAsnLeuArgThrAl 17
|||||
384 TATGTCTCGCATACGATTCGACAGATTCGGACAAATTCAGGACAAG 335

17 aLeuArgTyr 20
|||||

334 GTTGAGGTAT 325

seq_name: gb_est36:AV186046

seq_documentation_block: 360 bp mRNA EST 22-JUL-1999
LOCUS AV186046
DEFINITION AV186046 Yuji Kohara unpublished cDNA:Strain N2 hermaphrodite
embryo Caenorhabditis elegans cDNA clone yk494e6 5', mRNA sequence.
ACCESSION AV186046
VERSION AV186046.1 GI:5568029
KEYWORDS EST.
SOURCE Caenorhabditis elegans.
ORGANISM Caenorhabditis elegans
Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida;
Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
REFERENCE 1 (bases 1 to 360)
AUTHORS Kohara,Y., Shin-I,T., Thierry-Mieg,J., Thierry-Mieg,D., Mitsuki,H.,
Nishigaki,A., Motohashi,T., Zeng,Q., Watanabe,H., Sugimoto,A.,
Sano,M., Miyata,A., Mitani,Y., Iida,K., Uesugi,H., Sugiyama,Y. and
Namoto,H.
Expressed genes in C.elegans
Unpublished (1999)
On Dec 20, 1995 this sequence version replaced gi:1135120.
COMMENT
Contact: Yuji Kohara
Gene Library Lab
National Institute of Genetics
Yata 1111, Mishima, Shizuoka 411, Japan
Tel: 81-559-81-6854
Fax: 81-559-81-6855
Email: ykohara@lab.nig.ac.jp.
Location/Qualifiers

FEATURES
source
1..360
/organism="Caenorhabditis elegans"
/strain="N2"
/db_xref="taxon:6239"
/clone="yk494e6"
/clone_lib="Yuji Kohara unpublished cDNA:Strain N2
hermaphrodite embryo"
/sex="hermaphrodite"
/dev_stage="embryo"

BASE COUNT 103 a 90 c 109 g 58 t
ORIGIN

alignment_scores:
Quality: 46.00 Length: 19
Ratio: 3.067 Gaps: 0
Percent Similarity: 78.947 Percent Identity: 52.632

alignment_block:

US-08-653-294-30 x AV186046/rev ..

Align seg 1/1 to reverse of: AV186046 from: 1 to: 360

2 ArgLeuAlaThrArgLeuAsnGluArgGluAsnLeuArgThrAlaLe 18
|||||
174 CGTTTGTCTACCGGCTTCGGGAGCGACGACGATCCCGGCTTCGCT 125

18 uArgTyr 20
|||||
124 CCGATT 118

seq_name: gb_est33:AI777709

seq_documentation_block:

LOCUS AI777709 393 bp mRNA EST 29-JUN-1999
DEFINITION EST258504 tomato susceptible, Cornell Lycopersicon esculentum cDNA
clone CLES2H21, mRNA sequence.

ACCESSION AI777709
VERSION AI777709.1 GI:5275666
KEYWORDS EST.
SOURCE tomato.
ORGANISM Lycopersicon esculentum

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: February 8, 2000, 04:05:43 : Search time 133.56 seconds
(without alignments)
3.547 Million cell updates/sec

Title: US-08-653-294-31

Perfect score: 98

Sequence: 1 YRLAIRLNERYLRLAIRLNER 20

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 188963 seqs, 23686106 residues

Total number of hits satisfying chosen parameters: 188963

Minimum DB seq length: 0

Maximum DB seq length: 1000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : A_Geneseq_36.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	98	100.0	20	1 R92911	HLA-B2702 CTL modu
2	98	100.0	20	1 W33779	Immunomodulating d
3	54.5	55.6	20	1 R92907	HLA-B2702 CTL modu
4	54.5	55.6	20	1 R95428	HLA-B2702 84-75-84
5	54.5	55.6	20	1 W33778	Immunomodulating d
6	51.5	52.6	20	1 R92909	HLA-B2702 CTL modu
7	51.5	52.6	20	1 W33792	Peptide B2702.84-7
8	49.5	50.5	20	1 R92908	HLA-B2702 CTL modu
9	49.5	50.5	20	1 R95430	HLA-B2702 84-75T77
10	49.5	50.5	20	1 W33791	Peptide B2702.84-7
11	49.5	50.5	20	1 W47266	Immunomodulatory p
12	46.5	47.4	20	1 R92910	HLA-B2702 CTL modu
13	46.5	47.4	20	1 W33793	Peptide B2702.84-7
14	44.4	44.9	10	1 W47268	Immunomodulatory p
15	44.4	44.9	10	1 W47270	Immunomodulatory p
16	39.3	39.8	10	1 W47272	Immunomodulatory p
17	38.8	38.8	65	1 W20748	H. pylori cytoplas
18	38.8	38.8	272	1 W38650	S. pneumoniae alan
19	38.8	38.8	616	1 R65967	MS2 (male sterilit
20	38.8	38.8	672	1 P71200	Thermotoga beta
21	38.8	38.8	672	1 P60219	Sequence of thermo
22	38.8	38.8	706	1 W31199	Bacillus popilliae
23	38.8	38.8	872	1 W27658	Streptococcus pneu
24	38.8	38.8	3588	1 R34712	Bacillus subtilis
25	37.8	37.8	85	1 W60182	B. thuringiensis t
26	37.8	37.8	485	1 R20796	EHV-4 gc. Nucleic
27	37.8	37.8	597	1 R30168	Novel intestinal o
28	37.8	37.8	599	1 R72319	Laccase Rglac2 pro
29	37.8	37.8	599	1 W60879	Rhizoctonia solani
30	37.8	37.8	599	1 W76311	Rhizoctonia solani
31	36.5	37.2	149	1 W62901	Mutant of the first
32	36.5	37.2	149	1 W51846	Amino acid sequenc
33	36.5	37.2	247	1 W88359	Human lymphocyte a
34	36.5	37.2	338	1 W88361	Human lymphocyte a

35	36.5	37.2	380	1	R13272	Polyhedrin-soluble
36	36.5	37.2	422	1	W83360	Human lymphocyte a
37	36.5	37.2	498	1	R13270	Lymphocyte Activat
38	36.5	37.2	498	1	R87089	Human immunoglobul
39	36.5	37.2	243	1	P70483	Sequence encoded b
40	36.5	36.7	355	1	R77034	Rat brain-enriched
41	36.5	36.7	375	1	R95932	PDGF receptor beta
42	36.5	36.7	375	1	R96129	PR/TS protein, PRL
43	36.5	36.7	404	1	R94463	Creatine amidinohy
44	36.5	36.7	404	1	W11861	Creatine amidinohy
45	36.5	36.7	404	1	W22893	Creatine amidinohy

ALIGNMENTS

RESULT 1

R92911 ID R92911 standard; peptide; 20 AA.
AC R92911:
DE HLA-B2702 CTL modulating peptide (B2702.84-75/84-75).
KW Cytotoxic T lymphocyte; CTL; major histocompatibility complex; MHC;
KW Immunosuppressant; graft versus host disorder; transplantation; therapy;
KW class I MHC; HLA-B2702.
OS Synthetic.
PN W09526979-Al.
PD 12-OCT-1995.
PF 05-APR-1995; U04349.
PR 05-APR-1994; US-222851.
PA (STRD) UNIV LELAND STANFORD JUNIOR.
PI Clayberger C, Krensky AM, Parham P;
DR WPI: 95-359582/46
PT Extension of acceptance period of transplants from MHC unmatched
PT donor hosts - using Class I B75-84 MHC antigen of the recipient
PT host
PS Example 15; Page 36; 80pp; English.
CC R83061-R83085, R83090-R83096 and R92907-R92914 represent fragments of
CC class I major histocompatibility complex (MHC) antigens. This sequence
CC is a dimer of residues 75-84 of the alpha-1 domain of the class I MHC
CC HLA-B2702. These sequences can be used to extend the period of
CC acceptance of a recipient of a transplant from an MHC unmatched donor.
CC The peptides are administered to a patient in conjunction with a
CC subtherapeutic amount of an immunosuppressant. This is administered to
CC the patient for a limited period of time (compared to the lifetime
CC administration for current treatments). The peptides particularly
CC modulate (or inhibit) the activity of the cytotoxic T lymphocytes (CTLs)
CC of the patient.
SQ Sequence 20 AA;

Query Match 100.0%; Score 98; DB 1; Length 20;

Best Local Similarity 100.0%; Pred. No. 3.7e-10;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YRLAIRLNERYLRLAIRLNER 20

DB 1 YRLAIRLNERYLRLAIRLNER 20

RESULT 2

W33779 ID W33779 standard; peptide; 20 AA.

AC W33779:

DE 19-JUN-1998 (first entry)

KW Immunomodulating dimer; immunosuppressant drug; CTL activation;

KW Immunomodulating dimer; immunosuppressant drug; CTL activation;

KW transplantation; autoimmune disease; Class I HLA-B alpha-1 domain;

OS rejection.

OS Synthetic.

OS Homo sapiens.

PN W0744351-Al.

PD 27-NOV-1997.

PF 22-MAY-1997; U08689.
 PR 24-MAY-1996; US-653294.
 PA (STRD) UNIV LELAND STANFORD JUNIOR.
 PI Beulow R, Clayberger C, Krensky AM;
 DR WPI: 98-086530/08.
 PT New immunomodulating dimer peptide(s) - based on a Class I HLA-B
 PT alpha-1 domain, used for preventing rejection of transplants or
 PT treating autoimmune diseases
 PS Claim 16; Page 35; 41pp; English.
 CC This sequence represents a specifically claimed immunomodulating
 CC dimer peptide of the invention. A peptide-type compound or variant is
 CC claimed which has immunomodulating activity, including the N-terminal
 CC acylated and/or C-terminal amidated or esterified forms of up to 60
 CC amino acids, where the peptide-type compound comprises the formula: A-B,
 CC where A, B = (R aa76-77L) (aa79-84) or (aa84-79) (Laa77-76R); aa76 = E or
 CC V; aa77 = D, S or N; aa79 = R or G; aa80 = I or N; aa81, aa84 = a
 CC hydrophobic or small amino acid; aa82 = R or L; aa83 = G or R; and aa
 CC represents amino acid. The sequence in the brackets may optionally be
 CC absent or truncated at any peptide type bond within the brackets. The
 CC compounds comprise amino acid sequences related to a Class I HLA-B
 CC alpha domain (positions 79-84). They can be used to inhibit cytotoxic
 CC T-lymphocytes (CTL) from undesirably attacking cells in a host or in
 CC vitro. They can also be used in combination with antigenic peptides or
 CC proteins of interest to activate CTLs. They can also inhibit the
 CC proliferation of T cells in response to anti-CD3. The peptide can be
 CC used for preventing rejection of transplants or for treating autoimmune
 CC diseases, e.g. diabetes, rheumatoid arthritis and lupus erythematosus.
 CC The products can also be used for detection and diagnosis.
 SQ Sequence 20 AA;

Query Match 100.0%; Score 98; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 3.7e-10; Indels 0; Gaps 0;
 Matches 20; Conservative 0; Mismatches 0;

QY 1 YRLAIRLNERYRLAIRLNER 20
 |||||
 DB 1 YRLAIRLNERYRLAIRLNER 20

RESULT 3

ID R92907 standard; peptide; 20 AA.
 AC R92907: (first entry)
 DT 16-MAY-1996
 DE HLA-B2702 CTL modulating peptide (B2702.84-75/75-84).
 KW Cytotoxic T lymphocyte; CTL; major histocompatibility complex; MHC;
 KW immunosuppressant; graft versus host disorder; transplantation; therapy;
 KW class I MHC; HLA-B2702.
 OS Synthetic.
 PN W09528979-A1.
 PD 12-OCT-1995.
 PF 05-APR-1995; U04349.
 PR 05-APR-1994; US-222851.
 PA (STRD) UNIV LELAND STANFORD JUNIOR.
 PI Clayberger C, Krensky AM, Farham P;
 DR WPI: 95-358582/46.
 PT Extension of acceptance period of transplants from MHC unmatched
 PT donor hosts - using Class I B75-84 MHC antigen of the recipient
 PT host

PS Example 15; Page 36; 80pp; English.
 CC R83061-R83085, R83090-R83096 and R92907-R92914 represent fragments of
 CC class I major histocompatibility complex (MHC) antigens. This sequence
 CC is an inverted dimer of residues 75-84 of the alpha-1 domain of the class
 CC I MHC HLA-B2702. These sequences can be used to extend the period of
 CC acceptance by a recipient of a transplant from an MHC unmatched donor.
 CC The peptides are administered to a patient in conjunction with a
 CC subtherapeutic amount of an immunosuppressant. This is administered to
 CC the patient for a limited period of time (compared to the lifetime
 CC administration for current treatments). The peptides particularly
 CC modulate (or inhibit) the activity of the cytotoxic T lymphocytes (CTLs)
 CC of the patient.
 SQ Sequence 20 AA;

Query Match 55.6%; Score 54.5; DB 1; Length 20;
 Best Local Similarity 68.4%; Pred. No. 0.0047;
 Matches 13; Conservative 2; Mismatches 1; Indels 3; Gaps 1;

QY 1 YRLAIRLNER---YRLAIR 16
 |||||
 DB 1 YRLAIRLNERLRLAIR 19

RESULT 4

ID R95428 standard; peptide; 20 AA.
 AC R95428:
 DT 12-NOV-1996 (first entry)
 DE HLA-B2702 84-75-84 palindromic.
 KW HLA; p74; alpha1-helix; human-leucocyte-associated antigen; inhibitor;
 KW T-cell lysate; membrane protein; mammal; heat shock protein; Hsc70; APC;
 KW B cell; calcium influx; cytotoxic T lymphocyte; CTL; differentiation;
 KW cytolysis; antigen presenting cell.
 OS Synthetic.
 PN W09513288-A1.
 PD 18-MAY-1995.
 PF 10-NOV-1994; U12985.
 PR 10-NOV-1993; US-150493.
 PA (STRD) UNIV LELAND STANFORD JUNIOR.
 PI Clayberger C, Krensky AM;
 DR WPI: 95-194027/25.
 PT Compns. comprising lymphoid surface membrane proteins - which may
 PT inhibit cytolytic activity and differentiation of CTLs.
 PS Example; Page 12; 29pp; English.
 CC R95413, and R95415-R95431 represent palindromes and fragments of
 CC human-leucocyte-associated antigens. This sequence represents the
 CC HLA-B2702 84-75-84 palindromic. These sequences can be used to isolate
 CC the protein p74 from a T-cell lysate. p74 is a T-cell surface membrane
 CC protein associated with T-cell activation in mammalian T-cells, and is
 CC also immunologically cross reactive with the heat shock protein Hsc70.
 CC p74 is found in a limited number of cell types, but is particularly
 CC expressed on B and T cells. p74 can be isolated by lysis of a suitable
 CC cell with an amphoteric detergent, and then passed through an affinity
 CC column containing a covalently bound HLA-B2702 palindromic peptide.
 CC Compositions comprising the extracellular fragment of p74 combined with
 CC HLA-B2702.60-84 (see R95416), induces calcium influx, and inhibits
 CC cytotoxic T lymphocyte (CTL) differentiation or cytolysis. Candidate
 CC compounds can be screened for their effect on the cytolytic activity of
 CC T-cells, by combining them with the extracellular portion of p74 and
 CC determining the amount of binding between the candidate compound and p74.
 CC Modulation of CTL activity can be inhibited in a cellular composition
 CC containing T-cells and antigen presenting cells (APCs), by adding to the
 CC mix the extracellular portion of p74, in an amount sufficient to compete
 CC with p74 for the binding of the p74 ligand.
 SQ Sequence 20 AA;

Query Match 55.6%; Score 54.5; DB 1; Length 20;
 Best Local Similarity 68.4%; Pred. No. 0.0047;
 Matches 13; Conservative 2; Mismatches 1; Indels 3; Gaps 1;

QY 1 YRLAIRLNER---YRLAIR 16
 |||||
 DB 1 YRLAIRLNERLRLAIR 19

RESULT 5

ID W33778 standard; peptide; 20 AA.
 AC W33778:
 DT 19-JUN-1998 (first entry)
 DE Immunomodulating dimer peptide #1.
 KW Immunomodulating dimer; immunosuppressant drug; CTL activation;
 KW transplantation; autoimmune disease; Class I HLA-B alpha-1 domain;
 KW rejection.

OS Synthetic.
 OS Homo sapiens.
 PN W09744351-A1.
 PD 27-NOV-1997.
 PF 22-MAY-1997; U08689.
 PR 24-MAY-1996; US-653294.
 PA (STRD) UNIV LELAND STANFORD JUNIOR.
 PI Beulow R, Clayberger C, Krensky AM;
 DR WPI: 98-086530/08
 PT New immunomodulating dimer peptide(s) - based on a Class I HLA-B
 PT alpha-1 domain, used for preventing rejection of transplants or
 PT treating autoimmune diseases
 PS Claim 16; Page 35; 41pp; English.
 CC This sequence represents a specifically claimed immunomodulating
 CC dimer peptide of the invention. A peptide-type compound or variant is
 CC claimed which has immunomodulating activity, including the N-terminal
 CC acylated and/or C-terminal amidated or esterified forms of up to 60
 CC amino acids, where the peptide-type compound comprises the formula: A-B,
 CC where A, B = (R aa76-77L) (aa79-84) or (aa84-79) (Laa77-76R); aa76 = E or
 CC V; aa77 = D, S or N; aa79 = R or G; aa80 = I or N; aa81, aa84 = a
 CC hydrophobic or small amino acid; aa82 = R or L; aa83 = G or R; and aa
 CC represents amino acid. The sequence in the brackets may optionally be
 CC absent or truncated at any peptide type bond within the brackets. The
 CC compounds comprise amino acid sequences related to a Class I HLA-B
 CC alphas domain (positions 79-84). They can be used to inhibit cytotoxic
 CC T-lymphocytes (CTL) from undesirably attacking cells in a host or in
 CC vitro. They can also be used in combination with antigenic peptides or
 CC proteins of interest to activate CTLs. They can also inhibit the
 CC proliferation of T cells in response to anti-CD3. The peptide can be
 CC used for preventing rejection of transplants or for treating autoimmune
 CC diseases, e.g. diabetes, rheumatoid arthritis and lupus erythematosus.
 CC The products can also be used for detection and diagnosis.
 CC Sequence 20 AA;

Query Match 55.6%; Score 54.5; DB 1; Length 20;
 Best Local Similarity 68.4%; Pred. No. 0.0047;
 Matches 13; Conservative 2; Mismatches 1; Indels 3; Gaps 1;

QY 1 YRLAIRLNER---YRLAIR 16
 DB 1 YRLAIRLNERRENLTALR 19

RESULT 6

R92909
 ID R92909 standard; peptide; 20 AA.
 AC R92909;
 DT 16-MAY-1996 (first entry)
 DE HLA-B2702 CTL modulating peptide (B2702.84-75/75-84(T)).
 KW Cytotoxic T lymphocyte; CTL; major histocompatibility complex; MHC.
 KW Immunosuppressant; graft versus host disorder; transplantation; therapy;
 KW class I MHC; HLA-B2702.
 OS Synthetic.
 PN W09526979-A1.
 PD 12-OCT-1995.
 PF 05-APR-1995; U04349.
 PR 05-APR-1994; US-222851.
 PA (STRD) UNIV LELAND STANFORD JUNIOR.
 PI Clayberger C, Krensky AM, Parham P;
 DR WPI: 95-358582/46.
 PT Extension of acceptance period of transplants from MHC unmatched
 PT donor hosts - using Class I B75-84 MHC antigen of the recipient
 PT host
 PS Example 15; Page 36; 80pp; English.
 CC R83061-R83085, R83090-R83096 and R92907-R92913 represent fragments of
 CC class I major histocompatibility complex (MHC) antigens. This sequence
 CC is an inverted dimer of residues 75-84 of the alpha-1 domain of the class
 CC I MHC HLA-B2702. These sequences can be used to extend the period of
 CC acceptance by a recipient of a transplant from an MHC unmatched donor.
 CC The peptides are administered to a patient in conjunction with a
 CC -subtherapeutic amount of an immunosuppressant. This is administered to
 CC the patient for a limited period of time (compared to the lifetime

CC administration for current treatments). The peptides particularly
 CC modulate (or inhibit) the activity of the cytotoxic T lymphocytes (CTLs)
 CC of the patient.
 SQ Sequence 20 AA;

Query Match 52.6%; Score 51.5; DB 1; Length 20;
 Best Local Similarity 68.4%; Pred. No. 0.015;
 Matches 13; Conservative 1; Mismatches 2; Indels 3; Gaps 1;

QY 1 YRLAIRLNER---YRLAIR 16
 DB 1 YRLAIRLNERRENLTALR 19

RESULT 7

W33792
 ID W33792 standard; peptide; 20 AA.
 AC W33792;
 DT 19-JUN-1998 (first entry)
 DE Peptide B2702.84-75/75-84T tested for immunomodulating activity.
 KW Immunomodulating dimer; immunosuppressant drug; CTL activation;
 KW transplantation; autoimmune disease; Class I HLA-B alpha-1 domain;
 KW rejection.
 OS Synthetic.
 OS Homo sapiens.
 PN W09744351-A1.
 PD 27-NOV-1997.
 PF 22-MAY-1997; U08689.
 PR 24-MAY-1996; US-653294.
 PA (STRD) UNIV LELAND STANFORD JUNIOR.
 PI Beulow R, Clayberger C, Krensky AM;
 DR WPI: 98-086530/08.
 PT New immunomodulating dimer peptide(s) - based on a Class I HLA-B
 PT alpha-1 domain, used for preventing rejection of transplants or
 PT treating autoimmune diseases
 PS Example 1; Page 19; 41pp; English.
 CC Peptides W3784-98 and W3778-9 were assayed for their immunomodulating
 CC activity. A peptide-type compound or variant is claimed which has
 CC immunomodulating activity, including the N-terminal acylated and/or
 CC C-terminal amidated or esterified forms of up to 60 amino acids, where
 CC the peptide-type compound comprises the formula: A-B, where A, B =
 CC (R aa76-77L) (aa79-84) or (aa84-79) (Laa77-76R); aa76 = E or V; aa77 =
 CC D, S or N; aa79 = R or G; aa80 = I or N; aa81, aa84 = a hydrophobic or
 CC small amino acid; aa82 = R or L; aa83 = G or R; and aa represents amino
 CC acid. The sequence in the brackets may optionally be absent or truncated
 CC at any peptide type bond within the brackets. The compounds comprise
 CC amino acid sequences related to a Class I HLA-B alphas domain (positions
 CC 79-84). They can be used to inhibit cytotoxic T-lymphocytes (CTL) from
 CC undesirably attacking cells in a host or in vitro. They can also be
 CC used in combination with antigenic peptides or proteins of interest to
 CC activate CTLs. They can also inhibit the proliferation of T cells in
 CC response to anti-CD3. The peptide can be used for preventing rejection
 CC of transplants or for treating autoimmune diseases, e.g. diabetes,
 CC rheumatoid arthritis and lupus erythematosus. The products can also be
 CC used for detection and diagnosis.
 CC Sequence 20 AA;

Query Match 52.6%; Score 51.5; DB 1; Length 20;
 Best Local Similarity 68.4%; Pred. No. 0.015;
 Matches 13; Conservative 1; Mismatches 2; Indels 3; Gaps 1;

QY 1 YRLAIRLNER---YRLAIR 16
 DB 1 YRLAIRLNERRENLTALR 19

RESULT 8

R92908
 ID R92908 standard; peptide; 20 AA.
 AC R92908;
 DT 16-MAY-1996 (first entry)

DE HLA-B2702 CTL modulating peptide (B2702.84-75(T)/75-84).
 KW Cytotoxic T lymphocyte; CTL; major histocompatibility complex; MHC;
 KW immunosuppressant; graft versus host disorder; transplantation; therapy;
 KW class I MHC; HLA-B2702.
 OS Synthetic.
 PN W09526979-A1.
 PD 12-OCT-1995.
 PF 05-APR-1995; U04349.
 PR 03-APR-1994; US-222851.
 PA (STRD) UNIV LELAND STANFORD JUNIOR.
 PI Clayberger C, Krensky AM, Parham P;
 DR WPI: 95-358582/46.
 PT Extension of acceptance period of transplants from MHC unmatched
 PT donor hosts - using Class I B75-84 MHC antigen of the recipient
 PT host
 PS Example 15; Page 36; 80pp; English.
 CC R03061-R83085, R83090-R83096 and R92907-R92914 represent fragments of
 CC class I major histocompatibility complex (MHC) antigens. This sequence
 CC is an inverted dimer of residues 75-84 of the alpha-1 domain of the class
 CC I MHC HLA-B2702. These sequences can be used to extend the period of
 CC acceptance by a recipient of a transplant from an MHC unmatched donor.
 CC The peptides are administered to a patient in conjunction with a
 CC subtherapeutic amount of an immunosuppressant. This is administered to
 CC the patient for a limited period of time (compared to the lifetime
 CC administration for current treatments). The peptides particularly
 CC modulate (or inhibit) the activity of the cytotoxic T lymphocytes (CTLs)
 CC of the patient.
 SQ Sequence 20 AA;

Query Match 50.5%; Score 49.5; DB 1; Length 20;
 Best Local Similarity 63.2%; Pred. NO. 0.031;
 Matches 12; Conservative 2; Mismatches 2; Indels 3; Gaps 1;

QY 1 YRLAIRLN---ERYRLAIR 16
 ||||| ||||| | :|||
 Db 1 YRLATRLNERENLRALR 19

RESULT 9
 R95430
 ID R95430 standard; peptide: 20 AA.
 AC R95430;
 DT 12-NOV-1996 (first entry)
 DE HLA-B2702 84-75(T)/75-84T palindromic.
 KW HLA; p74; alpha1-helix; human-leucocyte-associated antigen; inhibitor;
 KW T-cell lysate; membrane protein; mammal; heat shock protein; Hsc70; APC;
 KW B cell; calcium influx; cytotoxic T lymphocyte; CTL; differentiation;
 KW cytolysis; antigen presenting cell.
 OS Synthetic.
 PN W09513288-A1.
 PD 18-MAY-1995.
 PF 10-NOV-1994; U12985.
 PR 10-NOV-1993; US-150493.
 PA (STRD) UNIV LELAND STANFORD JUNIOR.
 PI Clayberger C, Krensky AM;
 DR WPI: 95-194027/25.
 PT Compsns. comprising lymphoid surface membrane proteins - which may
 PT inhibit cytolytic activity and differentiation of CTLs.
 PS Example; Page 12; 29pp; English.
 CC human-leucocyte-associated antigens. This sequence represents the
 CC HLA-B2702 84-75(T)/75-84T palindromic. These sequences can be used to
 CC isolate the protein p74 from a T-cell lysate. p74 is a T-cell surface
 CC membrane protein associated with T-cell activation in mammalian T-cells,
 CC and is also immunologically cross reactive with the heat shock protein
 CC Hsc70. p74 is found in a limited number of cell types, but is
 CC particularly expressed on B and T cells. p74 can be isolated by lysis of
 CC a suitable cell with an amphoteric detergent, and then passed through an
 CC affinity column containing a covalently bound HLA-B2702 palindromic
 CC peptide. Compositions comprising the extracellular fragment of p74
 CC combined with HLA-B2702.60-84 (see R95416). Induces calcium influx, and
 CC inhibits cytotoxic T lymphocyte (CTL) differentiation or cytolysis.

CC Candidate compounds can be screened for their effect on the cytolytic
 CC activity of T-cells, by combining them with the extracellular portion of
 CC p74 and determining the amount of binding between the candidate compound
 CC and p74. Modulation of CTL activity can be inhibited in a cellular
 CC composition containing T-cells and antigen presenting cells (APCs), by
 CC adding to the mix the extracellular portion of p74, in an amount
 CC sufficient to compete with p74 for the binding of the p74 ligand.
 SQ Sequence 20 AA;

Query Match 50.5%; Score 49.5; DB 1; Length 20;
 Best Local Similarity 63.2%; Pred. NO. 0.031;
 Matches 12; Conservative 2; Mismatches 2; Indels 3; Gaps 1;

QY 1 YRLAIRLN---ERYRLAIR 16
 ||||| ||||| | :|||
 Db 1 YRLATRLNERENLRALR 19

RESULT 10
 W33791
 ID W33791 standard; peptide: 20 AA.
 AC W33791;
 DT 19-JUN-1998 (first entry)
 DE Peptide B2702.84-75(T)/75-84 tested for immunomodulating activity.
 KW Immunomodulating dimer; immunosuppressant drug; CTL activation;
 KW transplantation; autoimmune disease; Class I HLA-B alpha-1 domain;
 KW rejection.
 OS Synthetic.
 PN Homo sapiens.
 PN W09744351-A1.
 PD 27-NOV-1997.
 PF 22-MAY-1997; U08689.
 PR 24-MAY-1996; US-653294.
 PA (STRD) UNIV LELAND STANFORD JUNIOR.
 PI Beulow R, Clayberger C, Krensky AM;
 DR WPI: 98-086530/08.
 PT New immunomodulating dimer peptide(s) - based on a Class I HLA-B
 PT alpha-1 domain, used for preventing rejection of transplants or
 PT treating autoimmune diseases
 PS Example 1; Page 19; 41pp; English.

CC Peptides W33784-98 and W33778-9 were assayed for their immunomodulating
 CC activity. A peptide-type compound or variant is claimed which has
 CC immunomodulating activity, including the N-terminal acylated and/or
 CC C-terminal amidated or esterified forms of up to 60 amino acids, where
 CC the peptide-type compound comprises the formula: A-B, where A =
 CC (R aa76-77L) (aa79-84) or (aa84-79) (Laa77-76R); aa76 = E or V; aa77 =
 CC D, S or N; aa79 = R or G; aa80 = I or N; aa81, aa84 = a hydrophobic or
 CC small amino acid; aa82 = R or L; aa83 = G or R; and aa represents amino
 CC acid. The sequence in the brackets may optionally be absent or truncated
 CC at any peptide type bond within the brackets. The compounds comprise
 CC amino acid sequences related to a Class I HLA-B alpha1 domain (positions
 CC 79-84). They can be used to inhibit cytotoxic T-lymphocytes (CTL) from
 CC undesirably attacking cells in a host or in vitro. They can also be
 CC used in combination with antigenic peptides or proteins of interest to
 CC activate CTLs. They can also inhibit the proliferation of T cells in
 CC response to anti-CD3. The peptide can be used for preventing rejection
 CC of transplants or for treating autoimmune diseases, e.g. diabetes, be
 CC rheumatoid arthritis and lupus erythematosus. The products can also be
 CC used for detection and diagnosis.
 SQ Sequence 20 AA;

Query Match 50.5%; Score 49.5; DB 1; Length 20;
 Best Local Similarity 63.2%; Pred. NO. 0.031;
 Matches 12; Conservative 2; Mismatches 2; Indels 3; Gaps 1;

QY 1 YRLAIRLN---ERYRLAIR 16
 ||||| ||||| | :|||
 Db 1 YRLATRLNERENLRALR 19

RESULT 11

CC administration for current treatments). The peptides particularly modulate (or inhibit) the activity of the cytotoxic T lymphocytes (CTLs) of the patient.

SQ Sequence 20 AA;

Query Match 47.4%; Score 46.5; DB 1; Length 20;
Best Local Similarity 63.2%; Pred. NO. 0.095;
Matches 12; Conservative 1; Mismatches 3; Indels 3; Gaps 1

QY 1 YRLAIRLNER---YRLAIR 16
||||| ||||| | : : |
DB 1 YRLAIRLNERENRLTALR 19

RESULT 13
W33793
ID W33793 standard; peptide; 20 AA.
AC W33793;
DT 19-JUN-1998 (first entry)
DE Peptide B2702.84-75r/75-84t tested for immunomodulating activity.
KW Immunomodulating dimer; immunosuppressant drug; CTL activation;
KW transplantation; autoimmune disease; Class I HLA-B alpha-1 domain;
KW rejection.
OS Synthetic.
OS Homo sapiens.
PN WO9744351-A1.
PD 27-NOV-1997.
PF 22-MAY-1997; U06689.
PR 24-MAY-1996; US-653294.
PA (STRD) UNIV LELAND STANFORD JUNIOR.
PI Beulow R, Clayberger C, Krensky AM;
PT WPI; 98-086530/08.
PT New immunomodulating dimer peptide(s) - based on a Class I HLA-B alpha-1 domain, used for preventing rejection of transplants or treating autoimmune diseases
PT Example 1; Page 19; 41pp; English.
PS Peptides W33784-98 and W33778-9 were assayed for their immunomodulating activity. A peptide-type compound or variant is claimed which has immunomodulating activity, including the N-terminal acylated and/or C-terminal amidated or esterified forms of up to 60 amino acids, where the peptide-type compound comprises the formula: A-B, where A, B = (R aa76-77L) (aa79-84) or (aa84-79) (Laa77-76R); aa76 = E or V; aa77 = D, S or N; aa79 = R or G; aa80 = I or N; aa81, aa84 = a hydrophobic or small amino acid; aa82 = R or L; aa83 = G or R; and aa represents amino acid. The sequence in the brackets may optionally be absent or truncated at any peptide type bond within the brackets. The compounds comprise amino acid sequences related to a Class I HLA-B alpha-1 domain (positions 79-84). They can be used to inhibit cytotoxic T-lymphocytes (CTL) from undesirably attacking cells in a host or in vitro. They can also be used in combination with antigenic peptides or proteins of interest to activate CTLs. They can also inhibit the proliferation of T cells in response to anti-CD3. The peptide can be used for preventing rejection of transplants or for treating autoimmune diseases, e.g. diabetes, rheumatoid arthritis and lupus erythematosus. The products can also be used for detection and diagnosis.

SQ Sequence 20 AA;

Query Match 47.4%; Score 46.5; DB 1; Length 20;
Best Local Similarity 63.2%; Pred. NO. 0.095;
Matches 12; Conservative 1; Mismatches 3; Indels 3; Gaps 1

QY 1 YRLAIRLNER---YRLAIR 16
||||| ||||| | : : |
DB 1 YRLAIRLNERENRLTALR 19

RESULT 14
W47268
ID W47268 standard; peptide; 10 AA.
AC W47268;
DT 22-MAY-1998 (first entry)

CC administration for current treatments). The peptides particularly modulate (or inhibit) the activity of the cytotoxic T lymphocytes (CTLs) of the patient.

SQ Sequence 20 AA;

Query Match 47.4%; Score 46.5; DB 1; Length 20;
Best Local Similarity 63.2%; Pred. NO. 0.095;
Matches 12; Conservative 1; Mismatches 3; Indels 3; Gaps 1

QY 1 YRLAIRLNER---YRLAIR 16
||||| ||||| | : : |
DB 1 YRLAIRLNERENRLTALR 19

RESULT 14
W47268
ID W47268 standard; peptide; 10 AA.
AC W47268;
DT 22-MAY-1998 (first entry)

DE Immunomodulatory peptide.
 KW Immunomodulator; Class I HLA-B alpha-1 domain; inhibition;
 OS Homo sapiens.
 FT Key Location/Qualifiers
 FT Misc_difference 1. .10 /note= "at least one of the amino acids is the
 FT D-isomer
 PN WO9744052-A1.
 PD 27-NOV-1997.
 PF 23-APR-1997; U06705.
 PR 22-MAY-1996; US-651650.
 PA (STRD) UNIV LELAND STANFORD JUNIOR.
 PI Clayberger C, Krensky AM;
 DR WPI: 98-018220/02.
 PT Novel immunomodulatory peptide-type compound - useful for inhibiting
 PT transplant rejection
 PS Claim 10; Page 36; 41pp; English.
 CC The present sequence is an immunomodulatory peptide, which
 CC comprises a Class I HLA-B alpha-1 domain sequence. It can be used
 CC in a pharmaceutical composition together with a subtherapeutic dose
 CC of an immunosuppressant, to extend the period of acceptance of a
 CC transplant from a major histocompatibility complex (MHC) unmatched
 CC donor, i.e. to inhibit transplant rejection. It can also be used in
 CC the treatment of autoimmune diseases.
 CC Peptides using the D-form amino acids are more effective
 CC immunomodulators than their diastereomers or enantiomers.
 SQ Sequence 10 AA;

Query Match 44.9%; Score 44; DB 1; Length 10;
 Best Local Similarity 90.0%; Pred. No. 0.11;
 Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YRLAIRLNER 10
 DB 1 YRLAIRLNER 10
 ||| |||||

Search completed: February 8, 2000, 04:05:44
 Job time: 9361 sec

Query Match 44.9%; Score 44; DB 1; Length 10;
 Best Local Similarity 90.0%; Pred. No. 0.11;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YRLAIRLNER 10
 DB 1 YRLAIRLNER 10
 ||| |||||

RESULT 15
 W47270
 ID W47270 standard; peptide; 10 AA.
 AC W47270:
 DT 22-MAY-1998 (first entry)
 DE Immunomodulatory peptide.
 KW Immunomodulator; Class I HLA-B alpha-1 domain; inhibition;
 OS Homo sapiens.
 FT Key Location/Qualifiers
 FT Misc_difference 1. .10 /note= "at least one of the amino acids is the
 FT D-isomer
 PN WO9744052-A1.
 PD 27-NOV-1997.
 PF 23-APR-1997; U06705.
 PR 22-MAY-1996; US-651650.
 PA (STRD) UNIV LELAND STANFORD JUNIOR.
 PI Clayberger C, Krensky AM;
 DR WPI: 98-018220/02.
 PT Novel immunomodulatory peptide-type compound - useful for inhibiting
 PT transplant rejection
 PS Claim 10; Page 36; 41pp; English.
 CC The present sequence is an immunomodulatory peptide, which
 CC comprises a Class I HLA-B alpha-1 domain sequence. It can be used
 CC in a pharmaceutical composition together with a subtherapeutic dose
 CC of an immunosuppressant, to extend the period of acceptance of a
 CC transplant from a major histocompatibility complex (MHC) unmatched
 CC donor, i.e. to inhibit transplant rejection. It can also be used in
 CC the treatment of autoimmune diseases.
 CC Peptides using the D-form amino acids are more effective
 CC immunomodulators than their diastereomers or enantiomers.

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OM protein - protein search, using sw model

Run on: February 7, 2000, 18:04:39 ; Search time 111.22 seconds
(without alignments)
8.482 Million cell updates/sec

Title: US-08-653-294-31

Perfect score: 98

Sequence: 1 YRLAIRLNEYRLAIRLNER 20

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 142080 seqs, 47169319 residues

Total number of hits satisfying chosen parameters: 142080

Minimum DB seq length: 0

Maximum DB seq length: 1000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

PIR_62:**

1: pir1:**

2: pir2:**

3: pir3:**

4: pir4:**

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	42.5	43.4	414	2	T15947	hypothetical prote
2	42	42.9	846	2	A30889	integrin beta chai
3	41	41.8	223	2	F70685	probable phosphol
4	41	41.8	253	2	JS0595	rod-core linker po
5	41	41.8	254	2	S23475	rod-core linker po
6	41	41.8	289	2	A69405	hydroxymethylbilan
7	41	41.8	361	1	S34613	5-exo-hydroxycamph
8	41	41.8	413	2	F70211	hypothetical prote
9	41	41.8	584	2	S06696	hypothetical prote
10	40	40.8	192	2	H70375	conserved hypothet
11	40	40.8	388	2	S15593	hypothetical prote
12	40	40.8	473	2	A48949	beta-glucosidase,
13	40	40.8	526	2	S75812	hypothetical prote
14	40	40.8	579	2	A72367	oligopeptide ABC t
15	40	40.8	1502	1	RGB1H1	CyC1/CIP3 transcri
16	40	40.8	2208	2	A37860	calcium channel pr
17	40	40.8	2352	2	T05077	splicing factor-li
18	39.5	40.3	540	2	S76869	hypothetical prote
19	39.5	40.3	1110	1	A70652	probable serine/th
20	39	39.8	144	2	A21047	ribosomal mobile e
21	39	39.8	320	2	F70177	hypothetical prote
22	39	39.8	717	2	S31035	retrovirus-related
23	39	39.8	717	2	S31034	retrovirus-related
24	39	39.8	868	1	S45757	replication licens
25	39	39.8	2077	1	W2BE24	240K tegument prot
26	39	39.8	2078	2	T09326	tegument protein -
27	38.5	39.3	193	2	H72776	hypothetical prote
28	38.5	39.3	349	1	RGEGL	nitrogen regulatio
29	38	38.8	137	2	S43885	3-isopropylmalate
30	38	38.8	279	1	S32869	secretion protein

31	38	38.8	289	2	C72347	motility protein B
32	38	38.8	346	2	G64182	ADP-heptose--LPS h
33	38	38.8	372	2	S46344	env polyprotein -
34	38	38.8	387	2	D89752	two-component sens
35	38	38.8	393	2	JC6176	tumor suppressor p
36	38	38.8	395	2	T01392	leucine-rich repea
37	38	38.8	446	2	S59646	hypothetical prote
38	38	38.8	447	2	A72358	conserved hypothet
39	38	38.8	596	2	T04506	hypothetical prote
40	38	38.8	616	2	S33804	male sterility pro
41	38	38.8	616	2	T08096	male sterility pro
42	38	38.8	672	1	A29836	beta-galactosidase
43	38	38.8	747	1	HIBPC7	internal virion pr
44	38	38.8	1170	2	A72287	hypothetical prote
45	38	38.8	3588	2	I40485	surfactin syntheta

ALIGNMENTS

RESULT 1

T15947

Hypothetical protein F01F1.4 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C>Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999

C:Accession: T15947

R:Miller, N.

submitted to the EMBL Data Library, July 1995

A:Description: The sequence of C. elegans cosmid F01F1.

A:Reference number: Z18435

A:Accession: T15947

A:Status: preliminary; translated from GB/EMBL/DBDJ

A:Molecule type: DNA

A:Residues: 1-414 <MIL>

A:Cross-references: EMBL:U13070; NID:G529697; PID:G529701; PIDN:AAC46638.1; CESP:F01F

A:Experimental source: strain Bristol N2

C:Genetics:

A:Gene: CESP:F01F1.4

A:Introns: 17/3; 51/3; 120/3; 365/2

Query Match

Best Local Similarity 43.4%; Score 42.5; DB 2; Length 414;

Matches 10; Conservative 4; Mismatches 4; Indels 1; Gaps 1;

QY 2 RLAIRLNEYRLAIRLNER 20

DB 62 KAAMELNERYQLDLS-NER 79

RESULT 2

A30889

Integrin beta chain precursor - fruit fly (Drosophila melanogaster)

C:Species: Drosophila melanogaster

C>Date: 01-Dec-1989 #sequence_revision 01-Dec-1989 #text_change 20-Aug-1999

C:Accession: A30889

R:MacKrell, A.J.; Blumberg, B.; Haynes, S.R.; Fessler, J.H.

Proc. Natl. Acad. Sci. U.S.A. 85, 2633-2637, 1988

A:Title: The lethal myospheroid gene of Drosophila encodes a membrane protein homolog

A:Reference number: A30889; MUID:88190122

A:Accession: A30889

A:Molecule type: mRNA

A:Residues: 1-846 <MAC>

A:Cross-references: GB:J03251; NID:G157954; PIDN:AAA28714.1; PID:G157955

C:Genetics:

A:Gene: FlyBase:mys

A:Cross-references: FlyBase:FBgn0004657

C:Superfamily: integrin beta chain; laminin-type EGF-like homology

C:Keywords: cell adhesion; cytoskeleton; transmembrane protein

Query Match

Best Local Similarity 42.9%; Score 42; DB 2; Length 846;

Matches 10; Conservative 4; Mismatches 4; Indels 1; Gaps 1;

Matches 7; Conservative 7; Mismatches 4; Indels 0; Gaps 0;

Qy 2 RLALRLNRYRLAIRLNE 19
 |||:||||:|
 Db 162 RLALRVNEKHNIKISYSQ 179

RESULT 3
 F70685
 probable phosphoglycerate mutase 2 - Mycobacterium tuberculosis (strain H37RV)
 C:Species: Mycobacterium tuberculosis
 C:Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 17-Jul-1998
 C:Accession: F70685
 R:Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
 Nature 393, 537-544, 1998
 A:Authors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
 A:Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome
 A:Reference number: A70500; MUID:98295987
 A:Accession: F70685
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-223 <COL>
 A:Cross-references: GB:881368; GB:AL123456; NID:g3261656; PID:e1299808; PID:g3261659
 A:Experimental source: strain H37RV
 C:Genetics:
 A:Gene: RV2419C

Query Match 41.8%; Score 41; DB 2; Length 223;
 Best Local Similarity 40.0%; Pred. No. 21;
 Matches 8; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

Qy 1 YRLAIRLNERYLRLNER 20
 | | | | | | | | | |
 Db 62 YDTAVKLGERTGLVRVDTR 81

RESULT 4
 JS0595
 rod-core linker polypeptide cpcG4 - Anabaena sp. (strain PCC 7120)
 C:Species: Anabaena sp.
 C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 24-Oct-1997
 C:Accession: JS0595; PS0243
 R:Bryant, D.A.; Stirewalt, V.L.; Glauser, M.; Frank, G.; Sidler, W.; Zuber, H.
 Gene 107, 91-99, 1991
 A:Title: A small multigene family encodes the rod-core linker polypeptides of Anabaena
 A:Reference number: JS0592; MUID:92077441
 A:Accession: JS0595
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-253 <GRY>
 A:Cross-references: GB:M80435; NID:g142097; PID:g142102
 A:Accession: PS0243
 A:Molecule type: protein
 A:Residues: 2-23 <GRV1>
 C:Comment: Linker polypeptides determine the positions of phycobilliproteins within the P
 C:Genetics:
 A:Gene: cpcG4
 F:2-253/Product: rod-core linker polypeptide cpcG4 #status experimental <MAT>

Query Match 41.8%; Score 41; DB 2; Length 253;
 Best Local Similarity 53.8%; Pred. No. 23;
 Matches 7; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 1 YRLAIRLNERYLRL 13
 |||:|:|
 Db 95 YRLVSVNNRYRL 107

RESULT 5
 S23475
 rod-core linker polypeptide cpcG3 - Fischerella sp.
 C:Species: Fischerella sp.
 C:Date: 07-Apr-1994 #sequence_revision 07-Apr-1994 #text_change 07-May-1999
 C:Accession: S23475; S16060
 R:Glauser, M.; Stirewalt, V.L.; Bryant, D.A.; Sidler, W.; Zuber, H.
 Eur. J. Biochem. 205, 927-937, 1992
 A:Title: Structure of the genes encoding the rod-core linker polypeptides of Mastigoc
 A:Reference number: S23472; MUID:92249337
 A:Accession: S23475
 A:Molecule type: DNA
 A:Residues: 1-254 <GLA>
 A:Cross-references: EMBL:X59763; NID:g44397; PID:g44401
 A:Note: the source is designated as Mastigocladus laminosus
 C:Genetics:
 A:Gene: cpcG3

Query Match 41.8%; Score 41; DB 2; Length 254;
 Best Local Similarity 53.8%; Pred. No. 24;
 Matches 7; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 1 YRLAIRLNERYLRL 13
 |||:|:|
 Db 95 YRLVSVNNRYRL 107

RESULT 6
 A69405
 hydroxymethylbilane synthase (EC 4.3.1.18) - Archaeoglobus fulgidus
 N:Alternate names: porphobilinogen deaminase
 C:Species: Archaeoglobus fulgidus
 C:Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 16-Jul-1999
 C:Accession: A69405
 R:Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dod
 :; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E
 Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.
 Nature 390, 364-370, 1997
 A:Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artach, P.; Kaine, B.P.; Sykes,
 Smith, H.O.; Woese, C.R.; Venter, J.C.
 A:Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing arch
 A:Reference number: A69250; MUID:98049343
 A:Accession: A69405
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-289 <XLE>
 A:Cross-references: GB:AE001018; GB:AE000782; NID:g2689341; PID:AA90000.1; PID:g264
 C:Superfamily: hydroxymethylbilane synthase
 C:Keywords: ammonia-lyase; carbon-nitrogen lyase; porphyrin biosynthesis
 F:234/Modified site: dipyrrolylmethanemethyl (Cys) (covalent) #status predicted

Query Match 41.8%; Score 41; DB 2; Length 289;
 Best Local Similarity 50.0%; Pred. No. 27;
 Matches 8; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

Qy 2 RLALRLNRYRLAIRL 17
 :| | | | | | | |
 Db 19 KVAERLKERIEVEIRI 34

RESULT 7
 S34613
 5-exo-hydroxycamphor dehydrogenase (EC 1.1.1.-) - Pseudomonas putida plasmid CAM
 C:Species: Pseudomonas putida
 C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
 C:Accession: S34613; A29844
 R:Aramaki, H.; Koga, H.; Sagara, Y.; Hosoi, M.; Horiuchi, T.
 Biochim. Biophys. Acta 1174, 91-94, 1993
 A:Title: Complete nucleotide sequence of the 5-exo-hydroxycamphor dehydrogenase gene
 A:Reference number: S34613; MUID:93326643
 A:Accession: S34613
 A:Status: not compared with conceptual translation
 A:Molecule type: DNA

A:Residues: 1-361 <ARA>
A:Cross-references: GB:D14680; GB:D14452; GB:D14453; NID:g473744
A:Experimental source: PpG1; ATCC 17453; CAM plasmid
R.Koga, H.; Aramaki, H.; Yamaguchi, E.; Takeuchi, K.; Horiuchi, T.; Gunsalus, I.C.
J. Bacteriol. 166, 1089-1095, 1986
A:Title: camR, a negative regulator locus of the cytochrome P-450-cam hydroxylase operon
A:Reference number: A29844; MUID:86223770
A:Accession: A29844

A:Molecule type: DNA

A:Residues: 1-96, 'RAIAV' <KOG>

A:Cross-references: GB:M13471; NID:gl51117

A:Note: this sequence has been revised in reference S34613

C:Genetics:

A:Gene: camD

A:Genome: plasmid

C:Complex: homodimer

C:Function:

A:Description: catalyzes formation of 2,5-diketocamphane from 5-exo-hydroxycamphor

C:Superfamily: alcohol dehydrogenase; long-chain alcohol dehydrogenase homology

C:Keywords: NAD; oxidoreductase; zinc

F:25-350/Domain: long-chain alcohol dehydrogenase homology <LADH>

F:178-207/Region: beta-alpha-beta NAD nucleotide-binding fold

F:40-62,158/Binding site: zinc, catalytic (Cys, His, Cys) #status predicted

F:98,101,104,112/Binding site: zinc, noncatalytic (Cys) #status predicted

Query Match 41.8%; Score 41; DB 1; Length 361;

Best Local Similarity 47.4%; Pred. No. 34;

Matches 9; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 2 RLAIRLNRYRLAIRNER 20

DB 316 QLAARLQDRIPLADLTQR 334

||| ||| ||| ||| |||

RESULT 8

H70211

hypothetical protein BBA38 - Lyme disease spirochete plasmid A/lp54

C:Species: Borrelia burgdorferi (Lyme disease spirochete)

C>Date: 13-Feb-1998 #sequence_revision 13-Feb-1998 #text_change 05-Jun-1998

C:Accession: F70211

R:Fraser, C.M.; Casjens, S.; Huang, W.M.; Sutton, G.G.; Clayton, R.; Lathigra, R.; White

son, D.; Peterson, J.; Kervage, A.R.; Quackenbush, J.; Salzberg, S.; Hanson, M.; Vugt,

Bowman, C.; Garland, S.; Fujii, C.; Cotton, M.D.; Horst, K.; Roberts, K.; Hatch, B.

Nature 350, 580-586, 1997

A:Authors: Smith, H.O.; Venter, J.C.

A:Title: Genomic sequence of a Lyme disease spirochete, Borrelia burgdorferi.

A:Reference number: A70100; MUID:98065943

A:Accession: F70211

A>Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-413 <KLE>

A:Cross-references: GB:AE000790; NID:g2690224; PID:g2690299; TIGR:BBA38

A:Experimental source: strain B31

C:Genetics:

A:Genome: plasmid

Query Match

Best Local Similarity 41.8%; Score 41; DB 2; Length 413;

Matches 7; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 5 IRLNRYRLAIRNE 19

DB 351 LKLNRYRLNMFNE 365

||| ||| ||| |||

RESULT 9

S06696

hypothetical protein 1 - Zymomonas mobilis plasmid 2M2

C:Species: Zymomonas mobilis

C>Date: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 09-Sep-1997

C:Accession: S06696

R: Misawa, N.; Nakamura, K.
submitted to the EMBL Data Library, February 1989
A:Reference number: S06695
A:Accession: S06696
A:Molecule type: DNA
A:Residues: 1-584 <MIS>
A:Cross-references: EMBL:X14438; NID:g48656; PID:g48657
C:Genetics:
A:Genome: plasmid

Query Match 41.8%; Score 41; DB 2; Length 584;

Best Local Similarity 61.5%; Pred. No. 56;

Matches 8; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 7 LNERVRLAIRNE 19

DB 355 LNDLYRSKIRINE 367

||| ||| ||| |||

RESULT 10

H70375

conserved hypothetical protein aq_880 - Aquifex aeolicus

C:Species: Aquifex aeolicus

C>Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change 08-May-1998

C:Accession: H70375

R:Decker, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.;

V. Nature 392, 353-358, 1998

A:Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.

A:Reference number: A70300; MUID:98196666

A:Accession: H70375

A>Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-192 <AQF>

A:Cross-references: GB:AE000712; NID:g2983411; PID:g2983420; GB:AE000657

A:Experimental source: strain VF5

C:Genetics:

A:Gene: aq_880

Query Match

Best Local Similarity 40.8%; Score 40; DB 2; Length 192;

Matches 8; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 2 RLAIRLNRYRLAIR 16

DB 119 KLIALRLRYREALR 133

||| ||| ||| |||

RESULT 11

S15593

hypothetical protein (insertion sequence ISH27-3) - Halobacterium halobium

C:Species: Halobacterium halobium

C>Date: 19-Mar-1997 #sequence_revision 25-Apr-1997 #text_change 30-Jun-1998

C:Accession: S15593

R:Pfeiffer, F.; Blaseio, U.

Nucleic Acids Res. 18, 6921-6925, 1990

A:Title: Transposition burst of the ISH27 insertion element family in Halobacterium h

A:Reference number: S15591; MUID:91088266

A:Accession: S15593

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-388 <PFE>

A:Cross-references: EMBL:X54434

A:Note: the authors translated the initiation codon GTG for residue 1 as Val

C:Genetics:

A:Mobile element: insertion sequence ISH27-3

A:Start codon: GTG

Query Match

Best Local Similarity 40.8%; Score 40; DB 2; Length 388;

Matches 7; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 8 NERRRLAIR 16

Db 151 NKRYRLAVR 159

RESULT 12

A48949

beta-glucosidase, BglB - Microbispora bispora

C:Species: Microbispora bispora

C:Date: 19-Dec-1993 #sequence_revision 25-Apr-1997 #text_change 22-Jun-1999

C:Accession: A48949

R:Wright, R.M.; Yablonsky, M.D.; Shalita, Z.P.; Goyal, A.K.; Eveleigh, D.E.

Appl. Environ. Microbiol. 58, 3455-3465, 1992

A:Title: Cloning, characterization, and nucleotide sequence of a gene encoding Microbispora

A:Reference number: A48949; MUID:93128922

A:Contents: NRRL 15568

A:Accession: A48949

A>Status: preliminary

A:Molecule type: nucleic acid

A:Residues: 1-473 <WRI>

A:Cross-references: GB:M97265; NID:gl149827; PIDN:AAA25311.1; PID:gl149828

A:Note: sequence extracted from NCBI backbone (NCBIN:122282, NCBIP:122284)

C:Superfamily: Agrobacterium beta-glucosidase

Query Match 40.8%; Score 40; DB 2; Length 473;

Best Local Similarity 52.4%; Pred. No. 64;

Matches 11; Conservative 2; Mismatches 6; Indels 2; Gaps 1;

Qy 1 YRLAI--RLNERYRLAIRLNE 19

Db 176 YALAVHRLGDRVRCWITLNE 196

RESULT 13

S75812

hypothetical protein slr1270 - Synechocystis sp. (strain PCC 6803)

C:Species: Synechocystis sp.

A:Variety: PCC 6803

C:Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 21-Aug-1998

C:Accession: S75812

R:Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.;

O. K.; Okumura, S.; Shingo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda

DNA Res. 3, 109-136, 1996

A:Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis

S.

A:Reference number: S74322; MUID:97061201

A:Accession: S75812

A>Status: nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-526 <KAN>

A:Cross-references: EMBL:D90913; GB:AB001339; NID:gl653348; PID:d1019004; PID:gl653357

A:Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996

Query Match 40.8%; Score 40; DB 2; Length 526;

Best Local Similarity 52.6%; Pred. No. 72;

Matches 10; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

Qy 2 RLAIRLNERYRLAIRLNER 20

Db 98 RQAITLDAIDLALRNNEQ 116

RESULT 14

A72367

oligopeptide ABC transporter, periplasmic oligopeptide-binding protein - Thermotoga maritima

C:Species: Thermotoga maritima

C:Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 11-Jun-1999

C:Accession: A72367

R:Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hickey

Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, C.M.

Nature 399, 323-329, 1999

A:Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome

A:Reference number: A72200; MUID:99287316

A:Accession: A72367

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-579 <ARN>

A:Cross-references: GB:AE001728; GB:AE000512; NID:94981027; PID:94981044; TIGR:TM0531

A:Experimental source: strain MS98

C:Genetics:

A:Gene: TM0531

Query Match 40.8%; Score 40; DB 2; Length 579;

Best Local Similarity 50.0%; Pred. No. 79;

Matches 8; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

Qy 1 YRLAIRLNERYLRLAIR 16

Db 158 YTVKTLKETRYLRLAVR 173

RESULT 15

RGBYH1

CYC1/CYP3 transcription activator - yeast (Saccharomyces cerevisiae)

N:Alternate names: protein L9672.1; protein YLR255w; regulatory protein CYP1; regulat

C:Species: Saccharomyces cerevisiae

C:Date: 30-Sep-1991 #sequence_revision 23-Feb-1996 #text_change 16-Jul-1999

C:Accession: S59400; A31312; S15447; S05804; S15446

R:Johnson, D.

submitted to the EMBL Data Library, February 1995

A:Description: The sequence of S. cerevisiae cosmid 9672.

A:Reference number: S59386

A:Accession: S59400

A:Molecule type: DNA

A:Residues: 1-1502 <JOH>

A:Cross-references: EMBL:U20865; NID:g662330; PIDN:AAB67387.1; PID:g662331; MIPS:YLR2

A:Experimental source: strain S288C (AB972)

R:Preifer, K.; Kim, K.S.; Kogan, S.; Guarente, L.

Cell 56, 291-301, 1989

A:Title: Functional dissection and sequence of yeast HAP1 activator.

A:Reference number: A31312; MUID:89106221

A:Accession: A31312

A:Molecule type: DNA

A:Residues: 1-144, 'I', 146-322, 'R', 324-454, 'N', 456-507, 'M', 509-586, 'K', 588-882, 'N', 884

A:Cross-references: EMBL:J03152; NID:gl17645; PIDN:AAA34662.1; PID:gl17646

R:Creusot, F.; Verdier, J.; Gaisne, M.; Slonimski, P.P.

J. Mol. Biol. 204, 263-276, 1988

A:Title: CYPI (HAP1) regulator of oxygen-dependent gene expression in yeast. I. Overa

A:Reference number: S15447; MUID:89125585

A:Accession: S15447

A:Molecule type: DNA

A:Residues: 1-62, 'R', 64-1305, 'Y', 1306-1470, 'LVDFYRADFPPIWE' <CREI>

A:Cross-references: EMBL:X13793

A:Note: the sequence is from mutant CYP1-18

C:Genetics:

A:Gene: SGD:HAP1; CYP1

A:Cross-references: SGD:S0004246; MIPS:YLR256w

A:Map position: 12R

C:Superfamily: regulatory protein HAP1; GAL4 zinc binuclear cluster homology

C:Keywords: DNA binding; heme binding; transcription regulation; zinc finger

F:1-148/Domain: DNA binding #status predicted <DNA>

F:59-98/Domain: GAL4 zinc binuclear cluster homology <GAL4>

F:64-84/Region: zinc finger CCCC motif

F:177-189/Region: glutamine-rich

F:245-445/Domain: heme binding #status predicted <HEM>

F:299-304, 323-328, 347-352, 373-378, 389-394, 415-420/Region: 6-residue repeats

F:1308-1481/Domain: activation element #status predicted <ACT>

F:1388-1481/Region: acidic

Query Match 40.8%; Score 40; DB 1; Length 1502;
Best Local Similarity 38.9%; Pred. No. 2.1e+02;
Matches 7; Conservative 7; Mismatches 4; Indels 0; Gaps 0;

Qy 2 RLAIRLNERYRLAIRLNE 19
:| :|:::| |:::
Db 1124 KLTQLSKKRYNVAIRMNK 1141

Search completed: February 7, 2000, 18:04:40
Job time: 22206 sec

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: February 8, 2000, 01:26:00 ; Search time 68.63 seconds
(without alignments)
8.703 Million cell updates/sec

Title: US-08-653-294-31

Perfect score: 98

Sequence: 1 YRLAIRLNERYLRLAIRLNER 20

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 82229 seqs, 29864866 residues

Total number of hits satisfying chosen parameters: 82229

Minimum DB seq length: 0

Maximum DB seq length: 1000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : SwissProt_38:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	42	42.9	846	1	ITBX_DROME
2	41	41.8	252	1	P1584 drosophila
3	41	41.8	253	1	P29989 anabaena sp
4	41	41.8	289	1	P29733 mastigoclad
5	41	41.8	253	1	O29026 archaeoglob
6	41	41.8	361	1	P09347 pseudomonas
7	41	41.8	584	1	P15255 zymomonas m
8	40	40.8	323	1	P51947 xenopus lae
9	40	40.8	473	1	P38645 microbispor
10	39	39.8	312	1	P12351 saccharomyc
11	39	39.8	381	1	O31352 bacillus ce
12	39	39.8	868	1	O29537 canis fami
13	39	39.8	2077	1	P39469 saccharomyc
14	39	39.8	2077	1	P30002 herpes simp
15	38.5	39.3	349	1	P52340 herpes simp
16	38	38.8	137	1	P06712 escherichia
17	38	38.8	279	1	P50181 neisseria l
18	38	38.8	346	1	P31712 erwinia car
19	38	38.8	373	1	P45042 haemophilus
20	38	38.8	387	1	P79734 brachydanio
21	38	38.8	393	1	O09185 cricetus
22	38	38.8	446	1	O09718 schistosacch
23	38	38.8	616	1	O08891 arabidopsis
24	38	38.8	672	1	P19668 bacillus st
25	38	38.8	747	1	P03725 bacterioph
26	38	38.8	3587	1	P27206 bacillus su
27	37.5	38.3	342	1	P41788 salmonella
28	37	37.8	132	1	P03563 tomato gold
29	37	37.8	134	1	P29049 squash leaf
30	37	37.8	172	1	O02886 bacillus su
31	37	37.8	179	1	P54390 bacillus su
32	37	37.8	187	1	P50064 mycobacteri
33	37	37.8	189	1	P20464 leptospira
34	37	37.8	232	1	O55309 synechococc

35	37	37.8	287	1	Y030_HAEN	Q57092 haemophilus
36	37	37.8	327	1	EBGR_ECOLI	P06846 escherichia
37	37	37.8	396	1	P53_MESAU	Q00366 mesocricetu
38	37	37.8	424	1	PQ05_CAEEL	Q09535 caenorhabdi
39	37	37.8	445	1	PHR_MEITH	P12769 methanobact
40	37	37.8	485	1	VGLC_HSV4	P22596 equine herp
41	37	37.8	534	1	CN9A_MOUSE	O70628 mus musculu
42	37	37.8	580	1	GPC3_HUMAN	P51654 homo sapien
43	37	37.8	593	1	CN9A_HUMAN	O76083 homo sapien
44	37	37.8	597	1	GPC3_RAT	P13265 rattus norv
45	37	37.8	599	1	LAC2_THACU	Q02075 thanatephor

ALIGNMENTS

RESULT	1
ITBX_DROME	
ID	ITBX_DROME
AC	P11584;
DT	01-OCT-1989 (Rel. 12, Created)
DT	01-OCT-1989 (Rel. 12, Last sequence update)
DT	15-JUL-1998 (Rel. 36, Last annotation update)
DE	INTEGRIN BETA-SUBUNIT MYOSPHEROID PRECURSOR.
GN	L(1)MYS.
OS	Drosophila melanogaster (Fruit fly).
OC	Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC	Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC	Ephyroidea; Drosophilidae; Drosophila.
[1]	
RN	SEQUENCE FROM N.A.
RP	MEDLINE: 88190122.
RA	MACKRELL A.J., BLUMBERG B., HAYNES S.R., FESSLER J.H.;
RT	"The lethal myospheroid gene of Drosophila encodes a membrane protein
RT	homologous to vertebrate integrin beta subunits.";
RL	Proc. Natl. Acad. Sci. U.S.A. 85:2633-2637(1988).
[2]	
RN	CHARACTERIZATION.
RP	MEDLINE: 94163982.
RA	GRINBLAT Y., YEE G., HYNES R.O., KAFATOS F.C.;
RT	"Functions of the cytoplasmic domain of the beta PS integrin subunit
RT	during Drosophila development.";
RL	Development 120:91-102(1994).
CC	-1- FUNCTION: NOT KNOWN. PROBABLY PLAYS A ROLE IN CELL ADHESION.
CC	-1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN
CC	-1- SIMILARITY: BELONGS TO THE INTEGRIN BETA CHAIN FAMILY.
CC	
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CC	entities requires a license agreement (see http://www.isb-sib.ch/announce/
CC	or send an email to license@isb-sib.ch).
CC	
DR	EMBL: J03251; AAA28714.1; .
DR	PIR: A30889; A30889.
DR	FLYBASE: FBgn004657; mys.
DR	PROSITE: PS00243; INTEGRIN_BETA; 3.
DR	PROSITE: PS00022; EGF_1; UNKNOWN_2.
DR	PROSITE: PS01186; EGF_2; UNKNOWN_1.
DR	PFAM: PF00362; integrin_B; 1
KW	Integrin; Cell adhesion; Transmembrane; Glycoprotein; Repeat;
KW	Extracellular matrix; Cytoskeleton; Signal.
FT	SIGNAL 1 23 POTENTIAL.
FT	CHAIN 24 846 INTEGRIN BETA-SUBUNIT MYOSPHEROID.
FT	DOMAIN 24 776 EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM 777 799 POTENTIAL.
FT	DOMAIN 800 846 CYTOPLASMIC (POTENTIAL).
FT	DOMAIN 115 143 SER-RICH.
FT	DOMAIN 507 687 CYSTEINE-RICH REPEATS.
FT	REPEAT 507 560 I.
FT	REPEAT 561 605 II.

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FT REPEAT      506   546
FT REPEAT      547   587
FT CARBOHYD    72    72 POTENTIAL.
FT CARBOHYD    266   266 POTENTIAL.
FT CARBOHYD    277   277 POTENTIAL.
FT CARBOHYD    403   403 POTENTIAL.
FT CARBOHYD    428   428 POTENTIAL.
FT CARBOHYD    557   557 POTENTIAL.
FT CARBOHYD    603   603 POTENTIAL.
FT CARBOHYD    644   644 POTENTIAL.
FT CARBOHYD    718   718 POTENTIAL.
SQ SEQUENCE    846 AA; 92687 MW; 9906C2F9 CRC32;

Query Match          42.9%; Score 42; DB 1; Length 846;
Best Local Similarity 38.9%; Pred. No. 27;
Matches 7; Conservative 7; Mismatches 4; Indels 0; Gaps 0;

QY      2 RLAIRLNRYRLAIRLNE 19
        |||.:||.:|.:.:.
DB      162 RLALRVNEKHNIKISYSQ 179

RESULT 2
PYG4_ANASP
ID PYG4 ANASP STANDARD; PRT; 252 AA.
AC P29589;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 01-FEB-1994 (Rel. 28, Last annotation update)
DE PHYCOBILISOME ROD-CORE LINKER POLYPEPTIDE CPCG4 (L-RC 29.2).
DE CPCG4.
GN Anabaena sp. (strain PCC 7120).
OC Bacacteria; Cyanobacteria; Nostocales; Nostocaceae; Anabaena.
[1]
SEQUENCE FROM N.A., AND SEQUENCE OF 1-22.
MEDLINE; 92077441.
RA BRYANT D.A., STIREWALT V.L., GLAUSER M., FRANK G., SIDLER W.,
RA ZUBER H.;
RT "A small multigene family encodes the rod-core linker polypeptides of
RT Anabaena sp. PC7120 phycobilisomes.";
RL Gene 107:91-99(1991).
CC -!- FUNCTION: ROD-CORE LINKER PROTEIN REQUIRED FOR ATTACHMENT OF
CC PHYCYANIN TO ALLOPHYCOCYANIN IN CORES OF PHYCOBILISOMES.
CC -!- FUNCTION: LINKER POLYPEPTIDES DETERMINE THE STATE OF AGGREGATION
CC AND THE LOCATION OF THE DISC-SHAPED PHYCOBILIPROTEIN UNITS WITHIN
CC THE PHYCOBILISOME AND MODULATE THEIR SPECTROSCOPIC PROPERTIES IN
CC ORDER TO MEDIANE A DIRECTED AND OPTIMAL ENERGY TRANSFER.
CC -!- SUBUNIT: THE PHYCOBILISOME IS A HEMIDISCoidal STRUCTURE THAT IS
CC COMPOSED OF TWO DISTINCT SUBSTRUCTURES: A CORE COMPLEX (THAT
CC CONTAINS PHYCOBILIPROTEINS) AND A NUMBER OF RODS RADIATING FROM
CC THE CORE.
CC -!- SIMILARITY: TO OTHER PHYCOBILISOME LINKER PROTEINS.
-----
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-----
CC EMBL; M80435; AAA22039.1; -.
DR PIR; J50595; JS0595.
DR PFAM; PF00427; PBS_linker_poly; 1.
DR PHYCOBILISOME; Photosynthesis; Multigene family.
FT INIT MET 0
SQ SEQUENCE 252 AA; 29191 MW; 0C1A6468 CRC32;

Query Match          41.8%; Score 41; DB 1; Length 252;
Best Local Similarity 53.8%; Pred. No. 10;
Matches 7; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

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DR	EMBL:	D14580;	BAA03511.1;	-.	
DR	EMBL:	M13471;	AA025762.1;	ALT_SEQ.	
DR	PIR:	A29844;	A29844.		
DR	HSP:	P07846;	1SDG.		
DR	PROSITE:	PS00059;	ADH_ZINC;	1.	
DR	PFAM:	PF00107;	adh_zinc;	1.	
KW	Oxidoreductase:	Zinc;	NAD.		
FT	METAL	40	40	ZINC	(CATALYTIC) (BY SIMILARITY).
FT	METAL	52	52	ZINC	(CATALYTIC) (BY SIMILARITY).
FT	METAL	98	98	ZINC	(SECOND ATOM) (BY SIMILARITY).
FT	METAL	101	101	ZINC	(SECOND ATOM) (BY SIMILARITY).
FT	METAL	104	104	ZINC	(SECOND ATOM) (BY SIMILARITY).
FT	METAL	170	170	ZINC	(CATALYTIC) (BY SIMILARITY).
SO	SEQUENCE	361	AA:	38460	MW: E46D28F7 CRC32:

```

Query Match      41.8%; Score 41; DB 1; Length 361;
Best Local Similarity 47.4%; Pred. NO. 15;
Matches 9; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY      2 RLAIRLNERYRLAIRLNER 20
      : || || || || || : |
Db      316 OLAARLODRYPLADLITOR 334

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RESULT      5
65KD_ZYMMO
ID          65KD_ZYMMO      STANDARD;      PRT;      584 AA.
AC          P1255;
DT          01-APR-1990 (Rel. 14, Created)
DT          01-APR-1990 (Rel. 14, Last sequence update)
DT          15-DEC-1998 (Rel. 37, Last annotation update)
DE          65 KD PROTEIN (ORF 1).
OS          Zymomonas mobilis.
OG          Plasmid pZM2.
OC          Bacteria; Proteobacteria; alpha subdivision; zymomonas group;
OC          Zymomonas.
RN          [1]
RP          SEQUENCE FROM N.A.
RC          STRAIN-ATCC 10988 / ZM1;
RA          MISAWA N., NAKAMURA K.;
RT          "The nucleotide sequence of the 2.7 kilobase pair plasmid of Zymomonas

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ID AC CYPI_YEAST STANDARD; PRT; 1483 AA.
 DT P12351;
 DT 01-OCT-1989 (Rel. 12, Created)
 DT 01-OCT-1989 (Rel. 12, Last sequence update)
 DT 15-DEC-1999 (Rel. 39, Last annotation update)
 DE DE CYPI ACTIVATORY PROTEIN.
 GN CYPI OR HAP1 OR YLR256W.
 OS Saccharomyces cerevisiae (Baker's yeast).
 OC Eukaryota; Fungi; Ascomycota; Hemiascomycetes; Saccharomycetales;
 OC Saccharomycetaceae; Saccharomycetes.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 89125585.
 RA CREUSOT F., VERDIERE J., GAISNE M., SLONIMSKI P.P.;
 RA "CYPI (HAP1) regulator of oxygen-dependent gene expression in yeast.
 RT I. Overall organization of the protein sequence displays several
 RT novel structural domains.;
 RL J. Mol. Biol. 204:263-276(1988).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 89106221.
 RA PEIFFER K., KIM K.-S., KOGAN S., GUARENTE L.;
 RA "Functional dissection and sequence of yeast HAP1 activator.";
 RL Cell 56:291-301(1989).
 RN [3]
 RP MUTANT CYPI-18.
 RX MEDLINE; 89125586.
 RA VERDIERE J., GAISNE M., GUIARD B., DEFRANCOUX N., SLONIMSKI P.P.;
 RA "CYPI (HAP1) regulator of oxygen-dependent gene expression in yeast.
 RT II. Missense mutation suggests alternative Zn fingers as
 RT discriminating agents of gene control.";
 RL J. Mol. Biol. 204:277-282(1988).
 RN [4]
 RP DNA-BINDING.
 RX MEDLINE; 97042358.
 RA ZHANG L., GUARENTE L.;
 RA "The C6 zinc cluster dictates asymmetric binding by HAP1.";
 RL EMBO J. 15:4676-4681(1996).
 RN [5]
 RP STRUCTURE BY NMR OF 60-100.
 RX MEDLINE; 96275662.
 RA TIMMERMAN J., VUIDEPOT A.-L., BONTEMS F., LALLEMAND J.-Y., GERVAIS M.,
 RA SHECHTER E., GUIARD B.;
 RT "H, 15N resonance assignment and three-dimensional structure of CYPI
 RT (HAP1) DNA-binding domain.";
 RL J. Mol. Biol. 259:792-804(1996).
 CC -!- FUNCTION: REGULATION OF OXYGEN DEPENDENT GENE EXPRESSION. IT
 CC MODULATES THE EXPRESSION OF ISO-1 AND ISO-2 CYTOCHROME C. BINDS
 CC TO THE SEQUENCE 5'-CGGNNNTNCGG-3'.
 CC -!- SUBUNIT: BINDS DNA AS A HOMODIMER.
 CC -!- SUBCELLULAR LOCATION: NUCLEAR.
 CC -!- MISCELLANEOUS: CYPI-18 MUTANT ACTIVATES THE EXPRESSION OF CYP3
 CC (ISO-2) WHILE REDUCING THAT OF CYC1 (ISO-1).
 CC -!- MISCELLANEOUS: (SEE FT TABLE) MEDIATES HEME INDUCTION BY MASKING
 CC THE DNA-BINDING DOMAIN IN THE ABSENCE OF INDUCER.
 CC -!- SIMILARITY: CONTAINS A ZN(2)-CYS(6), FUNGAL-TYPE BINUCLEAR
 CC CLUSTER DOMAIN.
 CC -!- SIMILARITY: CONTAINS 7 HEME REGULATORY MOTIFS (HRM).
 CC
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 CC
 CC EMBL; X13793; CAA32032.1; -;
 CC EMBL; J03152; AAA34662.1; -;
 CC PIR; S05804; RBYH1.
 CC PDB; 1PYC; 01-AUG-96.
 CC TRANSFAC; T00346; -;

DR SGD; L0002665; HAP1.
 DR PROSITE; PS00463; ZN2_Cy6_FUNGAL_1; 1.
 DR PROSITE; PS00463; ZN2_Cy6_FUNGAL_2; 1.
 DR PFAM; PF00172; Zn_clus; 1.
 KW Transcription regulation; Activator; DNA-binding; Nuclear protein;
 KW Zinc; Metal-binding; Repeat; Heme; 3D-structure.
 FT DNA_BIND 64 93
 FT ZN(2)-CYS(6), FUNGAL-TYPE.
 FT VARIANT 63 63
 FT S -> R (IN CYPI-18 MUTANT).
 FT POLY-GLN.
 FT DOMAIN 177 189
 FT HRM 1 (POTENTIAL).
 FT DOMAIN 280 285
 FT HRM 2 (POTENTIAL).
 FT DOMAIN 323 328
 FT HRM 3 (POTENTIAL).
 FT DOMAIN 347 352
 FT HRM 4 (POTENTIAL).
 FT DOMAIN 389 394
 FT HRM 5 (POTENTIAL).
 FT DOMAIN 415 420
 FT HRM 6 (POTENTIAL).
 FT DOMAIN 1192 1197
 FT HRM 7 (POTENTIAL).
 FT CONFLICT 145 145
 FT T -> I (IN REF. 2).
 FT CONFLICT 323 323
 FT K -> R (IN REF. 2).
 FT CONFLICT 455 455
 FT S -> N (IN REF. 2).
 FT CONFLICT 508 508
 FT V -> M (IN REF. 2).
 FT CONFLICT 587 587
 FT N -> K (IN REF. 2).
 FT CONFLICT 883 883
 FT D -> N (IN REF. 2).
 FT CONFLICT 960 960
 FT H -> S (IN REF. 2).
 FT CONFLICT 1151 1151
 FT D -> N (IN REF. 2).
 FT CONFLICT 1157 1157
 FT S -> P (IN REF. 2).
 FT CONFLICT 1305 1305
 FT N -> Y (IN REF. 2).
 SQ SEQUENCE 1483 AA; 164150 MW; A46C7260 CRC32;
 QY 2 RLAIRLNERYRLAIRLNE 19
 DB 1124 KLTKQLSKKYNIAIRNKK 1141
 RESULT 10
 YOR3_BACCE
 ID YOR3_BACCE STANDARD; PRT; 312 AA.
 AC O31352;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 15-JUL-1998 (Rel. 36, Last annotation update)
 DE HYPOTHETICAL PROTEIN (ORF3) (FRAGMENT).
 OS Bacillus cereus.
 OC Bacteria; Firmicutes; Bacillus/Clostridium group;
 OC Bacillus/Staphylococcus group; Bacillus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-ATCC 10987;
 RA KOLSTO A.B., OKSTAD O.A., LINDBACK T., HEGNA I., LAGREID A.,
 RA RISHOVD A.L.;
 RL Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.
 CC -!- SIMILARITY: BELONGS TO THE ATG/TRZ FAMILY.
 CC
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 CC
 CC EMBL; Y11139; CAA72025.1; -;
 KW Hypothetical protein; Hydrolase.
 FT NON_TER 1
 SQ SEQUENCE 312 AA; 35208 MW; 165E9409 CRC32;
 Query Match 39.8%; Score 39; DB 1; Length 312;
 Best Local Similarity 39.1%; Pred. No. 26;

Query Match 40.8%; Score 40; DB 1; Length 1483;
 Best Local Similarity 38.9%; Pred. No. 1e+02;
 Matches 7; Conservative 7; Mismatches 4; Indels 0; Gaps 0;


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RESULT 14
ID TEGU_HSV6U STANDARD; PRT: 2077 AA.
AC P52340;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE LARGE TEGUMENT PROTEIN.
UN 031 OR HHRF1.
GN Herpes simplex virus (type 6 / strain Uganda-1102).
GC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Betaherpesvirinae; Roseolovirus.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 95266321.
RA COMPELS U.A., NICHOLAS J., LAWRENCE G., JONES M., THOMSON B.J.,
RA MARTIN M.E., EFSTATHIOU S., CRAXTON M., MACAULAY H.A.;
RT "The DNA sequence of human herpesvirus-6: structure, coding content,
RT and genome evolution.";
RL Virology 209:29-51(1995).
CC -!- FUNCTION: TEGUMENT PROTEIN.
CC -!- SIMILARITY: BELONGS TO FAMILY THAT GROUPS TOGETHER HSV-1 UL36,
CC EHv-1 24, EBV BPLF1, HSV-1 64, VZV 22, AND HCMV UL48.
CC -----
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CC -----
CC EMBL; X83413; CAA58411.1; -
DR SEQUENCE 2077 AA; 239946 MW; 36FCF7B1 CRC32;
SQ
Query Match 39.8%; Score 39; DB 1; Length 2077;
Best Local Similarity 50.0%; Pred. No. 2.2e+02;
Matches 6; Conservative 5; Mismatches 1; Indels 0; Gaps 0;
QY 9 ERYRLAIRLNR 20
DB 493 EKYKVAVLNKK 504
|:|:|:|:|:
RESULT 15
ID NTRB_ECOLI STANDARD; PRT: 349 AA.
AC P06712;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE NITROGEN REGULATION PROTEIN NR(II) (EC 2.7.3.-).
GN GLN1 OR NTRB OR GLNR.
OS Escherichia coli.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
CC [1]
RP SEQUENCE FROM N.A.
RX STRAIN-K12;
RA MEDLINE; 8714797.
RA MIRANDA-RIOS J., SANCHEZ-PESCADOR R., URDEA M., COVARRUBIAS A.A.;
RT "The complete nucleotide sequence of the glnA1 operon of Escherichia
RT coli K12.";
RL Nucleic Acids Res. 15:2757-2770(1987).
RN [2]
RP SEQUENCE FROM N.A.
RX STRAIN-K12 / MG1655;
RA MEDLINE; 93347969.
RA PLUNKETT G., III, BURLAND V.D., DANIELS D.L., BLATTNER F.R.;
RT "Analysis of the Escherichia coli genome. III. DNA sequence of the
RT region from 87.2 to 89.2 minutes.";

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RL Nucleic Acids Res. 21:3391-3398(1993).
RN [3]
RP SEQUENCE OF 1-22 FROM N.A.
RX MEDLINE; 85006814.
RA UENO-NISHIO S., MANGO S., REITZER L.J., MAGASANIK B.;
RT "Identification and regulation of the glnL operator-promoter of the
RT complex glnALG operon of Escherichia coli.";
RL J. Bacteriol. 160:379-384(1984).
RN [4]
RP SEQUENCE OF 1-24 FROM N.A.
RX MEDLINE; 86031370.
RA ROCHA M., VAZQUEZ M., GARCIAARRIBIO A., COVARRUBIAS A.A.;
RT "Nucleotide sequence of the glnA-glnL intercistronic region of
RT Escherichia coli.";
RL Gene 37:91-99(1985).
RN [5]
RP PHOSPHORYLATION SITE.
RX MEDLINE; 91201336.
RA NINFA A.J., BENNETT R.L.;
RT "Identification of the site of autophosphorylation of the bacterial
RT protein kinase/phosphatase NRII.";
RL J. Biol. Chem. 266:6888-6893(1991).
CC -!- FUNCTION: NTRB ACTS AS A SIGNAL TRANSDUCER WHICH RESPONDS TO THE
CC NITROGEN LEVEL OF CELL AND MODULATES THE ACTIVITY OF NTRC. IN
CC NITROGEN LIMITATION NTRB ACTIVATES NTRC BY PHOSPHORYLATING IT,
CC WHILE IN NITROGEN EXCESS NTRC IS DEPHOSPHORYLATED AND CONSEQUENTLY
CC INACTIVATED BY NTRB.
CC -!- SIMILARITY: TO OTHER PROKARYOTIC SENSORY TRANSDUCTION HISTIDINE
CC KINASES.
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CC -----
DR EMBL; X05173; CAA28807.1; -
DR EMBL; K02176; AAA23881.1; -
DR EMBL; L19201; AAB03003.1; -
DR EMBL; AE000462; AAC76866.1; -
DR PIR; Q00553; RGECGL.
DR PIR; B23970; B23970.
DR PIR; S40814; S40814.
DR ECOGENE; EGI0387; GLNL.
DR PFAM; PF00512; signal; 1.
KW Sensory transduction; Transferase; Kinase; Phosphorylation;
KW Nitrogen fixation; ATP-binding.
FT DOMAIN 116 349 TRANSMITTER DOMAIN (POTENTIAL).
FT MOD_RES 139 139 PHOSPHORYLATION (AUTO-).
FT BINDING 329 329 ATP (BY SIMILARITY).
SQ SEQUENCE 349 AA; 38556 MW; 6A017919 CRC32;

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Query Match          39.3%; Score 38.5; DB 1; Length 349;
Best Local Similarity 50.0%; Pred. No. 36;
Matches 10; Conservative 3; Mismatches 4; Indels 3; Gaps 1;

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QY 2 RLAIRL---NERYFLAIRLN 18
   | | | | | | | | | |
Db 265 RTAQLTLHGERYFLAIRID 284

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Search completed: February 8, 2000, 01:26:01
Job time: 1561 sec

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Result No.	Query			Length	DB	ID	Description
	Score	Match					
1	44.5	45.4	191	12	Q98543	Q98543 paramacium	
2	44	44.9	219	5	Q19332	Q19332 caenorhabdi	
3	44	44.9	2391	10	Q9X540	Q9X540 oryza sativ	
4	42.5	43.4	414	5	Q19088	Q19088 caenorhabdi	
5	42	42.9	188	8	Q35521	Q35521 phytopthor	
6	42	42.9	623	2	Q9X4J3	Q9X4J3 streptomyce	
7	41.5	42.3	2632	5	Q90736	Q90736 caenorhabdi	
8	41	41.8	223	2	P17724	P17724 mycobacteri	
9	41	41.8	413	2	Q50931	Q50931 borrellia bu	
10	41	41.8	471	5	Q9Y1X6	Q9Y1X6 ephydatia f	
11	40	40.8	192	2	O67035	O67035 aquifex aeo	
12	40	40.8	319	5	Q94499	Q94499 dictyostell	
13	40	40.8	369	13	Q9W678	Q9W678 barbus barb	
14	40	40.8	433	2	P71096	P71096 bacteroides	
15	40	40.8	526	2	P74182	P74182 synechocyst	
16	40	40.8	579	2	Q9WZ01	Q9WZ01 thermotoga	
17	40	40.8	741	2	Q9XAU3	Q9XAU3 pseudomonas	
18	40	40.8	1001	4	O75150	O75150 homo sapien	
19	40	40.8	1164	5	P92021	P92021 caenorhabdi	
20	40	40.8	1502	3	O06574	O06574 saccharomyc	

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RN  SEQUENCE FROM N.A.
RA  HARRIS B.;
RL  Submitted (AUG-1995) to the EMBL/GenBank/DBJ databases.
[2]
RN  SEQUENCE FROM N.A.
RX  MEDLINE: 94150718.
RA  WILSON R., AINSCOUGH R., ANDERSON K., BAYNES C., BERKS M.,
RA  BONFIELD J., BURTON J., CONNELL M., COPSEY T., COOPER J., COULSON A.,
RA  CRAXTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON L.,
RA  GARDNER A., GREEN P., HAWKINS T., HILLIER L., JIER M., JOHNSTON L.,
RA  JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LATREILLE P.,
RA  LIGHTNING J., LLOYD C., MCMURRAY A., MORTIMORE B., O'CALLAGHAN M.,
RA  PARSONS J., PERCY C., RIFKEN L., ROOPRA A., SAUNDERS D., SHOWNKEEN R.,
RA  SMALDON N., SMITH A., SONNHAMMER E., STADEN R., SULSTON J.,
RA  THIERRY-MIEG J., THOMAS K., VAUDIN M., VAUGHAN K., WATERSTON R.,
RA  WATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.;
RT  "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
RT  elegans.";
RL  Nature 368:32-38(1994).
DR  EMBL: Z50857; CAA90718.1;
SQ  SEQUENCE 219 AA; 25040 MW; 156231A7 CRC32;

Query Match 44.9%; Score 44; DB 5; Length 219;
Best Local Similarity 61.5%; Pred. No. 14;
Matches 8; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY  5 IRLNERYRLAIRL 17
DB  133 VRYNKKRLAURL 145
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RESULT 3
Q9XE40 PRELIMINARY; PRT; 2391 AA.
AC Q9XE40;
DT 01-NOV-1999 (TREMBlrel. 12, Created)
DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)
DT 01-NOV-1999 (TREMBlrel. 12, Last annotation update)
DE HYPOTHETICAL 27.9 KD PROTEIN.
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC euphyllophytes; Spermatophyta; Magnoliophyta; Liliopsida; Poales;
OC Poaceae; Oryza.
[1]
RN  SEQUENCE FROM N.A.
RC STRAIN-CV. NIPPONBARE;
RA SASAKI T., NAGAMURA Y., YAMAMOTO K.;
RT "Oryza sativa nipponbare(GA3) genomic DNA, chromosome 6, PAC
RT clone: P0680A03.";
RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: A8023482; BAA78744.1;
KW HYPOTHETICAL PROTEIN.
SQ SEQUENCE 2391 AA; 278546 MW; EBD126F9 CRC32;

Query Match 44.9%; Score 44; DB 10; Length 2391;
Best Local Similarity 57.1%; Pred. No. 1.8e+02;
Matches 8; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY  6 RLNERYRLAIRLNE 19
DB  870 RLKESYAVRLNQ 883
::|::|::|::|::|

RESULT 4
Q19088 PRELIMINARY; PRT; 414 AA.
AC Q19088;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-NOV-1999 (TREMBlrel. 10, Last annotation update)

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DE  SIMILARITY TO RODLIKE TAIL DOMAIN OF MYOSIN HEAVY CHAIN.
GN  F01F1.4.
OS  Caenorhabditis elegans.
OC  Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditi; Rhabditida;
OC  Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
[1]
RN  SEQUENCE FROM N.A.
RX  MEDLINE: 94150718.
RA  WILSON R., AINSCOUGH R., ANDERSON K., BAYNES C., BERKS M.,
RA  BONFIELD J., BURTON J., CONNELL M., COPSEY T., COOPER J., COULSON A.,
RA  CRAXTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON L.,
RA  JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LATREILLE P.,
RA  JARDNER A., GREEN P., HAWKINS T., HILLIER L., JIER M., JOHNSTON L.,
RA  LIGHTNING J., LLOYD C., MCMURRAY A., MORTIMORE B., O'CALLAGHAN M.,
RA  PARSONS J., PERCY C., RIFKEN L., ROOPRA A., SAUNDERS D., SHOWNKEEN R.,
RA  SMALDON N., SMITH A., SONNHAMMER E., STADEN R., SULSTON J.,
RA  THIERRY-MIEG J., THOMAS K., VAUDIN M., VAUGHAN K., WATERSTON R.,
RA  WATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.;
RT  "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
RT  elegans.";
RL  Nature 368:32-38(1994).
RN  [2]
RP  SEQUENCE FROM N.A.
RC STRAIN-BRISTOL N2;
RA MILLER N.;
RL Submitted (NOV-1994) to the EMBL/GenBank/DBJ databases.
[3]
RN  SEQUENCE FROM N.A.
RC STRAIN-BRISTOL N2;
RA WATERSTON R.;
RL Submitted (JUL-1995) to the EMBL/GenBank/DBJ databases.
DR EMBL: U13070; AAC46638.1;
DR PFW; PFO1363; FIVE; 1.
SQ SEQUENCE 414 AA; 47599 MW; 53B60FB7 CRC32;

Query Match 43.4%; Score 42.5; DB 5; Length 414;
Best Local Similarity 52.6%; Pred. No. 48;
Matches 10; Conservative 4; Mismatches 4; Indels 1; Gaps 1;

QY  2 RLAIRLNERYRLAIRLNER 20
DB  62 KAAMELNERYQLDLS-NER 79
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RESULT 5
Q35521 PRELIMINARY; PRT; 188 AA.
AC Q35521;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-NOV-1999 (TREMBlrel. 12, Last annotation update)
DE NADH UBIQUINONE OXIDOREDUCTASE SUBUNIT.
OS Phytophthora megasperma (Potato pink rot fungus).
OG Mitochondrion.
OC Eukaryota; stramenopiles; Oomycetes; Peronosporales; Pythiaceae;
OC Phytophthora.
[1]
RN  SEQUENCE FROM N.A.
RC STRAIN-695T; TISSUE-MYCELIUM;
RA CLARY S.A., HUDSPETH M.E.;
RL Submitted (OCT-1993) to the EMBL/GenBank/DBJ databases.
[2]
RN  SEQUENCE FROM N.A.
RC STRAIN-695T; TISSUE-MYCELIUM;
RA SACHAY D.J., HUDSPETH D.S.S., NADLER S.A., HUDSPETH M.E.S.;
RL Exp. Mycol. 17:7-23(1993).
DR EMBL: L16863; CAB24134.1;
DR PROSITE: PS00542; COMPLEX1_30K; 1.
DR PFW; PFO0329; complex1_30Kd; 1.
KW Ubiquinone; Mitochondrion.
SQ SEQUENCE 188 AA; 22638 MW; 61C1339B CRC32;

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Query Match 42.9%; Score 42; DB 8; Length 188;
 Best Local Similarity 47.1%; Pred. No. 25;
 Matches 8; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

OY 3 LAIRLNERYLRLNER 19
 I:|:| | | : | : | : |
 DB 76 LSIRFNSRLKVKITINE 92

RESULT 6
 ID Q9XAJ3 PRELIMINARY; PRT; 623 AA.
 AC Q9XAJ3;
 DT 01-NOV-1999 (TREMBLrel. 12, Created)
 DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)
 DT 01-NOV-1999 (TREMBLrel. 12, Last annotation update)
 DE PUTATIVE MEMBRANE PROTEIN.
 GN SC66T3.20.
 OS Streptomyces coelicolor.
 OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
 OC Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomycetes.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=A3(2);
 RA MURPHY L., HARRIS D.;
 RT "A set of ordered cosmids and a detailed genetic and physical map for the 8 Mb Streptomyces coelicolor A3(2) chromosome.";
 RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=A3(2);
 RA KENSBACH M., KISER H.M., DENAPATE D., EICHNER A., CULLUM J.,
 RA KINASHI H., HOPWOOD D.A.;
 RT "A set of ordered cosmids and a detailed genetic and physical map for the 8 Mb Streptomyces coelicolor A3(2) chromosome.";
 RL Mol. Microbiol. 21:77-96(1996).
 DR EMBL: AL079348; CAB45476.1;
 SQ SEQUENCE 623 AA; 65526 MW; 14E8FFCC CRC32;

Query Match 42.9%; Score 42; DB 2; Length 623;
 Best Local Similarity 58.8%; Pred. No. 89;
 Matches 10; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

OY 4 AIRLNERYLRLNER 20
 I:|:| | | : | : | : |
 DB 112 ARRLNRLRLRLRLN 128

RESULT 7
 ID P90736 PRELIMINARY; PRT; 2632 AA.
 AC P90736; 001311;
 DT 01-JAN-1999 (TREMBLrel. 09, Created)
 DT 01-JAN-1999 (TREMBLrel. 09, Last sequence update)
 DT 01-JAN-1999 (TREMBLrel. 09, Last annotation update)
 DE HYPOTHETICAL 305.8 KD PROTEIN B0365.7 IN CHROMOSOME V. B0365.7.
 GN Caenorhabditis elegans.
 OS Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditidae.
 OC Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BRISTOL N2;
 RA SIMS M.;

Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP REVISIONS.
 RC STRAIN=BRISTOL N2;
 RA JONES S.J.M.;
 RL Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RA PERCY C.;
 RL Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.
 CC -!- SIMILARITY: WEAK, TO DYEIN HEAVY CHAINS.
 DR EMBL: 281028; CAB02695.1;
 DR EMBL: 281096; CAB02695.1; JOINED.
 DR EMBL: 281096; CAB03163.1;
 DR EMBL: 281028; CAB03163.1; JOINED.
 DR WORMPEP; B0365.7; CRO7724.
 KW Hypothetical protein.
 SQ SEQUENCE 2632 AA; 305774 MW; 4F3356EF CRC32;

Query Match 42.3%; Score 41.5; DB 5; Length 2632;
 Best Local Similarity 43.5%; Pred. No. 4.9e+02;
 Matches 10; Conservative 5; Mismatches 5; Indels 3; Gaps 1;

OY 1 YRLAIRLNERYLRLNER 20
 I:|:| | | : | : | : |
 DB 557 YRSVRINEVQVQKMGNLEER 579

RESULT 8
 ID P71724 PRELIMINARY; PRT; 223 AA.
 AC P71724;
 DT 01-FEB-1997 (TREMBLrel. 02, Created)
 DT 01-AUG-1998 (TREMBLrel. 07, Last sequence update)
 DT 01-NOV-1999 (TREMBLrel. 12, Last annotation update)
 DE HYPOTHETICAL 24.2 KD PROTEIN.
 GN RV2419C.
 OS Mycobacterium tuberculosis.
 OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
 OC Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=H37RV;
 RX MEDLINE: 98295987.
 RA COLE S.T., BROSCHE R., PARKHILL J., GARNIER T., CHURCHER C., HARRIS D.,
 RA GORDON S.V., EIGLMEIER K., GAS S., BARRY III C.E., TEKAIA F.,
 RA BADCOCK K., BASHAM D., BROWN D., CHILLINGWORTH T., CONNOR R.,
 RA DAVIES R., DEVLIN K., FELTWELL T., GENTLES S., HAMLIN N., HOLROYD S.,
 RA HORNSBY T., JAGELS K., KROGH A., MCLEAN J., MOULE S., MURPHY L.,
 RA OLIVER S., OSBORNE J., QUAIL M.A., RAJANDREAM M.A., ROGERS J.,
 RA RUTTER S., SEEGER K., SKELTON S., SQUARES S., SQUARES R., SULSTON J.E.,
 RA TAYLOR K., WHITEHEAD S., BARRELL B.G.;
 RT "Deciphering the biology of Mycobacterium tuberculosis from the complete genome sequence.";
 RL Nature 393:537-544(1998).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=H37RV;
 RA PARKHILL J.;
 RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL: 281368; CAB03751.1;
 DR HSP; P00950; 3PGM.
 DR PFAM; PF00300; PGAM; 1.
 KW Hypothetical protein.
 SQ SEQUENCE 223 AA; 24174 MW; CECA2812 CRC32;

Query Match 41.8%; Score 41; DB 2; Length 223;
 Best Local Similarity 40.0%; Pred. No. 42;
 Matches 8; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

OY 1 YRLAIRLNERYLRLNER 20

Query Match 41.88; Score 41; DB 5; Length 471;

Query Match 40.8%; Score 40; DB 5; Length 319;
 Best Local Similarity 69.2%; Pred. No. 88;
 Matches 9; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 7 LNERYLRLRLNE 19
 |||| :|| :||
 DB 160 LNERKKLACRENE 172

RESULT 13

QY 09W678 PRELIMINARY; PRT; 369 AA.
 AC Q9W678;
 DT 01-NOV-1999 (TREMELrel. 12, Created)
 DT 01-NOV-1999 (TREMELrel. 12, Last sequence update)
 DT 01-NOV-1999 (TREMELrel. 12, Last annotation update)
 DE CELLULAR TUMOR ANTIGEN P53.
 GN P53.
 OS Barbus barbus (barbel).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Actinopterygii;
 OC Neoterygii; Teleostei; Euteleostei; Ostariophysi; Cypriniformes;
 OC Cyprinoidae; Cyprinidae; Cyprininae; Barbus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RA BHASKARAN A., MAY D., RAND-WEAVER M., TYLER C.R.;
 RT "Evolutionary conservancy of p53 gene sequences in fish."
 RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: P53 SEEMS TO ACT AS A TUMOR SUPPRESSOR IN SOME, BUT
 CC PROBABLY NOT ALL, TUMOR TYPES. P53 IS PROBABLY INVOLVED IN CELL
 CC CYCLE REGULATION, IT IS A TRANS-ACTIVATOR THAT ACTS TO NEGATIVELY
 CC REGULATE CELLULAR DIVISION BY CONTROLLING A SET OF GENES REQUIRED
 CC FOR THIS PROCESS. ONE OF THE GENES ACTIVATED IS AN INHIBITOR OF
 CC CYCLIN-DEPENDENT KINASES (BY SIMILARITY).
 CC -!- SUBCELLULAR LOCATION: NUCLEAR.
 DR EMBL; AF071570; AAD34212.1; -.
 DR PROSITE; PS00348; P53; 1.
 KW Anti-oncogene; DNA-binding; Transcription regulation; Activator;
 KW Nuclear protein; Phosphorylation.
 SQ SEQUENCE 369 AA; 41233 MW; 0D4E77F7 CRC32;

Query Match 40.8%; Score 40; DB 13; Length 369;
 Best Local Similarity 36.8%; Pred. No. 1e+02;
 Matches 7; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

QY 1 YRLAIRLNERYLRLNE 19
 || :|| :||
 DB 301 YTLQVRGKERYEMKKIND 319

RESULT 14

QY 09W678 PRELIMINARY; PRT; 433 AA.
 AC P71096;
 DT 01-FEB-1997 (TREMELrel. 02, Created)
 DT 01-FEB-1997 (TREMELrel. 02, Last sequence update)
 DT 01-AUG-1998 (TREMELrel. 07, Last annotation update)
 DE REGULATORY PROTEIN.
 GN SUS4.
 OS Bacteroides thetaiotaomicron.
 OC Bacteria; Cytophagales; Bacteroidaceae; Bacteroides.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-5842;
 RA D'ELIA J., SALYERS A.;
 RL Submitted (AUG-1996) to the EMBL/GenBank/DBJ databases.
 DR EMBL; U67052; AAB39215.1; -.
 SQ SEQUENCE 433 AA; 50646 MW; 13D3D4D5 CRC32;

Query Match 40.8%; Score 40; DB 2; Length 433;
 Best Local Similarity 52.6%; Pred. No. 1.2e+02;
 Matches 10; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

QY 1 YRLAIRLNERYLRLNE 19
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 DB 407 YSLATIYNSRIAIKLPE 425

RESULT 15

QY 09W678 PRELIMINARY; PRT; 526 AA.
 AC P74182;
 DT 01-FEB-1997 (TREMELrel. 02, Created)
 DT 01-FEB-1997 (TREMELrel. 02, Last sequence update)
 DT 01-JAN-1999 (TREMELrel. 09, Last annotation update)
 DE HYPOTHETICAL 57.7 KD PROTEIN.
 OS Synechocystis sp. (strain PCC 6803).
 OC Bacteria; Cyanobacteria; Chroococcales; Synechocystis.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-PCC6803;
 RA TABATA S.;
 RL Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-PCC6803;
 RX MEDLINE; 97061201.
 RA KANEKO T., SATO S., KOTANI H., TANAKA A., ASAMIZU E., NAKAMURA Y.,
 RA MIYAJIMA N., HIROSAWA M., SUGIURA M., SASAMOTO S., KIMURA T.,
 RA HOSOUCHI N., MURAKI A., NAKAZAKI N., NARUO K., OKUMURA S.,
 RA SHIMPO S., TAKEUCHI C., WADA T., WATANABE A., YAMADA M., YASUDA M.,
 RA TABATA S.;
 RT "Sequence analysis of the genome of the unicellular cyanobacterium
 RT Synechocystis sp. strain PCC6803. II. Sequence determination of the
 RT entire genome and assignment of potential protein-coding regions."
 RL DNA Res. 3:109-136(1996).
 DR EMBL; D90913; BAA18271.1; -.
 KW Hypothetical protein.
 SQ SEQUENCE 526 AA; 57735 MW; 7D6F9B34 CRC32;

Query Match 40.8%; Score 40; DB 2; Length 526;
 Best Local Similarity 52.6%; Pred. No. 1.5e+02;
 Matches 10; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 2 RLAIRLNERYLRLNER 20
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 DB 98 ROAITLDEAIDLALRNEQ 116

Search completed: February 8, 2000, 19:16:17
 Job time: 21504 sec

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	CEY38E10_2	200001	310000				
	CEY38E10_3	300001	393707				
Continuation (4 of 4) of Cey38E10 from base 300001 (AL021149 Caeenorh							

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Percent Identity: 60.000
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US-08-653-294-3

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Align seg 1/1 to reverse of: CEY38E10.3 from: 1 to: 93707

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1 TyrArgLeuAlaIleArgLeuAsnGluArgTyrArgLeuAlaIleArgLe 17
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AL110484.1
GI:5824723

KEYWORDS HTG.
SOURCE *Caenorhabditis elegans*.
ORGANISM *Caenorhabditis elegans*.

ORGANISM
Caenorhabditis elegans
Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia;
phabditina; phabditoidae. phabditidae. Deloderinae. C

REFERENCE

1 (bases 1 to 11932)

AUTHORS Wilson, R., Ainscough, R., Anderson, K., Baynes, C., Berk
Knapitallina; Knapitalloraea; Knapitallidae; Felouellinae;

AUTHORS

Fulton, L., Gardner, A., Green, P., Hawkins, T., Hillier, S.G., Johnston, L., Jones, M., Kershaw, J., Kirsten, J., Laister

Latreille, P., Lightning, J., Lloyd, C., McMurray, A., O'Callaghan, M., Parsons, J., Percy, C., Rifken, L., Roop

Saunders, D., Showkeen, R., Smaldon, N., Smith, A., Sonn-
Staden, R., Sulston, J., Thierry-Mieg, J., Thomas, K., Vag-

Vaughan, K., Waterston, R., Watson, A., Weinstock, L.,
Wilkinson-Sproat, J. and Wohldman, P.

TITLE	2.2 Mb of contiguous nucleotide sequence from chromosomes elegans	2.2 Mb of contiguous nucleotide sequence from chromosomes elegans
2.2 Mb of contiguous nucleotide sequence from chromosomes elegans	2.2 Mb of contiguous nucleotide sequence from chromosomes elegans	2.2 Mb of contiguous nucleotide sequence from chromosomes elegans

JOURNAL
Nature 368 (6466), 32-38 (1994)
MEDLINE
94150718
3 (Accession 142 110032)

REFERENCE
2 (pages 1 to 110932)
AUTHORS
Wallis, J.
DIRECT SUBMISSION

JOURNAL TITLE
Direct Submission
Submitted (19-NOV-1999) Louis, MO 63110, USA. E-mail: lois@asncr.ac.uk or ryan@ematode.wustl.edu

COMMENT
Coding sequences below are predicted from computer an-
jes@anger.ac.uk of iwemalcode.wustl.edu
predictions from Genefinder (P Green, U Washington)

predictions from generalizer (F. Green, U. Washington) available information.

see: -
for a graphical representation of this sequence and

http://webace.sanger.ac.uk/cgi-bin/display?db=wormaceclass=Sequence subject=y38e10a
 current sequence finishing criteria for the C. elegans genome sequencing consortium are that all bases are either sequenced unambiguously on both strands, or on a single strand with both a dye primer and dye terminator reaction, from distinct subclones. Exceptions are indicated by an explicit note.
 IMPORTANT: This sequence is NOT necessarily the entire insert of the specified clone. It may be shorter because we only sequence overlapping sections once, or longer because we arrange for a small overlap between neighbouring submissions.
 IMPORTANT: This sequence is not the entire insert of clone y38e10a. It may be shorter because we only sequence overlapping sections once, or longer because we arrange for a small overlap between neighbouring submissions.
 The left end of clone Y46G5 is at 110833 in this sequence. The true right end of clone F49C5 is at 100 in this sequence. The start of this sequence (1..100) overlaps with the end of sequence z81544. The end of this sequence (110833..110932) overlaps with the start of sequence A110485.

FEATURES
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gene

CDS

gene

CDS


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Percent Similarity: 84.211 Percent Identity: 57.895

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||||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
69396 AGCGTTAGGCTCAGGCTTAGCTTAGCTTAGCTTAGGCTTAGGCTCAGGCTGAA 69445

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18 nGluArg 20
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seq_name: gb_htg1:CEY51A2_3
seq_documentation_block:
WPCOMMENT
Sequence split into 4 fragments LOCUS CEY51A2 Accession Z99275

Fragment Name	Begin	End
CEV51A2_0	1	110000
CEV51A2_1	100001	210000
CEV51A2_2	200001	310000
CEV51A2_3	300001	402049

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alignment_block:
US-08-653-294-31 x CEV51A2 3/rev ..
Percent Similarity: 85.000 Percent Identity: 50.000
Ratio: 3.118 Gaps: 0
Quality: 31.000

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US-06-033-294-S1 X CH3JAN2_3rev ...

Align seg 1/1 to reverse of: CEY5IA2_3 from: 1 to: 102049

1 TyrArgLeuAlaIleArgLeuAsnGluArgTyrArgLeuAlaIleArgLe 17
:::||||| ::|||::|::|::|::|::|::|::|::|::|::|::|::|::|::|
44057 TTTAGGGCTTAGGTAGGCCTTAGACCTAGATTAGGCTTAGGCTTAGGCT 44008

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17  unsaturated 20
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LOCUS	DEFINITION	DNA	INV
CEV51A2D	139259 bp	cosmid Y51A2D, complete sequence	02-
CAENORHABDITIS			
ACCESSION	AL021497		
VERSION	AL021497.1		
KEYWORDS	HTG.		
SOURCE	Caenorhabditis elegans.		
ORGANISM	Caenorhabditis elegans		

Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia;
Rhabditina; Rhabditiidae; Rhabditae; Pelodidae; Codi-
1 (bases 1 to 139215)
Wilson, R., Alnscough, R., Anderson, K., Baynes, C., Berk-

REFERENCE
AUTHORS

Coulson, A., Craxton, M., Dear, S., Du, Z., Durbin, R., Farnham, J., Garside, J., Green, P., Hawkins, T., Hillier, P., Johnston, L., Jones, M., Kershaw, J., Kirsten, J., Laister, L., Lattelle, P., Lightning, J., Lloyd, C., McMurray, A., Moore, O'Callaghan, M., Parsons, J., Percy, C., Rifken, L., Roopnarain, S., Saunders, D., Showkeen, R., Smalldon, N., Smith, A., Sonni, Staden, K., Sulston, J., Thierrey-Mieg, J., Thomas, K., Vaughan, K., Waterson, R., Watson, A., Weinstock, L.,

TITLE 2.2 Mb of contiguous nucleotide sequence from chromosomes
wilkison-spirat, C. and Wollman, F.
elegans

JOURNAL Nature 368 (1994), 32-38 (1994)

MEDLINE
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

94150718
2. (bases 1 to 139259)
McMurray, A.
Direct Submission
Submitted (23-JAN-1998) Louis, MO 63110, USA. E-mail:
jes@sanger.ac.uk or rv@nematoe.wustl.edu
Coding sequences below are predicted from computer analysis, using
predictions from Genefinder (P. Green, U. Washington), and other
available information.
For a graphical representation of this sequence and its analysis
see: -

http://webcace.sanger.ac.uk/cgi-
bin/display?db=wormaceclass=Sequence&object=Y51A2D
Current sequence finishing criteria for the C. elegans genome
sequencing consortium are that all bases are either sequenced
unambiguously on both strands, or on a single strand with both a
dye primer and dye terminator reaction, from distinct subclones.
Exceptions are indicated by an explicit note.
IMPORTANT: This sequence is NOT necessarily the entire insert of
the specified clone. It may be shorter because we only sequence
overlapping sections once, or longer because we arrange for a small
overlap between neighbouring submissions.
IMPORTANT: This sequence is not the entire insert of clone Y51A2D.
It may be shorter because we only sequence overlapping sections
once, or longer because we arrange for a small overlap between
neighbouring submissions.
The true left end of clone Y69H2 is at 139160 in this sequence. The
true right end of clone ZK228 is at 104 in this sequence. The true
right end of clone Y37H2 is at 28891 in this sequence. The start of
this sequence (1..104) overlaps with the end of sequence Z82086.
The end of this sequence (139160..139259) overlaps with the start
of sequence Z98877.

FEATURES
source

Location/Qualifiers
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CDS

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CDS

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from this gene; cDNA EST yk240d11.5 comes from this gene;
cDNA EST yk243b6.5 comes from this gene; cDNA EST
yk305g3.5 comes from this gene; cDNA EST yk308e4.5 comes
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 NSSFNATSYVWQKHCTTSYILPVMGVYLLTFSCGFTSLPVLNSEFPYPMWARS
 TCVSITSLNNVFNILIALTSLTHATIKYGAFLWYAFITIAFIYFLVLPETTY
 SIDEVEMLFMKNRQRIAMQARQAKDAADKDKNSSTSLSTETITM
 58395 69879
 /gene="Y51A2D.7a"
 /gene="Y51A2D.7a"
 58395 69879
 /gene="Y51A2D.7b"
 /gene="Y51A2D.7b"
 join(58395..58445,58657..58792,59709..59891,61464..61787,
 63584..63948,64698..64888,66270..66366,68189..68665,
 69661..69879)
 /gene="Y51A2D.7b"
 /note="cDNA EST yk269a8.5 comes from this gene; cDNA EST
 yk269a8.3 comes from this gene; cDNA EST yk332b9.3 comes
 from this gene; cDNA EST yk332b9.5 comes from this gene;
 cDNA EST yk348d3.3 comes from this gene; cDNA EST
 yk348d3.5 comes from this gene; cDNA EST yk443f6.3 comes
 from this gene; cDNA EST yk443f6.5 comes from this gene;
 cDNA EST yk382c7.3 comes from this gene; cDNA EST
 yk575e9.3 comes from this gene; cDNA EST yk619h9.3 comes
 from this gene; cDNA EST yk673e8.3 comes from this gene"
 /codon_start=1
 /protein_id="CAA16406.1"
 /db_xref="GI:3881043"
 /translation="MQRNPELQEAQSOLIVDSLDKPAAGGGGVNRLGFAFFFKL
 VTCSLKTLQILVNTNCHLITPNVIRAIQVQTVKSLILPAITFSDFIKQIVDVP

alignment_scores:
 Quality: 53.00 Length: 20
 Ratio: 3.118 Gaps: 0
 Percent Similarity: 85.000 Percent Identity: 50.000

alignment_block:

US-08-653-294-31 x CEY51A2D/rev ..

Align seg 1/1 to reverse of: CEY51A2D from: 1 to: 139259

1 TyrArgLeuAlaIleArgLeuAsnGluArgTyArgLeuAlaIleArgLe 17

137264 TTTAGGCTTAGGCTAGGCTAGACCTAGATTAGGCTTAGGCTTAGGCT 137215

17 uAsnGluArg 20

|||||

137214 TAGACGTCG 137205

seq_name: gb_htg2:AC006889

seq_documentation_block:

LOCUS AC006889 267118 bp DNA HTG 26-FEB-1999
 DEFINITION Caenorhabditis elegans clone Y65B4, *** SEQUENCING IN PROGRESS ***,
 6 unordered pieces.

ACCESSION AC006889

VERSION AC006889.2 GI:4309908

KEYWORDS HTG; HTGS_PHASE1.

SOURCE Caenorhabditis elegans.

ORGANISM Caenorhabditis elegans.

REFERENCE
 1 (bases 1 to 267118)
 Rhabditia; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditidae;
 Eukaryota; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.

AUTHORS Waterston,R.H.

TITLE The sequence of Caenorhabditis elegans clone

JOURNAL Unpublished

REFERENCE 2 (bases 1 to 267118)

AUTHORS Waterston,R.H.

TITLE Direct Submission

JOURNAL Submitted (24-FEB-1999) Genome Sequencing Center, Washington
 University School of Medicine, 4444 Forest Park Parkway, St. Louis,
 MO 63108, USA

COMMENT On Mar 1, 1999 this sequence version replaced gi:4263459.

* NOTE: This is a 'working draft' sequence. It currently
 * consists of 6 contigs. The true order of the pieces
 * is not known and their order in this sequence record is
 * arbitrary. Gaps between the contigs are represented as
 * runs of N, but the exact sizes of the gaps are unknown.
 * This record will be updated with the finished sequence
 * as soon as it is available and the accession number will
 * be preserved.

* 1 5875: contig of 5875 bp in length
 * 5876 5889: gap of unknown length
 * 5890 13618: contig of 7729 bp in length
 * 13619 13632: gap of unknown length
 * 13633 28840: contig of 15208 bp in length
 * 28841 28854: gap of unknown length
 * 28855 110971: contig of 82117 bp in length
 * 110972 110985: gap of unknown length
 * 110986 174804: contig of 63819 bp in length
 * 174805 174818: gap of unknown length
 * 174819 267118: contig of 92300 bp in length.

FEATURES
 Location/Qualifiers

1..267118
 /organism="Caenorhabditis elegans"
 /db_xref="taxon:6239"
 /clone="Y65B4"

BASE COUNT 83652 a 50557 c 48664 g 84175 t 70 others
 ORIGIN

alignment_scores:

Quality: 53.00 Length: 19
 Ratio: 3.312 Gaps: 0
 Percent Similarity: 84.211 Percent Identity: 57.895

alignment_block:

US-08-653-294-31 x AC006889/rev ..

Align seg 1/1 to reverse of: AC006889 from: 1 to: 267118

2 ArgLeuAlaIleArgLeuAsnGluArgTyArgLeuAlaIleArgLeuAs 18

134720 AGGCTTAGTATTAGGCTAGGCTAGATTAGGCTTAGGCTTAGGCTTAG 134671

18 nGluArg 20

|||||

134670 TGTTAGG 134664

seq_name: gb_htg2:AC006792

seq_documentation_block:

LOCUS AC006792 299202 bp DNA HTG 23-FEB-1999
 DEFINITION Caenorhabditis elegans clone Y50C1a, *** SEQUENCING IN PROGRESS
 ***, 10 unordered pieces.

ACCESSION AC006792

VERSION AC006792.1 GI:4263146

KEYWORDS HTG; HTGS_PHASE1.

SOURCE Caenorhabditis elegans.

ORGANISM Caenorhabditis elegans.

REFERENCE
 1 (bases 1 to 299202)
 Rhabditia; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditidae;
 Eukaryota; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.

AUTHORS Waterston,R.H.

TITLE The sequence of Caenorhabditis elegans clone

JOURNAL Unpublished

REFERENCE 2 (bases 1 to 299202)

AUTHORS Waterston,R.H.

TITLE Direct Submission

JOURNAL Submitted (23-FEB-1999) Genome Sequencing Center, Washington
 University School of Medicine, 4444 Forest Park Parkway, St. Louis,
 MO 63108, USA

COMMENT

* NOTE: This is a 'working draft' sequence. It currently
 * consists of 10 contigs. The true order of the pieces
 * is not known and their order in this sequence record is
 * arbitrary. Gaps between the contigs are represented as

* runs of N, but the exact sizes of the gaps are unknown.
 * This record will be updated with the finished sequence
 * as soon as it is available and the accession number will
 * be preserved.

```

1      2371: contig of 2371 bp in length
*      2372      2385: gap of unknown length
*      2386      7309: contig of 4924 bp in length
*      7310      7323: gap of unknown length
*      7324      13580: contig of 6257 bp in length
*      13581      13594: gap of unknown length
*      13595      25198: contig of 11604 bp in length
*      25199      25212: gap of unknown length
*      25213      35779: contig of 10567 bp in length
*      35780      35793: gap of unknown length
*      35794      63108: contig of 27315 bp in length
*      63109      63122: gap of unknown length
*      63123      124970: contig of 61848 bp in length
*      124971      124984: gap of unknown length
*      124985      185093: contig of 60109 bp in length
*      185094      185107: gap of unknown length
*      185108      253768: contig of 68661 bp in length
*      253769      253782: gap of unknown length
*      253783      299202: contig of 45420 bp in length.

```

FEATURES

```

source
1. .299202
   /organism="Caenorhabditis elegans"
   /db_xref="taxon:6239"
   /clone="f50C1a"

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BASE COUNT  95054 a 54073 c 54425 g 95524 t 126 others
ORIGIN

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alignment_scores:

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Quality: 53.00      Length: 19
Ratio: 3.312      Gaps: 0
Percent Similarity: 84.211      Percent Identity: 57.895

```

```

alignment_block:
US-08-653-294-31 x AC006792

```

```

Align seg 1/1 to: AC006792 from: 1 to: 299202

```

```

2 ArgLeuAlaileArgLeuAsgnGluArgTyrArgLeuAlaileArgLeuAs 18
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
173748 AGGCTTAGTATTAGGCTAGGCTAGATTAGGCTTATACITAGGCTTAG 173797

```

```

18 nGluArg 20
: |||
173798 TGTTAGG 173804

```

```

seq_name: gb_pr3.AC003070

```

```

seq_documentation_block:
LOCUS      AC003070 129914 bp      DNA      PRI      10-FEB-1998
DEFINITION Homo sapiens chromosome 17, clone HCIT39G8, complete sequence.
ACCESSION  AC003070
VERSION     AC003070.1 GI:2865212
KEYWORDS   HTG.
SOURCE      human.

```

```

ORGANISM    Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.

```

```

REFERENCE   1 (bases 1 to 129914)
AUTHORS     Birren,B., Fasnman,K., McKernan,K., Nusbaum,C., Richardson,P. and
            Lander,E.

```

```

TITLE       Homo sapiens chromosome 17, clone HCIT39G8

```

JOURNAL

```

REFERENCE   2 (bases 1 to 129914)
AUTHORS     Birren,B., Fasnman,K., McKernan,K., Munro,C., Nusbaum,C.,
            Richardson,P., Lander,E., Baldwin,J., Barna,N., Cantu,C., Chang,A.,
            Cooke,P., Daly,M.J., Devon,K., Dewar,K., DuRette,B., Forrest,C.,
            Gage,D., Gensheimer,S., Geraghty,K., Gilmartin,T., Hagos,B.,
            Halphen,I., Harris,K., Howland,J.C., Huang,J., Hui,L., Jacotot,L.,

```

```

Kirby,A., Lane,M., Mackenzie,J., Marquis,N., McDermott,J.,
Molla,M., Morrow,J., Nachman,A., Naylor,J., O'Connor,T., Olotu,A.,
Peterson,K., Roberts,D., Rollins,G., Sarnaik,A., Shiup,P., Shyam,R.,
Stilwell,J., Stone,C., Strickland,C., Sydney,K., Tang,L.,
Zemtseva,I. and Zody,M.
Direct Submission
Submitted (06-NOV-1997) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA

```

TITLE

JOURNAL

REFERENCE

AUTHORS

```

3 (bases 1 to 129914)
Birren,B., Fasnman,K., McKernan,K., Nusbaum,C., Richardson,P.,
Lander,E., Allen,N., Baker,J., Baldwin,J., Barna,N., Beckerly,R.,
Boutwell,C., Byrne,S., Cantu,C., Castle,A., Cooke,P., Daly,M.J.,
Depayre,E., Devon,K., Dewar,K., DuRette,B., Etenadi,S.,
Ferreira,P., Forrest,C., Gage,D., Gardyna,S., Gensheimer,S.,
Geraghty,K., Gilmartin,T., Gray,D., Hagos,B., Harris,K.,
Howland,J.C., Hui,L., Jacotot,L., Linton,L.,
Mackenzie,J., Marquis,N., McEwan,P., McGurk,A., Meidrim,J.,
Molla,M., Morris,W., Morrow,J., Nachman,A., Naylor,J., O'Connor,T.,
Pavlin,B., Peterson,K., Ranganath,S., Riley,R., Roberts,D.,
Rollins,G., Rossello,R., Roy,A., Shyam,R., Soohoo,S., Stilwell,J.,
Stone,C., Strickland,C., Sydney,K., Tang,L., Vassiliev,H., Vo,A.,
Wagner,A., Wheeler,J., Wu,Y., Ye,W.J., Zemtseva,I., Zhao,J. and
Zody,M.
Direct Submission
Submitted (10-FEB-1998) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA

```

TITLE

JOURNAL

COMMENT

```

On Feb 11, 1998 this sequence version replaced gi:2665502.
The Staden databases, finishing information, and all
chromatographic files used in the assembly of this clone are
available from our anonymous ftp site.

```

```

All repeats were identified using RepeatMasker: Smit, A.F.A. &
Green, P. (1996-1997)

```

```

http://ftp.genome.washington.edu/RM/RepeatMasker.html.
location/Qualifiers
1. .129914
   /organism="Homo sapiens"
   /db_xref="taxon:9606"
   /clone="HCIT39G8"
   /clone_lib="Research Genetics/Cal Tech CITB978SK-B (plates
1-194)"
   /map="17"
   /chromosome="17"
   complement(708..790)
   /rpt_family="LINE2"
   complement(1014..1172)
   /rpt_family="AluJo"
   complement(1173..1468)
   /rpt_family="AluSx"
   complement(1492..1614)
   /rpt_family="AluJo"
   complement(2534..2835)
   /rpt_family="AluSg"
   3577..3670
   /rpt_family="MIR"
   complement(5082..5209)
   /rpt_family="FLAM_A"
   5758..5859
   /rpt_family="MIR"
   /rpt_family="(CAA)n"
   complement(5870..6043)
   /rpt_family="MIR"
   6096..6165
   /rpt_family="MIR"
   6205..6262
   /rpt_family="AT-rich"
   9133..9161
   /rpt_family="GC-rich"
   complement(9521..9628)
   /rpt_family="(CGG)n"
   complement(10099..10183)
   /rpt_family="LINE2"
   10514..10783
   /rpt_family="AluJo"

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FEATURES

source

repeat_region

repeat_region

repeat_region

repeat_region

repeat_region

repeat_region

repeat_region

repeat_region

repeat_region

repeat_region

repeat_region

repeat_region

repeat_region

repeat_region

repeat_region

repeat_region

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11280. 11348
/rpt_family="MIR"
complement(12323. 12380)
/rpt_family="WER20"
complement(12389. 12715)
/rpt_family="THEIC"
complement(12717. 13010)
/rpt_family="AluSx"
complement(13011. 13051)
/rpt_family="THEIC"
complement(13052. 13209)
/rpt_family="WER20"
complement(13218. 13360)
/rpt_family="MIR"
complement(13902. 14031)
/rpt_family="WER63B"
complement(14977. 15110)
/rpt_family="FLAM_C"
complement(15135. 15438)
/rpt_family="AluSx"
complement(15928. 15992)
/rpt_family="LINE2"
complement(15992. 16091)
/rpt_family="LINE2"
complement(16095. 16315)
/rpt_family="AluSg"
complement(16407. 16567)
/rpt_family="LINE2"
complement(16789. 16938)
/rpt_family="LINE2"
complement(17242. 17543)
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complement(17784. 18081)
/rpt_family="AluSx"
complement(18676. 18968)
/rpt_family="AluSg"
complement(19585. 19886)
/rpt_family="AluSx"
complement(19911. 20000)
/rpt_family="S5"
complement(20334. 20463)
/rpt_family="LINE2"
complement(20562. 20865)
/rpt_family="AluSx"
complement(21117. 21419)
/rpt_family="AluJo"
complement(21773. 22068)
/rpt_family="AluSg"
complement(22732. 22769)
/rpt_family="LINE2"
complement(22778. 23074)
/rpt_family="AluSg"
complement(23104. 23181)
/rpt_family="WER64B"
complement(23182. 23289)
/rpt_family="WER63B"
complement(23312. 23543)
/rpt_family="AluSg/x"
complement(23544. 23652)
/rpt_family="WER63A"
complement(23654. 24050)
/rpt_family="WER64B"
complement(24051. 24177)
/rpt_family="MIR"
complement(24179. 24309)
/rpt_family="FLAM_C"
complement(24336. 24627)
/rpt_family="AluSx"
complement(24630. 24664)
/rpt_family="MIR"
complement(24691. 24757)
/rpt_family="MIR"
complement(26560. 26719)

```



```

SOURCE
ORGANISM
Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditidae;
Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
REFERENCE
1 (bases 1 to 33673)
TITLE
The sequence of Caenorhabditis elegans clone
AUTHORS
Waterston,R.H.
JOURNAL
Unpublished
REFERENCE
2 (bases 1 to 33673)
TITLE
Direct Submission
AUTHORS
Waterston,R.H.
JOURNAL
Submitted (23-FEB-1999) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
COMMENT
* NOTE: This is a 'working draft' sequence. It currently
* consists of 1 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
*
* 1 33673: contig of 33673 bp in length.
*
FEATURES
Location/Qualifiers
source
1. .33673
/organism="Caenorhabditis elegans"
/db_xref="taxon:6239"
/clone="K08D12"
BASE COUNT 10444 a 6363 c 6792 g 10074 t
ORIGIN

alignment_scores:
Quality: 51.00 Length: 20
Ratio: 3.188 Gaps: 0
Percent Similarity: 80.000 Percent Identity: 55.000

alignment_block:
US-08-653-294-31 x AC006672 ..
Align seg 1/1 to: AC006672 from: 1 to: 33673

1 TyrArgLeuAlaIleArgLeuAsnGluArgTyrArgLeuAlaIleArgLe 17
CATAGGCTTGGCTTAGGCTTAAGCTTAGGCTTAGGCTTAGGCT 3921
17 uAsnGluArg 20
1::: |||
3922 TCGGCCTAGG 3931

seq_name: gb_htg2:AC006842

seq_documentation_block:
LOCUS AC006842 299015 bp DNA HTG 24-FEB-1999
DEFINITION Caenorhabditis elegans clone Y104H12x, *** SEQUENCING IN PROGRESS
***, 13 unordered pieces.
ACCESSION AC006842
VERSION AC006842.1 GI:4263506
KEYWORDS HTG; HTGS_PHASE1.
SOURCE
ORGANISM
Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditidae;
Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
REFERENCE
1 (bases 1 to 299015)
TITLE
The sequence of Caenorhabditis elegans clone
AUTHORS
Waterston,R.H.
JOURNAL
Unpublished
REFERENCE
2 (bases 1 to 299015)
TITLE
Direct Submission
AUTHORS
Waterston,R.H.
JOURNAL
Submitted (24-FEB-1999) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA

```

```

COMMENT
* NOTE: This is a 'working draft' sequence. It currently
* consists of 13 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
*
* 1 1993: contig of 1993 bp in length
* 2009: gap of unknown length
* 4578: contig of 2569 bp in length
* 4579: gap of unknown length
* 4595: contig of 2682 bp in length
* 7276: contig of 2682 bp in length
* 7277: gap of unknown length
* 7293: contig of 4213 bp in length
* 11505: contig of 4213 bp in length
* 11521: gap of unknown length
* 11506: contig of 5417 bp in length
* 11522: gap of unknown length
* 16934: contig of 3980 bp in length
* 20934: contig of 3980 bp in length
* 20935: gap of unknown length
* 20951: contig of 4235 bp in length
* 25185: contig of 4235 bp in length
* 25201: gap of unknown length
* 25186: contig of 23959 bp in length
* 25202: gap of unknown length
* 49161: contig of 15797 bp in length
* 49177: gap of unknown length
* 64974: contig of 36565 bp in length
* 64990: contig of 36565 bp in length
* 101555: gap of unknown length
* 101570: contig of 56116 bp in length
* 101571: gap of unknown length
* 157687: contig of 102657 bp in length
* 157703: gap of unknown length
* 260360: contig of 38640 bp in length.
* 260376: 299015: contig of 38640 bp in length.
*
FEATURES
Location/Qualifiers
source
1. .299015
/organism="Caenorhabditis elegans"
/db_xref="taxon:6239"
/clone="Y104H12x"
BASE COUNT 96423 a 53226 c 53209 g 95965 t 192 others
ORIGIN

alignment_scores:
Quality: 51.00 Length: 20
Ratio: 3.188 Gaps: 0
Percent Similarity: 80.000 Percent Identity: 55.000

alignment_block:
US-08-653-294-31 x AC006842 ..
Align seg 1/1 to: AC006842 from: 1 to: 299015

1 TyrArgLeuAlaIleArgLeuAsnGluArgTyrArgLeuAlaIleArgLe 17
:::|||||:::|||||::: ||| ||||| ::|||
69270 CATAGGCTTGGCTTAGGCTTAAGCTTAGGCTTAGGCTTAGGCT 69319
17 uAsnGluArg 20
1::: |||
69320 TCGGCCTAGG 69329

seq_name: gb_htg2:AC006874

seq_documentation_block:
LOCUS AC006874 306131 bp DNA HTG 24-FEB-1999
DEFINITION Caenorhabditis elegans clone Y54E10, *** SEQUENCING IN PROGRESS
***, 3 unordered pieces.
ACCESSION AC006874
VERSION AC006874.1 GI:4263474
KEYWORDS HTG; HTGS_PHASE1.
SOURCE
ORGANISM
Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditidae;
Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.

```


11454 TAGGCTTAGG 11445

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